

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 99742

TO: Minh-Tam Davis

Location:

Art Unit: 1642

July 25, 2003

Case Serial Number: 09/991681

From: P. Sheppard Location: CM1-1E03 Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

From: Sent:

Chan, Christina

To: √Subject: Friday, July 25, 2003 10:19 AM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/991681

RECEIVED

JUL 25 2003

(STIC)

Please rush! Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message----

From:

Davis, Minh-Tam

Sent:

Friday, July 25, 2003 10:18 AM

To:

Chan, Christina

Subject:

Rush search request for 09/991681

Please search for interference only:

SEQ IS NO:27-31.

Thank you. MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Edward Hart Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher: Phone: Location: Date Picked Up: Searcher Prep/Review Gerical: Online time:

TYPE OF SEARCH: NA Sequences: AA Sequences: Structures: 1 Bibliographic: Litigation:_ Full text: Patent Family:

Other:_

VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit: DRLink: Lexis/Nexis: Sequence Sys.: WWW/Internet: Other (specify):

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Sheppard, Paula

From:

Davis, Minh-Tam

Sent:

Tuesday, July 22, 2003 1:10 PM Sheppard, Paula

To:

Subject:

Rush search request for 09/991681

I am sorry that this is the third time that I ask you for this case. Since I could not find any decent art even for fragments of SEQ ID NO:27, could you please search in commercial database, PGPUB and issued patent files: Oligomer search for SEQ ID NOs: 27-31.

Thank you.

If you want me to submit a new search request to the library, please let me know. MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Point of Contact P. Sheppard Telephone number: (703) 308-4499

7/25/03

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Database :
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Maximum DB seq length: 2000000000
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Human liver pentid	human diad	protein SE	human diagno	prostate m	prostate-s	protein enco	prostate mai	Human prostate-spe	tion

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Monse Opt - 7 with The	1 0	-	complemen		Human stromalin-2.	Drosophila melanog	Human transporter	Drosophila melanog	mela	Human adipocyte Se	Human expressed pr	Human drug metabol		Human polypeptide		Human protein sequ				Human colon cancer	Human polypeptide	_	Novel central nerv	l signa	l centra	•	human	Human peptide enco	#2512	#2631	de #25	ne m	cain ex	#2506 enc	ide #2595	22

ALIGNMENTS

RESULT 1 AAO19169

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(BILL/)
(COHE/)
(COLP/)
(FRIE/)
(GORD/)
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          (GRAN/)
(HODG/)
                                                                              23-APR-1998;
23-APR-1997;
                                                                                                       26-NOV-2001; 2001US-0991681.
                                                                                                                         04-JUL-2002.
                                                                                                                                         US2002086316-A1.
                                                                                                                                                          Homo sapiens.
                                                                                                                                                                           Human; prostate; prostate-specific sequence; prostate cancer; PS118; EST; expressed sequence tag; cytostatic; gene therapy.
                                                                                                                                                                                                     Human prostate-specific PS118 protein fragment
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COLPITTS T L.
FRIEDMAN J N.
GORDAN J N.
GRANADOS E N.
HODGES S C.
KLASS M R.
                                                           BILLINGEL P A.
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97US-0842385.
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RESULT 2
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Best Local S
Matches 49
  Billing-Medel
Granados EN,
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Russell JC,
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GRANADOS E N.
HODGES S C.
KLASS M R.
KRATOCHVIL J D
ROBERTS-RAPP L
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RUSSELL J C.
STROUPE S D.
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Cohen
ges SC,
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Klass MR
M, Coplpitts TL, Friedman
Klass MR, Kratochvil JD,
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Pred. No. 3.3e-41;
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Kratochvil
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PN, Gordon C
Roberts-Rapp
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Roberts-Rapp
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comprising amino acids 393-441 of human prostate-specific PS118

comprising amino acids 393-441 of human prostate-specific PS118

comprise the sequence (see ABM50809). A PS118 consensus sequence (see ABM50815) is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, polynucleotides, and tibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostate; intraepithelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polymucleotides in transfected host cells, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
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Best Local S
Matches 49
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WPI; 1998-610000/51.
N-PSDB; AAV82812.
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25-FEB-1999
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Local Similarity 100.0%; 1
hes 49; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate tumour tissue; prostatic disease; cancer
                                                                                Cohen M, Colpitts TL, es SC, Klass MR, Kratpe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 23;
Pred. No. 3.3e-41;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  staging, monitoring, prognosticating, ing predisposition to prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogenic polypeptide
                                                                                                             Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                         PN,
                                                                                                          Robertsrapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                         Gordon
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RESULT 4
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Best Local S
Matches 49
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treatment
                             Billingel
Granados E
WPI; 2002-665429/71
                                                                                                   (BILL/)
(COHE/)
(COLP/)
(FRIE/)
(GORD/)
(GRAN/)
(HODG/)
(KLAS/)
                                                                                                                                                                                            23-APR-1998;
23-APR-1997;
                                                                                                                                                                                                                          26-NOV-2001; 2001US-0991681.
                                                                                                                                                                                                                                               04-JUL-2002
                                                                                                                                                                                                                                                                  US2002086316-A1
                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                   Human; prostate; prostate-specific sequence;
                                                                                                                                                                                                                                                                                                                                     Human prostate-specific PS118 protein fragment #1
                                                                                                                                                                                                                                                                                                                                                             27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                AA019165;
                                                                                                                                                                                                                                                                                                                                                                                                    AA019165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used for detection, diagnosis, staging, monitoring and prognosis of prostatic disease, particularly cancer, and to identify subjects at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant PS118 protein is used to detect PS118-specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a cDNA library made from prostate tumour tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17;
                                                                     (KRAT/)
(ROBE/)
(RUSS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated
                                                                                                                                                                                                                                                                                                          expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                      393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                          COHEN M.
COLPITTS T L.
FRIEDMAN P N.
GORDAN J.
GRANADOS E N.
HODGES S C.
                                                           ROBERTS-RAPP
RUSSELL J C.
STROUPE S D.
                   JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                       KLASS M R.
KRATOCHVIL J
                                                                                                                                                                        BILLINGEL P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid a
                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                       PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
llarity 100.0%;
Conservative (
                    Stroupe
                           Cohen
Hodges
                                                                                                                                                                                                                                                                                                                                                            (first
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A
                                                                                                                                                                                            98US-0065383
97US-0842385
                                                                                                                                                                                                                                                                                                          sequence
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                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 518
                                                                                                                                                                                                                                                                                                                                                             entry)
                   SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and proteins - used for diagnosis and cisease, especially cancer, and also
                                                                                                                                                                                                                                                                                                        tag;
                             Colpitts TL,
Klass MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                         cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                             , Friedman
Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
2.4e-40;
                                                                                                                                                                                                                                                                                                         prostate
le therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                            JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                            Roberts-Rapp
                                      Gordan
                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                   PS118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                      Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                              Billing-Medel
Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a number of prostate-specific sequence derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring prognosticating, preventing, treating, or determining predisposition individual to diseases and conditions of prostate, e.g. prostrate
                          preventing
disease -
                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                        (GRIE/)
(GORD/)
(GRAN/)
(HODG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                             Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2001055758-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM50809
                                                                                                                                                                                                                                                                                                      (ROBE/)
                                                                                                                                                                                                                                                                                                                                                    KLAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                       2002-187683/24.
)B; ABA91651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate marker partial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                             GORDON J.
GRANADOS E N.
HODGES S C.
KLASS M R.
                                                                                                                                                                                                                                                                                                    ROBERTS-RAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPLPITTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BILLING-MEDEL P
                                                                                                                                                                                                                                                                                                                                                                                                                                           FRIEDMAN P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COHEN M.
                                                                                                                                                                                                                                                                                                                               KRATOCHVIL J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Silarity 100.0%; Silarity 100.0%; Silarity 0;
                                                                                                                                                                                                           Stroupe
                                                                                                                                                                                                                                PA, Co
Hodges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0842385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9808-0065383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T L.
                                                                                                                                                                                                        Cohen
les SC,
lpe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58pp;
                                                                                                                                                                                                                                M, Coplpitts TL, Friedman Klass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB
Pred. No. 2.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.4e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                              PN, Gordon Roberts-Rapp
                                                                   prognosticating,
                                                                                                                                                                                                                                                      Gordon J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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RESULT 6
ABG09728
ID ABG0
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XX H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a human prostate-specific PS118 polypeptide, as predicted from a partial consensus cDNA sequence (see ABA91651), and lacking the N-terminal region. The PS118 consensus sequence is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, including derivatives of the present sequence, polynucleotides, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the prostate, such as benign prostatic hyperplasia, prostatitis, prostate intraepithelial neophasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polypeptides in transfected host cells. The methods and reagents of the invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and continuous cancer, which can differentiate cancers without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 49
                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 42-43; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #9719
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                         2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                   RT,
                                                                                                                                                                                                                                                                                                                                 AAS73915.
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                                                                                                                 SEQ ID No 40087; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
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Pred. No.
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to
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o assess
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo

Claim 20; SEQ ID 495; 394pp; English

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ABP64835
ID ABP6
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CC Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 49
                                                                                                                     WPI; 2002-590824/63
N-PSDB; ABQ99421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     haematopoletic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; antiallergic; antinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                             New isolated polynucleotide, useful in research, diagnostic therapeutic methods, e.g. preventing or treating disorders i aberrant protein expression or biological activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein SEQ ID 495.
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                                                                                                                                                                                                                                                                                              16-NOV-2001; 2001WO-US42950
                                                                                                                                                                                                                                                                                                                                                                    WO200259260-A2
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-2003
                                                                                                                                                                                           Tang
                                                                                                                                                                                                                                                             17-NOV-2000; 2000US-0714936
                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          .mmunostimulant; cerebroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1682
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                                                                                                                                                                         Xue AJ,
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                                                                                                                                                               Goodrich Rw,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 1730
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                                                                                                                                                                          Liu C, Zl
, Wehrman
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Pred. No. 6.7e-40;
; Mismatches 0;
                                                                                                                                                                         Zhou P, Asundi V,
an T, Drmanac RT;
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CC hybridisation probes, primers for PCR, for chromosome and gene mapping, CC for the recombinant production of protein, or in generation of anti-sense CC DNA or RNA. The polynucleotides are useful in diagnostics as expressed CC sequence tags (RSTs) for identifying expressed genes or for physical CC mapping of the human genome. The proteins may be used as molecular weight CC markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or CC pluripotential state useful for re-engineering damaged or diseased CC tissues, transplantation, manufacture of bio-pharmaceuticals or the CC development of bio-sensors. The polynucleotides and proteins are useful CC protein expression or biological activity, e.g. haematopoietic disorders, central/peripheral nervous system diseases, mechanical and traumatic CC disorders, non-healing wounds, immune deficiencies and disorders, CC disorders, or cancer. The polynucleotide sequences of the invention were diseases sequences obtained from one or more public databases.

CC note: The sequence data for this patent did not form part of the printed of specification, but was obtained in electronic format directly from WIPO careful parts. The polynucleotide in some cases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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Best Local S
Matches 49
                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                              WPI; 2001-639362/73
                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                         31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG09731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG09731 standard; Protein; 1982 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel human coding sequences (ABQ99268-ABQ99608) and proteins (ABP64682-ABP65022). The seq
                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                        AAS73918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic
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                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                         2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Pred. No. 6.8e-40;
; Mismatches 0;
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                                          mutations
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RESULT 9
ABG49938
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CC Note: The sequence data for this patent did not appear in the printed CC series wino intrinubnished not segmences of communications of the invention.
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                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                      WPI; 2001-488898/53.
                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00664
                                                                                                                                                                                                                                                                                                                                                   hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                            Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                           Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG49938;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide
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                                                                                                                                                                                                                                                                                             WO200157273-A2
                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                   SG
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                                                                                            MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPIGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1982 AA;
                                                                                                                                                                2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                            2000US-0180312
                                                                                                                                     2000US-0234687.
2000US-0236359.
                                                                  DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences.
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                                                                  Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to isolated
                                                                                                                                                                                                                                                                                                                                                   coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 22;
Pred. No. 7.3e-40;
, Mismatches 0;
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                                                                  Rank DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as hybridisation probes,
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Human genome-derived single exon nucleic acid probes useful analysing gene expression in human adult liver -

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RESULT 10
ABB29911
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Matches 8
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Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting
                                                                                           New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                  Claim
                                                                                                                                                                WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                            03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB29911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #2562 encoded by breast cell single exon nucleic acid probe.
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                                                                 SEQ
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                                                                                                                                                                                                                                                             2000GB-0024263.
                                                                 ID NO 12879;
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100.0%; Pred. No. 1;
                                                                                                                                                                                              Chen W,
                                                               327pp + sequence listing;
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RESULT 11
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CC Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly crom wife at figure in the published pct sequences.
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Best Local S
Matches 8
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
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                                                                                                           Claim 27;
                                                                                                                                        analyzing gene expression
                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #2595 encoded by human foetal liver single exon probe
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                                                                                                                                                                                                                     SG,
                                                                                                                                       genome-derived single exon nucleic acid probes useful zing gene expression in human fetal liver -
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                                                                                                           SEQ
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0207456.
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                                                                                                           ID NO 27724; 639pp + sequence listing;
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RESULT 12
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                       measuring human gene expression in a sample derived from human heart (see ABA2133-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                       Penn
                                     Sequence
                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                Claim 15;
                                                                                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing
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27-SEP-2000;
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                                                                                                                                                                                                                             SEQ ID No 22277; 530pp; English.
                                                                                                                                                                                                                                                                                                                      Hanzel DK,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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16.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heart; microarray; vascular system;
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Score 8;
Pred. No.
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DB 22;
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                                                                                                                                                                                                                                                                   gene expression in
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           Length 32;
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RESULT 14
AAM68280
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          AAM68280;
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                                                                                                                                                                                                  probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system
                                                                                                                                                     Sequence
                                                                                                                                                                                diseases such as Alzheimer's disease, multiple sclerosis, epilepsy and cancers. The present sequence is a protein en
                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                                                                                                              Single exon nucleic acid
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27-SEP-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain expressed single exon probe encoded protein SEQ ID
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                                                                                                                                                                        probes of the invention.
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8; Conserv
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                             standard;
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; 2000US-0207456.
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100.0%; Pred. No.
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schizophrenia;
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06-NOV-2001

(first entry)

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RESULT 15
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234887.
27-SEP-2000; 2000US-0236359.
             30-JAN-2001; 2001WO-US00670
                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used the gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bone marrow expressed probe encoded protein SEQ ID NO: 28586.
                                                                                                                                Homo
                                                                                                                                                                    cervical cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microarray; cancer; leukaemia; lymphoma; myeloma
                                                                                         WO200157278-A2
                                                                                                                                                                                      Probe; human; microarray;
                                                                                                                                                                                                                                                                                                                                          AAM16103 standard; Protein; 32 AA
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                                                                                                                                                                                                                         Peptide #2537 encoded by probe
                                                                                                                                                                                                                                                               12-OCT-2001
                                                                                                                                                                                                                                                                                                      AAM16103;
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                                                                                                                              sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       13 HSFSAGPE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 AA;
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                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                尺,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.3%; Score 8; DB
100.0%; Pred. No. 1;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28586; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                    gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                       for measuring cervical gene expression.
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Search completed: July 24, Job time: 15.4832 secs

2003, 12:21:21

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Best Local Similarity
Matches 8; Conserv
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SBP-2000; 2000US-0234687.
27-SBP-2000; 2000US-0234559.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                    The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                            Sequence
                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID No 20929; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn
                                                                                                                                                                                                        cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
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13
                               27
HSFSAGPE 20
                            HSFSAGPE 34
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                                                                                                                            32 AA;
                                                               Conservative
                                                      16.3%; bu
100.0%; Pro
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                                                                             Score 8;
Pred. No.
                                                               Mismatches
                                                                             DB 22;
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                                                                                            Length 32;
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                                                               Gaps
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Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match Length
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Gapop 60.0 , Gapext 60.0
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365.801 Million cell updates/sec
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49
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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          US-09-065-383-31
US-09-065-383-27
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US-09-065-383-27
US-09-065-383-27
US-09-252-991A-32535
US-09-252-991A-32472
US-09-252-991A-29708
US-09-252-991A-29708
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US-09-252-991A-3122
US-09-252-991A-3118
US-09-252-991A-3118
US-09-252-991A-3118
US-09-252-991A-3118
US-09-252-991A-3118
US-09-252-991A-31594
US-09-252-991A-31594
US-09-252-991A-31594
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US-09-252-991A-31595
US-09-252-991A-31595
US-09-252-991A-31595
US-09-252-991A-31595
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Sequence 27, Appl
Sequence 17084, A
Sequence 6376, Ap
Sequence 32535, A
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          e 10, Appl
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2, Appli
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324783, Appli
232708, Appl
223708, Appl
232129, Appl
232129, Appl
232129, Appl
232129, Appl
232129, Appl
232129, Appli
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δ	σ	σ	δ	σ	6	σ	6	თ	6	6	6	6	6	6	6	σ	6
12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2
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US-09-252-991A-29351	US-09-252-991A-28279	US-09-252-991A-27558	US-09-134-001C-5168	US-09-273-871A-12	US-09-636-499-7	US-09-543-141-2	US-09-470-512A-9	US-08-744-231-2	US-08-868-435-2	US-09-038-909-2	US-09-107-532A-4308	US-09-252-991A-28231	US-09-470-512A-8	US-09-252-991A-32284	US-09-191-879-2	US-09-252-991A-26239	US-09-252-991A-20438
Sequence 29351, A	Sequence 28279, A	Sequence 27558, A	Sequence 5168, Ap	Sequence 12, Appl	•	-	•	•	•	Sequence 2, Appli	Sequence 4308, Ap	Sequence 28231, A	Sequence 8, Appli	Sequence 32284, A	Sequence 2, Appli	Seguence 26239, A	Sequence 20438, A

ALIGNMENTS

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RESULT 1
US-09-065-383-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: BILLING
APPLICANT: COHEN,
APPLICANT: COLPITT
APPLICANT: FRIEDMA
APPLICANT: GORDON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/09065383 Patent No. 6391543
                                                                   COMPUTER: ISM COMPATIBLE
COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
FILING DATE:
CLASSIFICATION: DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/842,385
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.P1
TELEPAX: 847/938-1729
TELEPAX: 847/938-2623
                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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APPLICANT:
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APPLICANT:
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
LENGTH: 49 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRAVADOS, EDMARD N.
GRAVADOS, EDMARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
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                                      31:
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-065-383-27
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US-09-065-383-27
CQuery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US.
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPATIBLE COMPATIBLE
POS
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                                                                                                                                                                  NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROBERTS-R
APPLICANT: RUSSELL,
APPLICANT: STROUPE,
APPLICANT: STROUPE,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: No. 6391543e
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REGISTRATION UNMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/335-1729
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/8
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                         TYPE: amino acids
STRANDEDNESS: single
TOPOTOCY
                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                   TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
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6391543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPIGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
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RUSSELL, JOHN C.
STROUPE, STEPHEN D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLPITTS, TRACEY L. FRIEDMAN, PAULA N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abbott Laboratories
                                                                       No. 6391543e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE PROSTATE: 33
        100.0%;
                                                                                                                                                                                                                                                                                                                             08/842,385
                                                                                                                                                                    27:
                                                                                                                                                                                                                                                6084.US.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       °.
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Pred. No. 5.6e-41;
        Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
        DB 4;
4.1e-40;
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                     Length 518;
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17084
LENGTH: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-09-107-532A-6376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-17084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-17084
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Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

APPLICANT: Lynn A DOUCETTE ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: MATC J. RUBENFIELD et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                               APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          APPLICATION UNMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7310
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               NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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100.0%; Pred. No.
                                                             Pamela Deneke
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12;
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RESULT 6
US-08-426-627-10
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32535
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LOCATION: (B) LOCATION 1...285
SEQUENCE DESCRIPTION: SEQ ID NO: 6376:
US-09-107-532A-6376
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US-09-252-991A-32535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32535
LENGTH: 777
                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Marc J.
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Best Local (
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                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Amann, Egon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 637.
SEQUENCE CHARACTERISTICS:
                                                                          APPLICANT: Amann, Egon
APPLICANT: Otawara-Hamamoto, Yoko
APPLICANT: Kikuno, Reiko
APPLICANT: Takeshita, Sunao
APPLICANT: Tezuka, Kenichi
TITLE OF INVENTION: No. 5756664el Protein with Bone Formation
TITLE OF INVENTION: Ability and Process for Its Production.
                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 7; Conserva
                 ADDRESSEE: Finnegan, Henderson,
ADDRESSEE: Dunner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                          43 RSGSTGS 49
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 285 amino acids
                                                                                                                                                                                                                                         Application US/08426627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marc J. Rubenfield et al.

"ENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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100.0%; Pred. No. 41;
tive 0; Mismatches
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                                 Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 729;
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                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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; ORGANISM: Homo sapiens US-09-203-623-2
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                                                                                                                                                          SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09203623 Patent No. 6140084
                              Matches
                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICATION NUMBER: US 08/036,841
FILING DATE: 25-MAR-1993
APPLICATION NUMBER: JP 4-71501
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hammond, Alan W.
REGISTRATION NUMBER: 35,178
REFERENCE/DOCKET NUMBER: 02481-1285-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                        FILE REFERENCE: 97-62
CURRENT APPLICATION NUMBER: US/09/203,623
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: US 60/067,293
EARLIER FILING DATE: 1997-12-03
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                      APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: HUMAN THYROID PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                            TYPE: PRT
                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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RSGSTG 48
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                              Conservative
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                            Score 6; DB; Pred. No. 82
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                                             DB 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                            Length 114;
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                            Gaps
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Sequence 2, Application US/09523462
Patent No. 6486304
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
FILE OF INVENTION: HUMAN THYROID PROTEIN, ZSIG45
FILE REFERENCE: 97-62
CURRENT APPLICATION NUMBER: US/09/523,462
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: US 60/067,293
EARLIER FILING DATE: 1997-12-03
NUMBER OF SEQ ID NOS: 39
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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Best Local Similarity
Thes 6; Conserve
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US-09-523-462-2
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                                                                                                                                                                                                               RESULT 10
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APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: HUMAN THYROID PROTEIN, ZS.
FILE REFERENCE: 97-62
CURRENT APPLICATION NUMBER: US/09/522,980
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: US 60/067,293
EARLIER FILING DATE: 1997-12-03
NUMBER OF SEQ ID NOS: 39
                                                                                                                Sequence 32472, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 114
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Best Local Similarity
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
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100.0%; Pred. No.
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o. 82;
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US-09-252-991A-29708
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29708
LENGTH: 171
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US-09-252-991A-29708
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US-09-252-991A-24783
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32472
LENGTH: 139
TYPE- DET
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LENGTH: 153
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Matches 6; Conserv
Query Match
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APPLICANT: Marc J.
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION:
FILE REFERENCE: 107
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ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
                                                     ORGANISM: Pseudomonas aeruginosa
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NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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100.0%; Pred. No. 1.1e+02;
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100.0%; Pred. No.
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Length 171;
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; FEATURE:
, NAME/KEY: SITE
; LOCATION: (226)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-215
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                                                                                                                                   NUMBER OF SEQ ID NOS: 376
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 215
LENGTH: 226
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Best Local S
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: 98 Human Secreted Proteins FILE REFERENCE: PZ031P1
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                          ORGANISM: Homo sapiens
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les 6; Conserv
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ER FILING DATE: 1998-07-30
ER APPLICATION NUMBER: 60/095,486
ER FILING DATE: 1998-08-05
ER APPLICATION NUMBER: 60/096,319
ER APPLICATION NUMBER: 60/095,454
ER APPLICATION NUMBER: 60/095,454
ER APPLICATION DATE: 1998-08-06
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Matches 6
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Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 32129
LENGTH: 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32129, Apparent No. 6551799
                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                           TYPE: PRT
145 RPRSGS 150
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                               41 RPRSGS 46
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                   12.2%; Score 6;
100.0%; Pred. No.
                                                                     Mismatches
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Search completed: July 24, 2003, 12:28:40 Job time: 7.66764 secs

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Maximum DB
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Perfect score:
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49
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11:
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/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US090_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/JS06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result beir and is derived by analysis of the total score distribution. result being p printed,

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1	59	46	27	27	22	21	20	10	314	314	314	135	115	32	Query Match Length DB
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110 00 064 361 36330	US-09-764-872-354	US-09-864-761-41721	US-10-212-628-260	US-10-057-789-260	US-10-057-505-31	US-09-864-761-41759	US-10-057-505-30	US-09-572-404B-104	US-10-106-698-4725	US-09-925-299-934	US-09-925-299-934	US-09-916-790-31	US-09-764-868-815	US-09-864-761-35805	ID
יייייייייייייייייייייייייייייייייייייי	Sequence 354, App	Sequence 41721,	Sequence 260, A	Sequence 260, A	Sequence 31, Appl	Sequence 41759, A	Sequence 30, Appl	Sequence 104, A	Seguence 4725, Ap	Sequence 934, A	Sequence 934, Ap	Sequence 31, Appl	Sequence 815, A	Sequence 35805, A	Description

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.US-10-156-761-11458	115-10-290-631-2	-381	US-09-815-242-5263	US-10-080-170-86	-10-270-846-4	- 1	US-10-270-710-49	US-10-270-786-49	US-10-270-878-49	US-10-270-875-49	US-10-057-321-6	US-09-244-984-6	US-09-765-205-14	US-10-106-698-5221	US-09-769-787-46	US-09-976-451-2	US-09-976-451-8	US-09-764-864-1267	US-09-925-297-658	US-09-976-451-9	US-09-764-891-4162	US-09-864-761-39423	US-10-102-806-482	US-10-125-540-429	US-09-764-870-429	US-09-850-887-1	US-10-004-381-5	US-10-016-157A-187	US-U9-182-914C-26
		85.	5263,	, 98	49,		49,	49,	49,	49,	Sequence 6, Appli	Sequence 6, Appli	Sequence 14, Appl	Sequence 5221, Ap	Sequence 46, Appl	'n	w	Sequence 1267, Ap	σ	Sequence 9, Appli	Sequence 4162, A	Sequence 39423, A	Sequence 482, App	Sequence 429, App	42	Sequence 1, Appli	G	Sequence 187, Ap	Sequence 26, Appr

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US-09-864-761-35805
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                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PRIOR DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: US 60/236.36
PRIOR PILING DATE: 2000-10-04
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
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                                                         PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
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Hanzel, David K.
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,RESULT 3
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Best Local Similarity
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US-09-764-868-815
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
PILE REFERENCE: PTZ32
                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 815
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                                                                                                                                                                                                                                                                                                                                 Prior application data removed - refer to PALM or file wrapper
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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OTHER INFORMATION:
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FILING DATE: 2000-99-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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                                                                                                                          33 PELLROD 39
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8; Conserv
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     Application US/09916790
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N: EXPRESSED IN HELA, SIGNAL = 35

N: EXPRESSED IN HEART, SIGNAL = 1.2

N: EXPRESSED IN BRAIN, SIGNAL = 1.8

N: EXPRESSED IN BRAIN, SIGNAL = 1.8

N: EXPRESSED IN HELIO, SIGNAL = 3.9

N: EXPRESSED IN LUNG, SIGNAL = 3.1

N: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
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EXPRESSED IN PLACE
EXPRESSED IN HELA,
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Pred. No. 19;
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Pred. No.
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IN LUNG, SIGNAL = 3.1
IN BONE MARROW, SIGNAL = 1.5
IN ADULT LIVER, SIGNAL = 1.2
IN FETAL LIVER, SIGNAL = 0.9
INT: BE531168.1, EVALUE 3.90e-01
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FILE REFERENCE: 381552002700
CURRENT APPLICATION NUMBER: US/09/916,790
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/221,543
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 135
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                              US-09-925-299-934
Sequence 934, Application US/09925299
Publication No. US20030040617A9
GENERAL INFORMATION:
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US-09-925-299-934
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Best Local S
Matches 7
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SEQ ID NO 934
LENGTH: 314
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Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
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Best Local (
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 18431 AND 32374, NOVEL HUMAN PROTEIN
TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 1556
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nes 7; Conserv
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7; Conserv
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b; Pred. No. 21;
0; Mismatches
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5. 21;
                                                                              and Antibodies
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                                                                                                                                                                                                                                                                                                                                                                      Length 314;
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PRIOR FILING UALL. 1997 124
PRIOR APPLICATION NUMBER: 60/124
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 934
LENGTH: 314
TYPE: PRT
TYPE: PRT
                                                                                                                                                                                                   US-09-572-404B-104

Sequence 104, Application US/09572404B

; Publication No: US20030078374A1

; GENERAL INFORMATION:
APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
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; OTHER INFORMATION: sequence located in BTF3L3 at 25-34 and may interact with Sequence; OTHER INFORMATION: in this patent.
US-09-572-404B-104
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-106-698-4725
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                                                                                                    SOFTWARE: ProtPatent version 1.0
SEQ ID NO 104
LENCTH: 10
TYPE: PRT
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SEQ ID NO 4725
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
-09-925-299-934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide FILE REFERENCE: PA005P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8564
                                                                                                                                                                                        TUMBER OF SEQ ID NOS: 4203
                                                                             ORGANISM: Homo Sapiens
                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 LLRODKR 99
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Conservative 0; Mismatches
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US-10-057-505-30
                                 FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 41759, Application US/09864761 Patent No. US20020048763A1
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Best Local Similarity
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Best Local
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CUBITY, ANDYEM
TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
FILE REFERENCE: REGEN1260-3
CURRENT APPLICATION NUMBER: US/10/057,505
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR FILING DATE: 1997-01-31
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                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION: Linker sequence
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TYPE: PRT
                 APPLICATION NUMBER: PCT/US01/00666
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2001-01-30
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Best Local
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 22
                                                                                             CURRENT APPLICATION NUMBER: US/10/057,505
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: US 09/396,003
                                                                                                                                                                                               APPLICANT: CUBITT, Andrew
TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
FILE REFERENCE: REGEN1260-3
                                                                                                                                                                                                                                                                           APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA APPLICANT: AURORA BIOSCIENCES CORPORATION APPLICANT: TSIEN, ROGER
                                                             PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 31
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OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00661
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No. US20020164674A1
                                                                                                                                                                                                                                                          HEIM, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXPRESSED IN BRAIN, SIGNAL = 2
EXPRESSED IN PLACENTA, SIGNAL = 2
EXPRESSED IN ADULT LIVER, SIGNAL = 2
EXPRESSED IN BONE MARROW, SIGNAL = 1.6
PYDRESSED IN FETAL LIVER, SIGNAL = 2.6
PYDRESSED IN FETAL SIGNAL = 3.3
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N HELA, SIGNAL = 3
N HEART, SIGNAL = 3
N LUNG, SIGNAL = 5.4
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o. 39;
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Sequence 260, Application US/10212628 Publication No. US20030087329A1 GENERAL INFORMATION:

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APPLICANT: Paul Haynes
APPLICANT: Jing Wei
APPLICANT: Jing Wei
APPLICANT: John Yates
APPLICANT: Nancy Andon
TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES
FILE REFERENCE: NADII.022CP1
CURRENT APPLICATION NUMBER: US/10/212,628
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/264,576
PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: US 60/305,232 PRIOR FILING DATE: 2001-07-13

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RESULT 12
US-10-212-628-260
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US-10-057-789-260
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                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 260
LENGIH: 27
                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
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APPLICANT: Paul Hay:
APPLICANT: Jing We
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                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES FILE REFERENCE: NADII.022A CURRENT APPLICATION NUMBER: US/10/057,789 CURRENT FILING DATE: 2002-06-28 PRIOR APPLICATION NUMBER: US 60/264,576 PRIOR PILING DATE: 2001-01-26 PRIOR PILING DATE: 2001-01-26 PRIOR PILING DATE: 2001-07-13 PRIOR FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jing Wei
APPLICANT: John Yates
APPLICANT: Nancy Andon
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 311
                                                                                                                                                                                                                  TYPE: PRT
ORGANIAM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: VARIANT
LOCATION: 8
OTHER INFORMATION: Xaa = Modified Cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Linker sequence
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US20030082522A1
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100.0%; Pred. No.
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100.0%; Pred. No.
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D. 41;
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RESULT 13
US-09-864-761-41721
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NUMBER OF SEQ ID NOS: 311
SOFTWARE: FastSEQ for Windows Version
BEQ ID NO 260
LENGTH: 27
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT LOCATION: 8
OTHER INFORMATION: Xaa
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TYPE: PRT
ORGANISM: Saccharomyces
FEATURE:
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FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-10-04
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
                                                        FILING DATE: 2000-09-21
                                                                       APPLICATION NUMBER: US 60/234,687
                                                                                           FILING DATE:
                                                                                                            APPLICATION NUMBER: PCT/US01/00670
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                                      APPLICATION NUMBER: US 09/608,408
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Pred. No.
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o. 49;
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US-09-864-761-36328
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: SITE
; LOCATION: (14)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
US-09-764-872-354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-764-872-354
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NUMBER OF SEQ ID NOS: 957
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 354
LENGTH: 59
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                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: Nucleic Acids, Protei:
FILE REFERENCE: PA125
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                             APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                             APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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FILING DATE:
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EST_HUMAN HIT: BF310134.1, EVALUE 2.00
SWISSPROT HIT: Q56815, EVALUE 2.80e+00
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EXPRESSED IN BRAIL
EXPRESSED IN PLACE
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100.0%;
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100.0%; Pred. No.
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IN BOME MARROW, SIGNAL = 1.8
IN HEART, SIGNAL = 2
IN LUNG, SIGNAL = 4.3
IN LUNG, SIGNAL = 4.3
HIT: BF310134.1, EVALUE 2.00e-15
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CREATURE:

PEATURE:

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PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOPTWARR: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36328
LENGTH: 75
TYPE: PRT
Search completed: July 24, 2003, 12:48:30 Job time : 9.32211 secs
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                   60 LLORPO 65
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                        12.2%; Score 6; DB 9; Length 75; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
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Result
No.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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Perfect score:
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                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                 Score
               4 9
9
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Match Length DB ID
               100.0
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/ Cgn2_6/ptodata/1/paa/US081_COMB.pep:*
/ Cgn2_6/ptodata/1/paa/US081_COMB.pep:*
/ Cgn2_6/ptodata/1/paa/US082_COMB.pep:*
/ Cgn2_6/ptodata/1/paa/US083_COMB.pep:*
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/ Cgn2_6/ptodata/1/paa/US092_COMB.pep:*
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/ Cgn2_6/ptodata/1/paa/US101_COMB.pep:*
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               49
49
            12
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         US-08-842-385-10
US-09-991-681-31
                                                                                                                                                                                    SUMMARIES
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Sequence 10, Appl
Sequence 31, Appl
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equence 54297, Sequence 709, Sequence 148,	equence equence quence	equence 266913	Sequence 759, App Sequence 438, App	equence 759,	equence 1163	e 65261	equence 64883,	equence 14062	equence 1403715	Sequence 1354743,	equence 17560,	e 2772	equence 12879,	equence 12879,	equence 28863,	equence 28586.	equence 27486.	22220	equence 20929,	2227	equence 28015,	Sequence 3580	quence 28863	٠,	ייני מיני	equence 32,	Sequence 49	equence 495,	quence 400	Sequence 44,	quence 44	27	emience 6

ALIGNMENTS

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US-08-842-385-10

US-08-842-385-10

; Sequence 10, Application US/08842385

; GENERAL INFORMATION:
   APPLICANT: Russell, John
   APPLICANT: COlpitts, Tracey
   TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
   TITLE OF INVENTION: FOR DETECTING DISEASE OF THE PROSTATE
   NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
   ADDRESSE: ADDORACE ADDRESS:
   ADDRESSET: 100 Abbott Laboratories
   STREET: 100 Abbott Park Road
   CITY: Abbott Park
   STATE: IL
   COUNTRY: USA
   ZIP: 60064-3500
   COMPUTER READABLE FORM:
   MEDIUM TYPE: Diskette
   COMPUTER: IBM Compatible
   OPERATING SYSTEM: DOS
   SOFTWARE: FastSEG for Windows Version 2.0
   CURRENT APPLICATION NUMBER: US/08/842,385
   FILING DATE:
   CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE

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US-09-991-681-31
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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NAME: POTEMBRI, Priscilla B
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6884
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
APPLICATION UNMER: 09/065,383
PILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US
TELECHONE: 847/935-1729
TELEPHONE: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 49 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-NOV-2001
CLASSIFICATION: <UNKNOWND
PRIOR APPLICATION DATA:
OF THE PRIOR APPLICATION DATA:
OF THE PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
ROBERTS-RAPP, LISA
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Abbott Park
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 49; DB 12; 100.0%; Pred. No. 9.9e-40;
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                                                                   6084.US.P1
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                                                                                                                                            US-08-842-385-6
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GENERAL INFORMATION:
APPLICANT: Russell, John
APPLICANT: Colpitts, Trav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 49; Conserv
                                                                      Matches.
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                        NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6084.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                             MOLECULE TYPE: None
                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/842,385 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 31:
342 EPIGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 390
                    1 EPLGPRGODSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
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TYPE: amino acid
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                                                                                                                                                                                                                                    467 amino acids
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                                                                                                                                                                           یمی: single
linear
                                                                    100.0%; Score 49; DB 12; ilarity 100.0%; Pred. No. 7.4e-39; Conservative 0; Mismatches 0;
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FOR DETECTING DISEASE OF THE PROSTATE
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                                                                                                        Length 467;
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                                                                                                          Sequence 44, Application PC/TUS0301943 GENERAL INFORMATION:
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Best Local :
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GENERAL INFORMATION
               APPLICANT: ORIGENE TECHNOLOGIES INC
TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 10/054,935
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
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MEDIUM TYPE: Diskette
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ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Abbott Laboratories
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                                                                                                                                                                                                                       393 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 441
                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                               1 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441 REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-NOV-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 518 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HODGES, STEVEN C.
KLASS, MICHAEL R.
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Pred. No. 8.1e-39;
); Mismatches 0;
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TYPE: PRT
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APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                    PCT-US01-08631-40087
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Best Local Similarity
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                                                                 SEQ ID NO 40087
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GENERAL INFORMATION
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CURRENT FILING DATE: 2002-05-14
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TITLE OF INVENTION: Regulated Prostate Cance Genes
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PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR FILING DATE: 2002-05-14
                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: Custom
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PRIOR FILING DATE: 2002-03-22
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ORGANISM: Homo sapiens
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                                            ENGTH: 1807
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les 49; Conserv
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Pred. No. 2.4e-38;
); Mismatches 0;
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                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-416-993-495
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PCT-US01-42950-495
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                                                              Matches
                                                                                                                                                                                                                                                                                                                              Sequence 495, Application US/10416993
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
SEQ ID 495
LENGTH: 1839
TYPE: PRT
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 495
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
                                                                                            Query Match
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Best Local Similarity
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/416,993
CURRENT FILING DATE: 2003-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
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OTHER INFORMATION: Helper component proteinase domain identified by PFam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam score of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX, OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw so
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                                                                           Local
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                                                            49;
                                                                           Similarity
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EPIGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                        100.0%; ! ilarity 100.0%; ! Conservative 0;
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Pred. No. 2.5e-38;
                                                        Score 49; DB 30;
Pred. No. 2.5e-38;
Mismatches 0;
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Pred. No. 2.5e-38;
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RESULT 11
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CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 93
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Query Match
Best Local S
Matches 49
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LENGTH: 1982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/1
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/6
PRIOR FILING DATE: 2000-08-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: IDEC PHARMACEUTICALS APPLICANT: GATELY, DENNIS
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 60736
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                                                                                             NAME/KEY: DOMAIN
LOCATION: (1065)..(1074)
OTHER INFORMATION: Helper component proteinase domain identified by PFam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
                                                                                                                                                                              OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX, OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw sc
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                                                                                                                                                                                                                      NAME/KEY: DOMAIN
LOCATION: (11)..(25)
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                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                       TYPE: PRT
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  l Similarity
49; Conserv
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Pred. No. 2.5e-38;
                  Score 49; DB 1;
Pred. No. 2.7e-38;
  Mismatches
                                     Length 1982;
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  Gaps
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1796 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 1844

PCT-US03-01943-30

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RESULT 14
PCT-US01-00663-28863
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CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 10/054,935
PRIOR FILING DATE: 2002-01-25
PRIOR PPLICATION NUMBER: US 60/356,130
PRIOR APPLICATION NUMBER: US 60/356,130
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/117,229
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR APPLICATION NUMBER: US 10/197,824
PRIOR APPLICATION NUMBER: US 10/197,824
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GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prostate Car
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
Sequence 28863, Application PC/TUS0100663
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0 SEQ ID NO 30
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NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2221
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                           100.0%; Score 49; DB 27; Length 2221; larity 100.0%; Pred. No. 3e-38; Conservative 0; Mismatches 0; Indels 0.
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Pred. No. 3e-38;
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CURRENT FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 Pebruary 2000 (04.02.00)
PRIOR PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,667
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR PILING DATE: 21 September 2000 (21.09.00)
PRIOR PILING DATE: 30 June 2000 (30.06.00)
PRIOR PILING DATE: 30 June 2000 (30.06.00)
PRIOR PILING DATE: 30 June 2000 (30.06.00)
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                                     PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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LENGTH: 32
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Best Local
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: PB 0004 WO 7
CURRENT ADDITION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
FILE REFERENCE: PB 0004 WO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
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FEATURE:
OTHER INFORMATION: MAP TO AC007688.15
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EST_HUMAN HIT: BES31168.1, EVALUE 3.90e-01
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                 APPLICATION NUMBER: PCT/US01/00664
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Chen, Wensheng
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Hanzel, David K.
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COGANISM: Homo sapiens

FEATURE:

FEATURE:

FEATURE:

FOTHER INFORMATION: MAP TO ACO07688.15

COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

COTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2

COTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8

COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8

COTHER INFORMATION: EXPRESSED IN HIL100, SIGNAL = 3.9

COTHER INFORMATION: EXPRESSED IN HOLDON, SIGNAL = 3.1

COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9

COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9

COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9

COTHER INFORMATION: EXPRESSED IN BONE MARROW SIGNAL = 0.9

COTHER INFORMATION: EXPRESSED IN BESSII68.1, EVALUE 3.90e-01
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PRIOR FILING DATE: 2001-01-30

PRIOR PPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PPLICATION NUMBER: PCT/US01/00670

PRIOR PPLICATION NUMBER: US 60/234,687

PRIOR PPLICATION NUMBER: US 69/234,687

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 35805

LENGTH: 32
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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HSFSAGPE 20
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Best Local Similarity
Matches 8; Conserve
Search completed: July 24, 2003, 12:45:57 Job time: 74.8228 secs
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    and is derived by analysis of the total score distribution.
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US-10-294-433-224

US-10-462-850-104

US-10-273-573-901

US-10-273-573-689

US-10-273-573-689

US-10-360-849A-15

US-10-360-849A-15

US-10-361-910A-27

US-10-311-910A-27

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US-10-462-850-2094

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224, App
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9548, Ap
 7474, Appl
62, Appl
63, Appl
63, Appl
612, Appl
1172, App
2092, Ap
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-978-32
                                                                                                                                         Sequence 99, Application US/09291417D GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Pa
                                                       APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: MHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 036602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
CURRENT FILING DATE: 1999-04-13
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5 10.2 81 6 US-10-316-175-73 5 10.2 88 1 PCT-US02-41612A-559 5 10.2 92 6 US-10-273-573-9360 5 10.2 107 1 PCT-US02-18934-119 5 10.2 107 1 PCT-US03-18934-119 5 10.2 110 6 US-10-273-573-9385 5 10.2 110 6 US-10-273-573-8138 5 10.2 110 6 US-10-273-573-8138 5 10.2 110 6 US-10-273-573-8513 5 10.2 120 6 US-10-273-573-8535 5 10.2 132 6 US-10-273-573-5535 5 10.2 132 6 US-10-273-573-9166 5 10.2 135 6 US-10-273-573-9178 5 10.2 155 6 US-10-273-573-9178 5 10.2 157 6 US-10-273-573-913 5 10.2 164 6 US-10-273-573-914 5 10.2 196 6 US-10-273-573-9114	10.2 86 10.2 88 10.2 92 10.2 107 10.2 110 10.2 110 10.2 110 10.2 110 10.2 112 10.2 132 10.2 135 10.2 153 10.2 157 10.2 164 10.2 1	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27
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ALIGNMENTS

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Sequence 32, Application US/10367978
; Sequence 32, Application US/10367978
; GENERAL INFORMATION:
APPLICANT: GATELY, DENNIS
; TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND TITLE OF INVENTION: OR THERAPEUTICS
; FILE REFERENCE: 037003-0301988
; CURRENT APPLICATION NUMBER: US/10/367,978
; CURRENT APPLICATION NUMBER: 60/357,140
pRIOR APPLICATION NUMBER: 60/357,140
pRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/356,082
pRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 60/366,759
; PRIOR FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2002-06-10
                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 49; Conservative C
1747 EPIGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 1795
                                    1 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
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                                                                                                      Score 49; DB 6; 1
Pred. No. 8.9e-39;
); Mismatches 0;
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LENGTH: 418

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-99
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US-10-462-850-104
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                                                Sequence 104, Application US/10462850
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/10/462,850
CURRENT APPLICATION NUMBER: US/10/462,850
NUMBER OF SEQ ID NOS: 4203
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SOFTWARE: ProtPatent version 1.0
EQ ID NO 104
LENGTH: 10
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CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/US01/14826
PRIOR FILING DATE: 2001-05-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 792CIP4
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1162
TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 5.2;
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; FEATURE:
NAME/KEY: misc feature
; LOCATION: (1)...(173)
; OTHER INFORMATION: Xaa = X or *
US-10-273-573-9548
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OTHER INFORMATION: sequence located
OTHER INFORMATION: in this patent.
US-10-462-850-104
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                                                                                                                                                            SOFTWARE: Custom
SEQ ID NO 9548
LENGTH: 173
TYPE: PRT
                                                                                                                                                                                                                                                                                Sequence 9548, Application US/10273573

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
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SEQ ID NO 9011
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Best Local :
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Matches 6; Conserv
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Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
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PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/770,160
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                                                                                                                                         ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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100.0%; Pr
12.2%;
100.0%;
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k; Pred. No. 2.2
0; Mismatches
Score 6;
Pred. No.
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                 Length 173;
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US-10-360-849A-15
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; LOCATION: (1)...(238)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-273-573-6890
 Query Match
Best Local Similarity
""" hes 6; Conserva
                                                                                     ; ORGANISM: mus musculus US-10-360-849A-15
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                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/354,978
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15
LENGTH: 261
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GENERAL INFORMATION
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                                                                                                                                                                                                                                   APPLICANT: Wadman, Shannon
TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
FILE REFERENCE: 3021.05US02
CURRENT APPLICATION NUMBER: US/10/360,849A
CURRENT FILING DATE: 2003-02-07
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APPLICANT: Hackett, Perry
APPLICANT: Nasevicius, Aidas
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PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
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CURRENT FILING DATE: 2002-10-18
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
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PRIOR FILING DATE: 2000-04-18
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                                                                                                                        TYPE: PRT
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ORGANISM: Homo sapiens
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Clark, Karl
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              12.2%; Score 6; DB 6; ilarity 100.0%; Pred. No. 30; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Scenedesmus obliquus
US-10-411-910A-27
                RESULT 11
US-10-73-573-7423
; Sequence 7423, Application US/10273573
; GENERAL INFORMATION:
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US-10-411-910A-27
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Best Local Similarity
Matches 6; Conserv
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GENERAL INFORMATION:
APPLICANT: Dillon, Harrison F.
APPLICANT: DIVENTION: Methods and Compositions for Evolving Hydrogenase Genes
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/360,849A
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/354,978
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 72
APPLICANT: Hyseq, Inc
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TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
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TYPE: PRT
ORGANISM: home sapiens
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                                                                                                                        165 PRSGST 170
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Ekker, Stephen
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100.0%; Pred. No.
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Best Local Similarity
Thehes 6; Conserv
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7511813CD1
PCT-US03-19660-37
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; OTHER INFORMATION: Carboxyl transferase domain identified by PFam, accession
; OTHER INFORMATION: name Carboxyl_trans, E-value=4.3e-72, PFam score of 252.9
US-10-273-573-7423
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 98
SOFTWARE: PERL Program
SEQ ID NO 37
SEQ ID NO 37
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Best Local Similarity
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SEQ ID NO 7423
LENGTH: 697
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CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/396,196
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TITLE OF INVENTION: KINASES AND PHOSPHATASES
FILE REFERENCE: PF-1454 PCT
                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/770,160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: INCYTE CORPORATION; MARQUIS, Joseph P., APPLICANT: BAUGHN, Mariah R.; TRAN, Uyen K.; APPLICANT: HAFALIA, April J.A.; KABLE, Amy E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equence 37, Application PC/TUS0319660 ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                             ENGTH: 729
143 PRSGST 148
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                                    PRSGST 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BULLOCH, Sean A.; JIN, Pei;
BHATIA, Umesh G.; BURRILL, John D.;
LEE, Sally; BLAKE, Julie;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAWLA, Narinder K.; BECHA, Shanya D.; MASON, Patricia M.; HAWKINS, Phillip R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMERLING, Brooke M.; ELLIOTT, Vicki S.;
LINDOUIST, Erika A.; RICHARDSON, Thomas W.;
KHARE, Reena; SWARNAKAR, Tanita;
                                                                       12.2%; Score 6; DB ilarity 100.0%; Pred. No. 70 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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RESULT 15
US-10-316-175-63
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Sequence 63, Application US/10316175 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 7424
LENGTH: 1264
                                                                                                                                                                                      Matches
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Best Local :
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 532862000100
CURRENT APPLICATION NUMBER: US/10/316,175
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/338,188
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thederahn, Ted
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING HYPOTRICHOSIS SIMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/770,160 PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hyseq, Inc
                                                                                                                                                                                                                                                                                                                LENGTH: 6
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b; Pred. No. 3.2
0; Mismatches
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APPLICANT: WELLA AG

Pras, Elon Levy-Nissenbaum, Etgar Frydman, Moshe

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APPLICANT: Thederahn, Ted
ITILE OF INVENTION. METHODS AND COMPOSITIONS FOR DIAGNOSING
ITILE OF INVENTION: AND TREATING HYPOTRICHOSIS SIMPLEX
FILE REFERENCE: 532862000100
CURRENT APPLICATION NUMBER: US/10/316,175
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/338,188
PRIOR FILING DATE: 2001-12-07
NUMBER OF SED ID NOS: 73
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 63
SEQ ID NO 63
LENGTH: 6
TYPE: PRT
CORGANISM: Homo sapiens
US-10-316-175-63

Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e-04;
Watches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Watches 5; Conservative 0; Mismatches 0; Indels 0; Gaps Db
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Search completed: July 24, 2003, 12:46:20
Job time: 2.63485 secs
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49
1 EPIGPRGQDSPLLQRPQHLM......
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

Post-processing: Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

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6 12.2	12.	12.	12.	12.	12.	12.	•	12.	12.	12.	•	•		6 12.2	6 12.2	12.			٠	7 14.3	7 14.3	7 14.3	7 14.3		4.	7 14.3	7 14.3	7 14.3	Query e Match
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hypothetical prote	conserved hypothet	transcription regu	hypothetical	Orf50 (bacteriopha	probable transcrip	ribulose-bisphosph	Ca2+-transporting	conserved hypothe	hypothetical	\mathbf{r}	photosystem II	hypothetical	hypothetical	hypothetical	hypothetical	hypothetical	hypothetical	nuclear protein	dihydroorotase	OD.	conserved hypothet		a		ribosomal protein	pathogenesis-rela	pathogenesis-	ьe	Description

pathogenesis-related protein 4B - common tobacco (Species: Nicotiana tabacum (common tobacco (Species: Nicotiana tabacum (common tobacco) C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 23-Mar-2001 C;Accession: S23800 R;Linthorst, H.J.M.; Danhash, N.; Brederode, F.T.; van Kan, J.A.L.; de Wit, P.J.G.M.; Bo Mol. Plant Microbe Interact. 4, 586-592, 1991 A;Title: Tobacco and tomato PR proteins homologous to win and pro-hevein lack the "heveir A;Reference number: S23799; MUID:92208317; PMID:1804403 A;Accession: S23800 A;Status: preliminary A;Molecule type: mRNA

RESULT 2 S23800

ALIGNMENTS

유 성	Query Match Best Local Matches	C95304 hypothetical tran C;Species Sinorh C;Date: 24-Aug-20 C;Accession: C953 R;Barnett, M.J.; ; Kalman, S.; Ke Proc. Natl. Acad. A;Title: Nucleoti A;Reference numbe A;Accession: C953 A;Status: prelimi A;Reference interence A;Roserimental : 1-86 A;Cross-reference A;Roserimental : 1-86 A;Cross-reference C;Galibert, F.; F pela, D.; Chain, L.; Hyman, R.W.; Science 293, 668- A;Authors: Kahn A;Authors: Kahn A;Authors: Kahn A;Authors: Kahn A;Authors: Kahn A;Authors: Mand A;Title: The comp A;Reference numbe A;Contents: C;Genetics: A;Genetics: A;Genetics: A;Genee: SMa0643 A;Genome: plasmid
31 AGPELLR 37 66 AGPELLR 72	atch 14.3%; cal Similarity 100.0%; 7; Conservative (C95304 C95304 C95304 Cypothetical transposase, partial match [imported] - Sinorhizobium meliloti (strain 1021 C;Species: Sinorhizobium meliloti C;Species: C95304 C; Ralman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Barloy-Hubler, F.; Bows C; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001 A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Recession: C95304 A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Recession: C95304 A;Reference SMa0643 A;Genome: plasmid C95304 A;Reference SMa0643 A;Genome: plasmid
	Score 7; DB 2; Leng Pred. No. 4.4;); Mismatches 0;	Imported] - S; Aug-2001 #tea Komp, C.; Abs sck, M.C.; Su B, 2001 Gfunctions of PMID:114814: Lasmid pSymA buhler, A.; Al v.; Dreano, S V.; Weidner, S i, Weidner, S pMID:1147410
	Length 86; 0; Indels	Inorhizobii tt_change : tt_change : lla, A.P.; rzycki, R.; grzycki,
	0; ດູ	um mel: 30-Sep. Barlo; Welli; Welli re Sin re Sin el, N iel, N iel, N mel.
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٠	0;	(strain 102 er, F.; Bow l.; Yeh, K.C bium melilo 65 fisher, R.F. isher, R.F. C.; Lelaure K.; Yeh, K

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RESULT 5
AG2760
conserved hypothetical protein Atul495 [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosomal protein $4, chloroplast - Iris pallida chloroplast (fragment)
C;Species: chloroplast Iris pallida
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 13-Aug-1999
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R;Friedrich, L.; Moyer, M.; Ward, E.; Ryals, J.
Mol. Gen. Genet. 230, 113-119, 1991
A;Title: Pathogenesis-related protein 4 is structurally homologous to the c;A;Reference number: S18598; MUID:92079884; PMID:1745223
A;Accession: S18598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-139 <LIN>
A;Cross-references: EMBL:X58547; NID:g19965; A;Cross-references: EMBL:X58547; NID:g19965; C;Superfamily: pathogenesis-related protein 4 F;18-139/Domain: barwin homology <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-147 <FRI>
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                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-196 <NAD>
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Best Local S
Matches 7
                                                                                                                                                                                                                                                            Gene: rps4;
Genome: chloroplast;
                                                                                                                                                                                                                             Superfamily: Escherichia coli ribosomal protein S4; Reywords: chloroplast; protein biosynthesis; ribosome
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                                                                                          KRPRSGS
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100.0%; Pred. No.
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o. 9.3;
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5. 7.2;
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                                                                                                                                                                                             Length 196;
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     Agrobacterium tumefaciens
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RESULT 7
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                   R; Kaneko, T.; Sato, S.; Kotani, o, K.; Okumura, S.; Shimpo, S.; DNA Res. 3, 109-136, 1996
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C;Date: 11-Jan-2002 #sequence_revisi
C;Accession: AG2760
A; Title: Sequence
                                                                                 C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
C;Accession: S74737
                                                                                                                                                                       conserved hypothetical protein sll0926 - Synechocystis sp.
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A;Molecule type: DNA
A;Residues: 1-269 <KUR>
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A;Reference number: A973:
A;Accession: E97541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein AGR_C_2756 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
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A;Experimental source: strain C58 (Dupont)
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A;Accession: AG2760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Lerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: AGR_C_2756
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  analysis of the genome of
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A97359; MUID:21608551; PMID:11743194
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100.0%; Pred. No. 12
Live 0; Mismatches
                                            H.; Tanaka, A.; Asamizu, E.; Nakar
Takeuchi, C.; Wada, T.; Watanabe,
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Yamada, M.; Ya
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Markelz, B.;
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RESULT 8
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C; Geneti
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R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: C75592
                                                                                                                                                                                                              A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77508
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-433 <KANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S77508
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Io, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamadi DNA Res. 3, 109-136, 1996
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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A; Residues: 1-415 < WHI>
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       14.3%;
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       Score
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       2;
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       Length
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Zalewski,
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hypothetical protein F28016.11 [imported] - Arabidopsis thaliana (F28016.11 (imported) - Arabidopsis thaliana (F28016.11 (imported) - Arabidopsis thaliana (imported) - Arabidop
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C;Superfamily:
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R;Kaneko, T.; Nakamura,
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A; Accession: T30194
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A;Molecule type: DNA
A;Residues: 1-439 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74002.1; PID:g17131395; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                  nuclear protein SA2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 201
A;Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anai
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                          A; Cross-references: EMBL: AJ002636;
                                                                                                                                                          A;Status: preliminary; translated A;Molecule type: mRNA
                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 1997 A;Description: Homologue to human nuclear protein SA2
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 Conservative
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              14.3%;
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100.0%; Pred. N
; Score 7; DB 2
%; Pred. No. 47;
0; Mismatches
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                                                                                                                          PIDN: CAA05638.1
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, Y.; Lin, S.X.; Liu, S.X.; Liu, S.X.; Liuros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wordson and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                     R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, N. A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein R11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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T24161
                        A; Reference number: A97359; A; Accession: D97460
                                                                                                                                                                                   hypothetical protein AGR_C_1518 [imported] - Agrobacterium tumefaciens (strain C58, Cere C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: D97460
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A; Status: preliminary
                                                    A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun
A;Reference number: A97359; MUID:21608551; PMID:11743194
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A;Residues: 1-90 <WIL>
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A;Residues: 1-1532 <STO>
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RESULT 15
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A;Experimental source: strain Bristol N2; clone F56F4
                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-118 <MUR>
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A; Accession: T15239
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STRAIN-cv. Xanthi; TISSUE-Leaf;
MEDLINE-92079884; PubMed=1745223;
Friedrich L., Moyer M., Ward E., Ryals J.;
"Pathogenesis-related protein 4 is structurally homologous
"Pathogenesis-related protein 4 is structurally homologous".";
               Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
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PRODOm; PD004535; Barwin; 1.
PROSITE; PS00771; BARWIN 1; 1.
PROSITE; PS00772; BARWIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carboxy-terminal domains of hevein, Win-1 and
Mol. Gen. Genet. 230:113-119(1991).
-!- INDUCTION: By TMV infection.
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                                                                                                                                        Chloroplast
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pathogenesis-related protein PR-4B precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - !- SIMILARITY: BELONGS TO THE BARWIN FAMILY.
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3 (Rel. 41, Tast annotation)
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                                                                                                                                        1. 37, Last sequence update)
1. 41, Last annotation updat
ribosomal protein S4 (Fragm
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PATHOGENESIS-RELATED PROTEIN PR-4B.
BY SIMILARITY.
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S4 (Fragment).
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                                           Embryophyta; Tracheophyta;
                 Asparagales;
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Plant Syst. Evol. 204:109-123(1997).
-!- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the body of the 30S subunit (By similarity).
-!- FUNCTION: With S5 and S12 plays an important role in translational accuracy (By similarity).
                                                                                                Haemanthus magnificeas. Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z68235; CAA92533.1; -. HSSP; P81288; 1C05. HAMAP; MF_01306; -; 1. InterPro; IPR001912; Ribosomal_S4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A. Souza-Chies T.T.,
                                                                                                                              RPS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002942; S4.
InterPro; IPR005709; S4 bact_org.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
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                                     NCBI_TaxID=59038;
                                                        Haemanthus
                                                                  Spermatophyta; Magnoliophyta;
                                                                                    Eukaryota; Viridiplantae;
                                                                                                                                        Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGRO1017; rpsD_bact; proSITE; PS00632; RIBOSOMAL_S4; PROSITE; PS50889; S4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00363; S4; 1.
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of translational fidelity (By similarity).
SUBCELUUAR LOCATION: Chloroplast.
SIMILARITY: Contains 1 S4 RNA-binding domain.
SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5. The interaction surface between S4 and S5 is involved in control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; RNA-binding; rRNA-binding;
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182
182 AA;
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation updat
30S ribosomal protein S4 (Fragm
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Bittar G.,
                                                                                                                                                                                                                                                                                                                                                                                                    21048 MW;
                                                                     Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Asparagales; Amaryllidaceae;
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Nadot S.,
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Mismatches
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HSSP; P81288; 1C05.
HAWAP; MF 01306; -; 1.
InterPro; IPR001912; Ribosomal_S4.
InterPro; IPR002942; S4.
InterPro; IPR005709; S4 bact_org.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
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Plant Syst. Evol. 204:109-123(1997).
-I- FUNCTION: One of the primary rRNA binding proteins, i directly to 16S rRNA where it nucleates assembly of t the 30S subunit (By similarity).
-I- FUNCTION: With 55 and S12 plays an important role in
"Phylogenetic analysis of Iridaceae with parsimony and distance methods using the plastid gene rps4."; Plant Syst. Evol. 204:109-123(1997).
                                             SEQUENCE FROM N.A.
Souza-Chieg T.T., Bittar G.,
                                                                                                                                                     Hymenocallis littoralis
                                                                                                                                                                    RPS4.
                                                                                                                                                                              Chloroplast
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00363; S4; 1.
TIGREAMS; TIGRO1017; rpsD_bact; 1.
PROSITE; PS00632; RIBOSOMAL_S4; 1.
PROSITE; PS50889; S4; 1.
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                                                                                                                                         Chloroplast
                                                                                      NCBI_TaxID=59040;
                                       Lejeune B.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The interaction surface between S4 and S5 is involved in cor of translational fidelity (By similarity). SUBCELLULAR IOCATION: Chloroplast. SIMILARITY: Contains 1 S4 RNA-binding domain. SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
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SUBUNIT: Part of the 30S ribosomal subunit.
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182 AA;
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(Rel. 37, Last sequenc
(Rel. 41, Last annotat
30S ribosomal protein
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100.0%; Pred. No.
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yta; Liliopsida; Asparagales; Amaryllidaceae;
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(Fragment).
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                                                Carter L.,
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Pfam; PF01479; S4; 1.
SMART; SM00767.
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-!- FUNCTION: With S5 and S12 plays an important role in translat accuracy (By similarity).
-!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein The interaction surface between S4 and S5 is involved in cont translational fidelity (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Contains 1 S4 RNA-binding domain.
         "Phylogenetic analysis of Iridaceae with parsimony and dimethods using the plastid gene rps4.";
Plant Syst. Evol. 204:109-123(1997).
-i- FUNCTION: One of the primary rRNA binding proteins,
directly to 16S rRNA where it nucleates assembly of
the 30S subunit (By similarity).
                                                                                            SEQUENCE FROM N.A.
Souza-Chies T.T., Bittar G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS0632; RIBOSOMAL 54; PROSITE; PS50889; RIBOSOMAL 54; 1.
                                                                                                                                                              Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
                                                                                                                                                                                                                  RPS4.
                                                                                                                                                                                                                             Chloroplast
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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InterPro; IPR001912; Ribosomal_S4.
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                                                                                      Lejeune B.P.;
                                                                                                                                     NCBI_TaxID=58956;
                                                                                                                                                                                                     Iris lutescens.
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  FUNCTION: With S5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; RNA-binding; rRNA-binding;
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IPR005709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 AA;
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(Rel.
(Rel.
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37,
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S12 plays an
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Pred. No.
                                                                                                 Nadot S.,
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S4 (Fragment).
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 important role
                                                                                                  Carter L.,
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                                                                         and distance
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 in translational
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"Phylogenetic analysis of Iridaceae with parsimony and distance methods using the plastid gene rps4";
Plant Syst. Evol. 204:109-123(1997).
-!- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 168 rRNA where it nucleates assembly of the body the 308 subunit (By similarity).
-!- FUNCTION: With S5 and S12 plays an important role in translat accuracy (By similarity).
-!- SUBUNIT: Part of the 308 ribosomal subunit. Contacts protein The interaction surface between S4 and S5 is involved in cont of translational fidelity (By similarity).
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PROSITE; P
PROSITE; P
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Souza-Chies T.T., Bittar G., Nadot
Lejeune B.P.;
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InterPro; IPR002942; S4.
InterPro; IPR005709; S4_bact_org.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
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HAMAP; MF_01306; -; 1.
                                                                                                                                                                                                                                                                                                                                       sophysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accuracy (By similarity).

SUBUNIT: Part of the 30s ribosomal subunit. Contacts protein S5.

The interaction surface between S4 and S5 is involved in control of translational fidelity (By similarity).

SUBCELLULAR LOCATION: Chloroplast.

SIMILARITY: Contains 1 S4 RNA-binding domain.

SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL
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PS00632; RIBOSOMAL_S4;
PS50889; S4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; RNA-binding; rRNA-binding; Chloroplast
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yta; Magnoliophyta;
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182 /
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
30S ribosomal protein S4 (Fragment).
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182
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/ta; Liliopsida;
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o. 4.3;
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                                                                                                                                                                                                                                                   Carter L.,
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a; Asparagales; Iridaceae;
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Souza-Chies T.T., Bittar G., Nadot S.,
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PROSITE; PS00632; RIBOSOMAL_S4; 1.
PROSITE; PS50889; S4; 1.
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Pfam; PF00165; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinfi
the European Bioinformatics Institute
                                                                            "Phylogenetic analysis of Iridaceae with parsimony and distance methods using the plastid gene rps4.";
Plant Syst. Evol. 204:109-123(1997).
Plant Syst. Evol. 204:109-123(1997).
I FUNCTION: One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the body of the 30S subunit (By similarity).
I FUNCTION: With S5 and S12 plays an important role in translation accuracy (By similarity).
SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5.
                                                                                                                                                                                                                                                             NCBI_TaxID=58960;
                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta;
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SIMILARITY: Contains 1 S4 RNA-binding domain.
SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
           SIMILARITY: Contains 1 S4 RNA-binding domain. SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL
                                     The interaction surface between S4 and S5 of translational fidelity (By similarity). SUBCELLULAR LOCATION: Chloroplast.
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182 AA;
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yta; Liliopsida; Asparagales; Iridaceae;
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28-PEB-2003 (Rel. 41, Last annotat
Chloroplast 30S ribosomal protein
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                                                                                                                                                                                                                                                                    methods using the plastid gene rps4.",

Plant Syst. Evol. 204:109-123(1997).

-i-FUNCTION: One of the primary rNNA binding proteins, i

directly to 16S rRNA where it nucleates assembly of t

the 30S subunit (By similarity).

-i-FUNCTION: With S5 and S12 plays an important role in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
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TIGRPAMS; TIGRO1017; rpsD bact; 1.
PROSITE; P800632; RIBOSOMĀL_S4; 1.
PROSITE; PS50889; S4; 1.
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InterPro; IPR005709; S4 bact_org.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
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InterPro; IPR001912; Ribosomal_S4
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                                                                                                                                                                              accuracy (By similarity).
SUBUNIT: Part of the 30S ribosomal subunit. C
The interaction surface between S4 and S5 is
of translational fidelity (By similarity).
                                                                                                           SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: Contains 1 S4 RNA-binding domain.
SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS
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182 AA;
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RRESULT 10

RR4_NERBO

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Best Local S
Matches
                                                                                                                                                                                                                                                                                          "Phylogenetic analysis of Iridaceae with parsimony and dist methods using the plastid gene rps4.";

Plant Syst. Evol. 204.109-123 (1997).

-i- FUNCTION: One of the primary rRNA binding proteins, it directly to 168 rRNA where it nucleates assembly of the the 308 subunit (By similarity).

-i- FUNCTION: With S5 and S12 plays an important role in the accuracy (By similarity).

-i- SUBUNIT: Part of the 308 ribosomal subunit. Contacts professional stranslations surface between S4 and S5 is involved of translational fidelity (By similarity).
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020265;
15-DEC-1998
15-DEC-1998
15-DEC-1998
28-FEB-2003
Chloroplast
                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                   This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Contains 1 S4 RNA-binding domain.
-!- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOWAL PROTEINS
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Souza-Chies T.T., Bittar G., Nadot S.,
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InterPro; IPR001912; Ribosomal_S4.
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37, Last sequence update)
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Left Plant Syst. Evol. 204:109-123(1997).

Cill Financy rena binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the body of the 30S subunit (By similarity).

Cill FUNCTION: With S5 and S12 plays an important role in translational accuracy (By similarity).

Cill FUNCTION: By similarity).

Cill FUNCTION: One of the 30S ribosomal subunit. Contacts protein S5.

Cill FUNCTION: One of the 30S ribosomal subunit. Contacts protein S5.

Cill FUNCTION: One of the 30S ribosomal subunit. Contacts protein S5.

Cill FUNCTION: One of the 30S ribosomal subunit. Contacts protein S5.

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Cill FUNCTION: One of the 30S ribosomal subunit. Contacts protein S5.

Cill FUNCTION: One of the 30S ribosomal subunit. Contacts protein S5.

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InterPro; IPR001912; Ribosomal_S4.
InterPro; IPR002942; S4.
InterPro; IPR002709; S4_bact_org.
Pfam; PF0013; Ribosomal_S4; 1.
SMART; SM00363; S4; 1.
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SEQUENCE
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PROSITE; P
Ribosomal
                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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EMBL; Z68233; CAA92531.1; -.
EMBL; Z68232; CAA92530.1; -.
HSSP; P81288; 1C05.
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Souza-Chies T.T., Bittar G., Nadot S.,
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HSSP; P81288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=58983,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lejeune B.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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7; Conserv
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182
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182
; 21054 MW;
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                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carter L.,
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RESULT 12
RR4_BABST
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                                                                                                                                                                                                                                                                                                                                                                                        Phylogenetic analysis of Iridaceae with parsimony and distance methods using the plastid gene rps4.";

Le plant Syst. Evol. 204-109-123 (1997).

C -!- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the body of the 30S subunit (By similarity).

C -!- FUNCTION: With S5 and S12 plays an important role in translational accuracy (By similarity).

C -!- SUBUNIT; Part of the 30S ribosomal subunit. Contacts protein S5.

The interaction surface between S4 and S5 is involved in control of translational fidelity (By similarity).

C -!- SUBCELLULAR LOCATION: Chloroplast.

-!- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 7
EMBL; Z68234; CAA92532.1; -.
HSSP; P81288; 1C05.
HAMAP; MF_01306; -; 1.
InterPro; IPR001912; Ribosomal_S4.
InterPro; IPR002942; S4.
InterPro; IPR005709; S4_bact_org.
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019995;
15-DEC-1998
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Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
Babiana.
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InterPro; IPR005709; S4 bact org
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOUZA-Chies T.T., Bittar G., Nadot S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=58942;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast 30S ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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InterPro; IPR001912; Ribosomal_S4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 AA;
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183
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Conservative 0; Misma
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                                                                                                                                                                                                                agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S4 RNA-BINDING
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methods using the plastid gene rps4";

L Plant Syst. Evol. 204:109-123(1997).

C -!- FUNCTION: One of the primary rRNA binding proteins, it binds
directly to 16S rRNA where it nucleates assembly of the body of
the 30S subunit (By similarity).

C -!- FUNCTION: With S5 and S12 plays an important role in translation
accuracy (By similarity).

C -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5.
The interaction surface between S4 and S5 is involved in control
of translational fidelity (By similarity).

C -!- SUBCELLULAR LOCATION: Chloroplast.

C -!- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                     EMBL; Z68237; C
EMBL; Z68241; C
EMBL; Z68246; C
HSSP; P81288; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RR4_CRONU STANDARD; PRT; 183 AA.
020100; O20216; O20261;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein S4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal
NON_TER
DOMAIN
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR01017; rpsD_bact; 1.

PROSITE; PS00632; RIBOSOMAL_S4; 1.

PROSITE; PS50889; S4; 1.

Ribosomal protein; RNA-binding; rRNA-binding; Chloroplast.
                                                  HAMAP; MF_01306;
                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Souza-Chies T.T., Bittar G., Nadot S., Carter L., Besin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Micranthus juncus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gladiolus communis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crocus nudiflorus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00163; Ribosomal_S4; 1. Pfam; PF01479; S4; 1.
SSP; P81288; 1....

LAMAP; MF_01306; -; 1.

LINTERPRO; IPR001912; Ribosomal_S4.

INTERPRO; IPR002942; S4.

INTERPRO; IPR005709; S4_bact_org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ejeune B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
183
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                                                                                 CAA92535.1; -.; CAA92539.1; -.; CAA92544.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58992,
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183
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100.0%; Pred. No. 4.:
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S4 RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A7ADD354908BEAD3
                                                                                                                                                                                                                                                                                                                                                                          an important role in translational
                                                                                                                                                           (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 183;
                                                                                                                                                                                                                                                                                                                              is involved in control
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RESULT 14
RR4_CROSP
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RR4 CROSP
020103;
15-DEC-1998
15-DEC-1998
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                     Pfam;
                                                                                                                                                                                                                                                      accuracy (By similarity).

-!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5.

The interaction surface between S4 and S5 is involved in control of translational fidelity (By similarity).

-!- SUBCELLULAR LOCATION: Chloroplast.

-!- SIMILARITY: Contains 1 S4 RNA-binding domain.

-!- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                    methods using the plastid gene rps4.";
Plant Syst. Evol. 204:109-123(1997).
-!- FUNCTION: One of the primary rRNA binding proteins,
directly to 16S rRNA where it nucleates assembly of
the 30S subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Schiza-Chies T.T., Bittar G.,
                                                                                     EMBL; Z68236; CAA92534.1;
HSSP; P81288; 1C05.
HAMAP; MF 01306; -; 1.
                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                           the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Uentities requires a license agreement (See httentities requires a license agreement)
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00363; S4; 1
TIGRPAMS; TIGRO1017; rpsD_bact;
PROSITE; PS00632; RIBOSOWAL_S4;
PROSITE; PS50889; S4; 1
                         Ptam,
                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: With S5 and S12 plays an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=58948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast
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                                                    InterPro; IPR005709;
                                                                InterPro; IPR002942;
                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Phylogenetic analysis of Iridaceae with
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lejeune B.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crocosmia
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                      PF00163; Ribosomal S4; PF01479; S4; 1.
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7; Conserv
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                                                                             IPR001912; Ribosomal_S4
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183 /
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation updat
30S ribosomal protein S4 (Fragm
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                                                                                                                                                                                                                                                                                                                                                                                                             plastid gene rps4.";
204:109-123(1997).
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183
; 21138 MW;
                                             S4_bact_org.
                                                                S4.
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100.0%; Pred. No.
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). 4.3;
                                                                                                                                                             (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                          important role in translational
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                                                                                                                                                                                          its content
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TIGR01017;

rpsD_bact; 1

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Best Local Similarity
Thes 7; Conserva
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PROSITE; P
PROSITE; P
Ribosomal
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DOMAIN
NON TER
SEQUENCE
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020215;
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-!- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 165 rRNA where it nucleates assembly of the body of the 305 subunit (By similarity).
-!- FUNCTION: with S5 and S12 plays an important role in translational accuracy (By similarity).
-!- SUBUNIT: Part of the 305 ribosomal subunit. Contacts protein S5.
The interaction surface between S4 and S5 is involved in control
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15-DEC-1998
15-DEC-1998
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Souza-Chies T.T., Bittar G., Nadot S., Carter L., Besin E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: Contains 1 S4 RNA-binding domain.
SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 KRPRSGS 23
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PS50889; S4; 1.
protein; RNA-binding; rRNA-binding; Chloroplast.
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183
183 AA;
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
30S ribosomal protein S4 (Fragment).
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183
; 21124 MW;
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Matches 7
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NON TER
SEQUENCE
17
                40
                                  l Similarity
7; Conserv
KRPRSGS 23
                KRPRSGS 46
                                                                     183 AA;
                                                                           183
                                 14.3%; Score 7; DB ilarity 100.0%; Pred. No. 4. Conservative 0; Mismatches
                                                                    143
183
21143
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                                                                                      S4 RNA-BINDING
                                                                     A7B96C19B1CF3763 CRC64;
                                           DB 1;
). 4.3;
                                   <u>.</u>
                                                   Length 183;
                                   Indels
                                   0
                                   Gaps
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Search completed: July 24, 2003, 12:22:11 Job time: 4.2284 secs

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Regult
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
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sp_bacteriap:*
sp_archeap:*
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
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sp_phage:*
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Q96CH9
Q91LH6
Q92ZV9
Q9WKP7
Q8WKP7
Q8WKP5
Q8WKA5
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Q8WL414
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OBN444 homo sapien
OSOLO sapien
OSULH6 homo sapien
OSULH6 homo sapien
OSULH6 homo sapien
OSULTO rhizobium m
OSOKOT zephyra ele

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Q96CH9
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Q8N4Y4
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Q8p410 xanthomonas	xant	Q9p110 homo sapien	m	w	ь	0	Q9tjw8 dioscorea b	laurus	alism	Q9tjx7 arum italic	sagitta	Q9tjw1 musa x para		typha a	Q9tjx2 costus luca	elettar					Q8wkq1 watsonia an	٠.		_	ixia	6 olsynium	galax	Q8wkv7 orthrosanth

ALIGNMENTS

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SEPPPRE
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Best Local Similarity 100.0%;
Matches 49; Conservative 0;
Q96CH9 PRDATE...
Q96CH9;
Q96CH9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBN4Y4;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
5imilar to KIAA1244 protein (Fragment).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC033191; AAH33191.1; -.
NON TER 1
SEQUENCE 589 AA; 66086 MW; 8041EEA348DE65F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                               464 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 512
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                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 4; Length 589; Pred. No. 2e-42;
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RESULT 4
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Q9ULH6
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Best Local S
Matches 49
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Best Local S
Matches 49
                                                                  Q92ZY9;
Q92ZY9;
Q92ZY9;
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical transposase, partial match.
RA0339 OR SMA0643.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Plasmid pSymA (megaplasmid Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
                      SEQUENCE FROM N.A. STRAIN=1021;
                                                                                                                                                                                                                                                                                                                                                          Q92ZV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "KIĀA1244 as a novel distantly related member (BIG3) of the BIG1/Sec7p subfamily of AFF GEFs.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413080; AAL04174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ULH6; Q96P46;
01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
NON_TER
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MEDLINE=21396509; PubMed=11481432;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1770 AA;
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Primates;
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22,
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 4; 1
Pred. No. 5.3e-42;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49;
Pred. No.
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RESULT 6
Q8WKQ0
ID Q8WK
AC Q8WK
DT 01-M
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DT 01-M
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Q8WKP7
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Matches
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Best Local
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Q8WKQ0;
01-MAR-2002
01-MAR-2002
01-MAR-2003
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                            regions.";
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Tecophilaeaceae; Zephyra.
                                                Q8WKQ0
                                                                                                                                                                                                                                                                          InterPro; IPR005709; S4_bact_org
Pfam; Pf00163; RibosomaI_S4; 1.
Pfam; Pf01479; S4; 1.
SMART; SM00363; S4; 1.
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                                                                                                                                                                                                                                       Chloroplast.
                                                                                                                                                                                                                                                   TIGRFAMS; TIGR0101 PROSITE; PS00632;
                                                                                                                                                                                                                                                                                                                                 EMBL; AJ409052; CAC83931.1; -.
InterPro; IPR001912; Ribosomal_S4
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                                                                                                                               KRPRSGS 46
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174 AA;
 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                     14.3%; Score 7; DB ilarity 100.0%; Pred. No. 21 Conservative 0; Mismatches
                                                PRELIMINARY;
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174
; 19912 MW;
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RIBOSOMAL_S4;
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100.0%;
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s T.;
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                     96BF6433CBCBF3B5 CRC64;
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5. 11;
                                                                                                                                                                   DB 8;
                                                                                                                                                                             Length 174;
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update)

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RESULT 7
Q8WKRS
ID Q8WKRS
AC Q8WK
DT 01-M
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Best Local S
Matches 7
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InterPro; IPR002942; S4.
InterPro; IPR002942; S4. bact_org.
InterPro; IPR005709; S4 bact_org.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
ITIGRPAMS; TIGR01017; TPSD_bact; 1.
PROSITE; PS00632; RIBOSOMAL_S4; 1.
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NON_TER
SEQUENCE
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Am. J. B
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Spermatophyta; Magnoliophyta;
Tecophilaeaceae; Tecophilaea.
NCBI_TaxID=49737;
                       NON_TER
                                                                   TIGRFAMS; TIGR010
PROSITE; PS00632;
Chloroplast.
                                                                                                                                   EMBL; AJ409049; CAC83928.1; ...
InterPro; IPR001912; Ribosomal_S4.
InterPro; IPR002942; S4.
InterPro; IPR005709; S4 bact_org.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
                                                                                                                                                                                                                                                                                                  regions.";
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Reeves G., Chase M.W., Goldblatt P.,
Lejeune B., Souza-Chies T.;
"Molecular systematics of Iridaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tecophilaea cyanocrocus.
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01-MAR-2003
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EMBL; AJ409048; CAC83927.1; -.
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Reeves G., Chase M.W., (
Lejeune B., Souza-Chies
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                                                                                   1479; S4; 1.
TIGR01017; rpsD_bact;
PS00632; RIBOSOMAL_S4;
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2 (TrEMBLrel. 20, Last s
3 (TrEMBLrel. 23, Last a
protein S4 (Fragment).
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174
174 AA;
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174 AA;
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  19906 MW;
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yta; Liliopsida; Asparagales;
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  7A8B2A7389B1F26F CRC64;
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RESULT 8
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ID COWL48
AC QOWL
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Best Local S
Matches 7
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Best Local
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Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
TICRFAMB; TICRO1017; rpsD bart.
PROSITE: PROACCA
                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 20, Last sequence update) Ribosomal protein S4 (Fragment).
                                                                                                                                                                                                                                                Q8WKS8; PRELIMINARY;
Q8WKS8; Q1-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
Syringodea.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                     Syringodea bifucata.
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Lejeune B., Souza-Chies T.;
"Molecular systematics of Iridaceae:
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Chloroplast.
SEQUENCE FROM N.A.
Reeves G., Chase M.W., C
Lejeune B., Souza-Chies
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InterPro; IPR002942; S4.
InterPro; IPR005709; S4 bact org.
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SMART; SM00363; S4; 1.
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Lejeune B., Souza-Chies T.;
"Molecular systematics of Iridaceae:
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01-MAR-2003 (TrEMBLrel. 23, Last
Ribosomal protein S4 (Fragment).
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Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
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Am. J. Bot. 88:2074-2087(2001)
EMBL; AJ409026; CAC83844.1; -.
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Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
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EMBL; AJ409022; CAC83795.1; -.
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PROSITE; PS00632; RIBOSOMAL_S4; 1.
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InterPro; IPR002942; S4.
InterPro; IPR005709; S4 bact_org.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
SMART; SN00363; S4; 1.
TIGRFAMG; TIGR01017; TPSD_bact; 1.
PROSITE; PS00632; RIBOSOMAL_S4; 1.
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Q8WL25; CPEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
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Interpro; IPR002942; S4.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
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Lejeune B., Souza-Chies T.;
"Molecular systematics of Iridaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regions.";
Am. J. Bot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reeves G., Chase M.W.,
Lejeune B., Souza-Chie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solenomelus pedunculatus. Chloroplast.
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Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
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EMBL; AJ409038; CAC83920.1; -.
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EMBL; AJ409019; CAC79546.1; -.
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s T.;
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InterPro; IPR002942; S4.
InterPro; IPR005709; S4. bact org.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
ICREPAMS; TIGR01017; rpsD bact; 1.
PROSITE; PS00632; RIBOSOMĀL_S4; 1.
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OBWL41;

OBWL41;

OHM241;

O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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QBWL34;
QBWL34;
Q1-MAR-2002 (TrEMBLrel. 20, Last ol-MAR-2003 (TrEMBLrel. 23, Last ol-MAR-20
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Gynandriris sisyrinchium.
                            Spermatophyta; Magnoliophyta; Ferraria.
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Eukaryota; Viridiplantae;
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Reeves G., Chase M.W., Goldblatt P.,
Lejeune B., Souza-Chies T.;
"Molecular systematics of Iridaceae:
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Reeves G., Chase M.W., Go?
Reieune B., Souza-Chies T
Freieune B., Svatematics of
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
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pfam; PF00163; Ribosomal_S4; 1.
pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
TIGRFAMs; TIGR01017; rpsD_bact; 1
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PROSITE; PS00632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Reeves G., Chase M.W.,
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RIBOSOMAL_S4;
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Search completed: July 24, 2003, 12:25:54 Job time: 17.0659 secs

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pland is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB DB
                                                                                                                                                                                                            Score
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        260
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length: 2000000000
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Match
        100.0
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260
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986_DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/geneseq/geneseqp-embl
/SIDS1/gcgdata/geneseq/geneseqp-embl
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1807
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1982
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        22323333233
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                         AAO19169
AAM50813
AAW85472
AAO19165
AAM50809
ABG09728
ABP64835
ABP64835
                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488.334 Million cell updates/sec
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/AA1987.DAT:*
                                                          Human prostate-spe
PS118 prostate mar
PS118 protein enco
Human prostate-spe
PS118 prostate mar
Novel human diagno
                                                                                                                                                                                                        Description
                           Human
Novel
8 protein enco
n prostate-spe
8 prostate mar
1 human diagno
n protein SEQ
1 human diagno
1 human secret
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Mutated thymidylat	AAW75762	. 19	313	21.7	56.5	•
Mutated thymidylat	AAW75761	19	313	21.7	56.5	_
	AAW75760	19	313	21.7		_
	AAW75759	19	313	21.7	٥,	
	AAW75758	19	313	21.7	٥.	•
	AAW75757	19	313	21.7	σ	Ŭ
	AAW75756	19	313	21.7	٥.	_
Mutated thymidylat	AAW75755	19	313	21.7	٥.	_
Human thymidylate	ABP53743	23	284	21.7	٥,	_
human	ABG20773	22	189		56.5	٠,
human	ABG23688	22	558	۲.	57	٠.
prote	AAM79977	22	514		57	_
prote	AAM78993	22	495		57	_
acid	AAY69392	21	485	21.9	57	
-	AAY69385	21	485	۲.	57	
	ABG27597	22	331	۲	57	Ŭ
Human foetal prote	AAM06884	22	152		57	•
Encoded by human G	AAR28992	13	83	21.9	57	_
Arabidopsis thalia	AAG10797	21	79	۲.	57	`
	AAG61469	21	71		57	٠,
ç	AAW75754	19	313		57.5	٠.
Mutated thymidylat,	AAW75752	19	313	2	57.5	_
Human NF-ATc1/C pr	ABP96278	24	930	٢	58	_
Drosophila melanog	ABB60011	22	3429	2	58.5	
Human immune/haema	AAM84901	22	54	2	58.5	
Propionibacterium	AAU66156	22	122	2	59	_
Human translocatio	ABG95113	23	2004		59.5	•
	ABP73759	23	1671	ω.	60	_
O	AAB87657	22	87	·	62	7
human di	ABG22251	22	171	.4	63	٠.
pride	ABG43753	23	70	24.2	63	٠.
de #80	AAM34047	22	70			_
bone n	AAM73865	22	70	Α.		-
ain ex	AAM61151	22	70	4.		
de #7852 en	034	22	70	Α.	ప	_
Human liver peptid	ABG55616	22	70	24.2	63	_

ALIGNMENTS

RESULT 1 AAO19169

AAO19169;

AAO19169 standard; Protein; 49

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(BILL/)
(COHE/)
(COLP/)
(FRIE/)
(GORD/)
        (GRAN/)
(HODG/)
                                                                                                                       04-JUL-2002.
                                                                                                                                                       Homo sapiens
                                                                                                                                                                      Human; prostate; prostate-specific sequence; prostate cancer; PS118; EST; expressed sequence tag; cytostatic; gene therapy.
                                                                                                                                                                                                                 27-NOV-2002 (first entry)
                                                                             23-APR-1998;
23-APR-1997;
                                                                                                      26-NOV-2001; 2001US-0991681.
                                                                                                                                      US2002086316-A1.
                                                                                                                                                                                                Human prostate-specific PS118 protein fragment
COHEN M.
COLPITTS T L.
FRIEDMAN P N.
GORDAN J.
GRANADOS E N.
HODGES S C.
KLASS M R.
                                                           BILLINGEL P A.
                                                                            98US-0065383.
97US-0842385.
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RESULT 2
AAM50813
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Best Local S
Matches 49
                                                                                                                                                                                                                                                     PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
Billing-Medel
Granados EN,
                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                              PS118 prostate marker immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                    01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                           AAM50813 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-665429/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Granados EN, Russell JC,
                                                                                                                                                                       23-APR-1998;
                                                                                                                                                                                            27-DEC-2001
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(RUSS/)
(STRO/)
                                                                (GORD/)
(GRAN/)
(HODG/)
                                                                                                                                                   23-APR-1997;
                                                                                                (FRIE/)
                                                                                                                              (BILL/)
                                                                                                                    COHE/)
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                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                             COPLPITTS T L.
FRIEDMAN P N.
                                                     GORDON J.
GRANADOS E N.
HODGES S C.
KLASS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRATOCHVIL J
ROBERTS-RAPP
RUSSELL J C.
STROUPE S D.
                                  KRATOCHVIL J
ROBERTS-RAPP
                                                                                                                               BILLING-MEDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                              EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Cohen
, Hodges
Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,
    PA, Cohen
Hodges SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                    97US-0842385
                                                                                                                                                                       98US-0065383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58pp; English.
                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                  r o
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    M, Coplpitts TL, Friedman Klass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colpitts T. Klass MR,
                                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 260; DB 23;
Pred. No. 1.5e-28;
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Kratochvil
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   PN, Gordon J
Roberts-Rapp
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Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                               49
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RESULT 3
AAW85472
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Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of an immunogenic polypeptide comprising amino acids 39.441 of human prostate-specific PS118 polypeptide (see AM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, antibodies, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benjgn prostateic hyperplasia, prostaticits, for prostate, such as benjgn prostateic hyperplasia, prostaticits, for prostate, such as benjgn prostateic hyperplasia, prostaticits, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
                                         Billing-medel PA,
Granados EN, Hod
Russell JC, Stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
WPI; 1998-610000/51.
N-PSDB; AAV82812.
                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                           AAW85472;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAW85472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 44; 57pp;
                                                                                                                                     23-APR-1997;
                                                                                                                                                                                                                            WO9848054-A1
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                  PS118 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                without the use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Russell JC,
                                                                                                      (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-187683/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              μ,
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49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       standard; Protein; 518
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ilarity 100.0%;
Conservative (
                                            Hodges
Stroupe
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                                                                                                                                                                                                                                                                                                                                              (updated) .
(first entry)
                                                                                                                                                                                                                                                                                                                  encoded by consensus sequence
                                                                                                                                     97US-0842385
                                                                                                                                                                  98WO-US08239
                                                                                                                                                                                                                                                                                   prostate tumour tissue; prostatic
                                           Cohen M, Colpitts TL, es SC, Klass MR, Krat pe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 260; DB 23;
Pred. No. 1.5e-28;
; Mismatches 0;
                                                          s TL, Friedman
Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                      disease;
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New P118 nucleic acid and

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prostatic

and proteins -disease, espec

ins - used for diagnosis and especially cancer, and also

for gurb

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RESULT 4
AAO19165
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Best Local
                  Billingel
Granados E
Russell JO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a cDNA library made from prostate tumour tissue. Recombinant PS118 protein is used to detect PS118 specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of used for detection, diagnosis, staging, monitoring and prognosis of potential constatic disease, particularly cancer, and to identify subjects at
                                                                                                                      (BILL/)
(COHE/)
(COLP/)
(FRIE/)
(GORD/)
(GORD/)
                                                                                                                                                                                              23-APR-1998;
23-APR-1997;
                                                                                                                                                                                                                             26-NOV-2001; 2001US-0991681.
                                                                                                                                                                                                                                                 04-JUL-2002
                                                                                                                                                                                                                                                                      US2002086316-A1
                                                                                                                                                                                                                                                                                                           Human; prostate; prostate-specific sequence; persence; persence tag; cytostatic; gene
                                                                                                                                                                                                                                                                                                                                          Human prostate-specific PS118 protein fragment #1.
                                                                                                                                                                                                                                                                                                                                                                27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                     AAO19165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page
                                                                                          (KLAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on
                                                                               ROBE/)
                                                                                                              (HODG/)
2002-665429/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                           393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                          COLPITTS T L.
FRIEDMAN P N.
GORDAN J.
GRANADOS E N.
HODGES S C.
              PA,
EN,
JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>بــر</u>
                                                                             KLASS M R.
KRATOCHVIL J
ROBERTS-RAPP
                                                           RUSSELL
STROUPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                               COHEN
                                                                                                                                                                         BILLINGEL P A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
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ilarity 100.0%;
Conservative (
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                   Stroupe
                             Cohen
Hodges
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                                                                                                                                                                                             98US-0065383
97US-0842385
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                                                                                                                                                                                                                                                                                                                                                               entry)
                   SC,
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                             Colpitts TL,
Klass MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 260; DB 19;
Pred. No. 2.4e-27;
; Mismatches 0;
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                             Kratochvil
                                                                                                                                                                                                                                                                                                                      prostate
                                                                                                                                                                                                                                                                                                             therapy
                             JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                            Gordan J;
Roberts-Rapp
                                                                                                                                                                                                                                                                                                                      cancer;
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RESULT 5
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                                                                                                  Billing-Medel
Granados EN,
Russell JC, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a number of prostate-specific sequer derived from the human PS118 gene. These can be used in the detection monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                   Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                                                                                                                                                           PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
                                                                                                                                                                                                                  (BILL/)
(COHE/)
(COPL/)
(FRIE/)
                                                                                                                                                                                                                                                                                                    23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 42-43;
                                                                                                                                                                                                                                                                             23-APR-1997;
                                                                                                                                                                                                                                                                                                                                                  US2001055758-A1
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PS118
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                                                                                                                                                                                              (GRAN/)
                                                                                                                                                                                                          (GORD/)
                                                                                                                                                                       KLAS/
                                                                                                                                                                                   HODG/
                                                                   2002-187683/24.
DB; ABA91651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393
                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate marker partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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                                                                                                                                                                              GORDON J.
GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                 ROBERTS-RAPP
                                                                                                                                                                                                                  COPLPITTS T L
FRIEDMAN P N.
                                                                                                                                                                                                                                                     BILLING-MEDEL P
                                                                                                                                                           KLASS M R.
KRATOCHVIL J
                                                                                                                                                                                                                                            COHEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                    Stroupe
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                                                                                                             Hodges
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es SC,
pe SD;
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                                                                                                              M, Coplpitts TL, Friedman
Klass MR, Kratochvil JD,
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Pred. No. 2.4e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate-specific sequences be used in the detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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                                                                                                                          PN,
                                                                                                              Roberts-Rapp
                                prognosticating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518;
                                                                                                                         Gordon J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate than in non-prostate tissue. PSIME polypeptides, including derivatives of the present sequence, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the prostate, such as benign prostatic hyperplasia, prostatitis, prostate, such as benign prostatic hyperplasia, prostatitis, and prostatic intraepithelial neoplasia, prostate cancer, tumours and metastases. The PSIME polypeptides can be produced by expression of PSIME polynucleotides in transfected host cells. The methods and reagents of the invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo plants of the primers of 
                                                                                                                                       Claim 20;
                                                                                                                                                                                             biodiversity
                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutatesponsible for genetic disorders or other traits and to asse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                       2001-639362/73.
DB; AAS73915.
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                                                                                                                                    SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic protein #9719.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
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                                                                                                                                 40087; 103pp; English.
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Pred. No. 2.4e-27;
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                                                                                                                                                                                                                                                   mutations
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags cc for identifying expressed genes. (II) is useful in gene therapy techniques cc (II). (II) is useful in generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as cc a food supplement. (II) and its binding partners are useful in medical cl imaging of sites expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. Cc The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and cc produce other types of data and products dependent on DNA and cc amino acid sequences. ABG00010-ABG30377 represent novel human cc diagnostic amino acid sequences of the invention.
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Best Local S
Matches 49
                                                                                                             WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                  antiallergic; antiinflammatory; immunosuppressive; neuroprotective cytostatic; haemostatic; virucide; antibacterial; fungicide; immunostimulant; cerebroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; fungal infection; autoimmune disorder; coagulation disorder; nootropic;
                                             New isolated polynucleotide, useful in research, diagnostic therapeutic methods, e.g. preventing or treating disorders i aberrant protein expression or biological activity -
                                                aberrant
                                                                                                                                                                                                                                                                                 16-NOV-2001; 2001WO-US42950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                17-NOV-2000; 2000US-0714936
                                                                                                                                                                                                                                                                                                                                                   WO200259260-A2
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
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                                                                                                               2002-590824/63
DB; ABQ99421.
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                                                                                                                                                                , Goodrich RW,
Xue AJ, Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                              Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                Liu
                                                                                                                                                                  iu C, Zh
Wehrman
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Pred. No. 1.1e-26;
; Mismatches 0;
                                                                                                                                                                Zhou P, Asundi V,
an T, Drmanac RT;
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Claim

20; SEQ

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495;

394pp; English

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CC mapping of the human genome. The proteins may be used as molecular weight commarkers, or as nutritional sources or supplements. The proteins may be used as molecular weight commarkers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or cC pluripotential state useful for re-engineering damaged or diseased cC tissues, transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The polynucleotides and proteins are useful for preventing, treating or ameliorating disorders involving aberrant cC protein expression or biological activity, e.g. haematopoietic disorders, central/peripheral nervous system diseases, mechanical and traumatic cdisorders, non-healing wounds, immune deficiencies and disorders, cC infectious diseases caused by viral, bacterial or fungal infection, cC autoimmune disorders, allergic reactions and conditions, coagulation cC assembled from ESTs isolated mainly by sequences of the invention were assembled from ESTs isolated mainly by sequencing by hybridisation, and consecutions, but was obtained from one or more public databases.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO are from wipo introublehed for sequences.
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Best Local :
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The polynucleotides are useful in diagnostics as expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel human coding sequences (ABQ99268-ABQ99608) and proteins (ABP64682-ABP65022). The sequence useful in therapeutic, diagnostic and research methods. The polynucleotides may be used in the field of molecular biology as
                                                                                                                                                                                           WPI; 2001-639362/73.
N-PSDB; AAS73918.
                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forension supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #9722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG09731 standard; Protein; 1982 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1714 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                         RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Pred. No. 1.1e-26;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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The invention relates to novel human secreted polypeptides.

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RRESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for identifying expressed genes. (1) is useful in gene therapy techniques (1) or restore normal activity of (II) or to treat disease states involving (II) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations (1) and to produce other types of data and products dependent on DNA and (2) and to produce other types of data and products dependent on DNA and (2) and to produce other types of data and products dependent on DNA and (2) and to sequences. ABG00010-ABG30377 represent novel human (2) apecification, but was obtained in electronic format directly from WIPO (2) specification, but was obtained in electronic format directly from WIPO (2) apecification, but was obtained in electronic format directly from WIPO
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags polynucleotides.
                                                            Claim 20; Page 548-549; 765pp; English
                                                                                                                            Nucleic acids encoding a range or vaccination, testing and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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26-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1982 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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2001US-0770160.
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                                                                                                                                                              range of human polypeptides, useful in
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Pred. No. 1.2e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                 genetic
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RESULT 10
ABG55616
ID ABG55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Sim
Matches 18;
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-02345359.
04-OCT-2000; 2000GB-0024263.
The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult
                                                                                                                                                                                Claim 27;
                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful analysing gene expression in human adult liver - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human liver peptide, SEQ ID No 34264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG55616 standard;
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                                                                                                                                                                                                                                                                                                                                   2001-488898/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKNGQGEPAVVRCSHLL----VKHSQSRRPSSWRQEKITRTKGGGPGS
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                                                                                                                                                                                SEQ
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                                                                                                                                                                             No 34264; 658pp; English
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                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
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0.44;
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Query Match

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Score

63; BB

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Length

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RESULT 11
ABB40346
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct secmences
                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes mapples derived from human measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
Sequence
                                                       Note:
                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                Claim 27; SEQ
                                                                                                                                                                                                             analyzing gene expression
                                                                                                                                                                                                                                                                                         Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #7852 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB40346
                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
                                                                                                                                                                                                                                                                                                                       (MOLE-)
                             WIPO
                                                                                                                                                                                                                                                           2001-483447/52
                                                                                                                                                                                                                                                                                         SG,
                         The sequence data for this patent did not form part of the ed specification, but was obtained in electronic format dir WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful zing gene expression in human fetal liver -
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19; Conserv
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                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPGQ-----QQPPHLHHRGGRRHSEAVHSHRPGPGVRIHLQAVRQDEAGLGGATG
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70 AA;
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                                                                                                                                                                                                                                                                                                                                                ; 2000US-0180312.

2000US-0207456.

; 2000US-0608408.

; 2000US-0632366.

; 2000US-0234687.

; 2000US-0236359.

; 2000US-0236359.
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                                                                                                                                                                               ID NO 32981; 639pp + sequence listing; English
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                                                                                                                                                                                                                                                                                         Chen W,
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; Pred. No. 0.48;
7; Mismatches
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                                                                                                                                                                                                                                                                                         Rank DR;
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                                            format directly
                                                                                      a single exon
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RESULT 13
AAM73865
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                                                                                                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                              Penn
              AAM73865 standard; Protein;
                                                                                                                       Sequence
                                                                                                                                                                                                    Example 4; SEQ ID NO: 33256; 650pp + Sequence Listing; English
                                                                                                                                                                                                                             Single exon nucleic acid probes
                                                                                                                                                                                                                                               WPI; 2001-483446/52
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                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                    microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human brain
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                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                       70 AA;
                                                                                                                                       of the invention.
                                                                                                                                                                                                                                                                                            ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632368.
; 2000US-0632368.
; 2000US-0234687.
; 2000US-0234685.
; 2000US-0236359.
                                                                                      Conservative
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                                                      -OOPPHLHHRGGRRHSEAVHSHRPGPGVRIHLQAVRQDEAGLGGATG
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                                                                                      Mismatches
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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30-JAN-2001; 2001WO-US00663.
                                             09-AUG-2001
                                                                                                                                                                        Probe; microarray; human; placenta; antenatal diagnosis genetic disorder.
                                                                                                                                                                                                                                     Peptide #8084 encoded by probe
                                                                                                                                                                                                                                                                                17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                        AAM34047 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
27-SEP-2000;
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microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                     WO200157272-A2
                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; SEQ ID NO: 34171; 658pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; DB 2
Pred. No. 0.48;
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RESULT 15
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Best Local Similarity
                  04-FEB-2000; 2000US-180312P.
26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-236359P.
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-02346359.
04-OCT-2000; 2000GB-0024263.
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                              chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease;
                                                                                                                                                                                                                                                                                                                                                                                                        Human peptide encoded by genome-derived single exon probe SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG43753 standard; Peptide; 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta -
                                                                                                                              30-JAN-2001; 2001WO-US00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRGQDSPLLQRPQHLMDQGQMRHSFSA-----GP-----ELLRQDKRPRSGSTG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID No 34316; 654pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 AA;
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Pred. No.
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Search completed: July 24, Job time: 16.9268 secs

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                                                                                                                                                                                                            CC probes: Also included are a microarray comprising the movel set of probes; the novel set of probes which hybridise at high stringency to a conucleic acid expressed in the human lung; measuring gene expression in a CC sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung (comprising (a)) contacting the array with CC mRNA, and (b) measuring the labeled nucleic acids derived from human lung comprising (a) algorithmically predicting at least one exon from genomic sequences (c) in the enkaryote; and (b) detecting specific hybridisation of detectably comprising (a) identifying exons from genomic sequences (c) having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, (c) tissues and/or cell types using hybridisation to a single exon in several (c) tissues and/or cell types using hybridisation to a single exon (c) microarrays having a probe with the exon, where a common pattern of (c) expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one (c) floors and the probed are used for gene (c) the exons and for identifying exons in a gene, particularly (c) using human lung derived mRNA and for the study of lung diseases (COPP), interstitial lung diseases (ILD), familial idiopathic pulmonary disease, nulmonary harmansky-Pudlak syndrome, sarcoidosis, pulmonary concert, chronic obstructive pulmonary disease, pulmonary harmansky-Pudlak syndrome, sarcoidosis, pulmonary h
                                                                                                  Query Match
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Matches 19
                                                                                                                                                                                                                                                                                                                                    haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a spatially-addressable set of single exception in a sample derivation comprise for measuring gene expression in a sample derivation human lung comprising single exon nucleic acid probes having 12614 nucleic acid sequences mentioned in the specification, or the complements or the 12387 open reading frames derived from the 1260.
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                     of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measure gene expression in human
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                                                                                                       Conservative
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                                                                                                  Score 63; DB 2:
Pred. No. 0.48;
7; Mismatches
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
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                                                                                       US-09-065-383-31

US-09-065-383-27

US-09-252-991A-21596

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US-09-252-991A-28435

US-09-252-991A-28436

US-09-252-991A-28987

US-09-252-991A-28917

US-09-252-991A-2817

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US-09-258-912A-2
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-252-991A-21250
-252-991A-16841
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Sequence
31, Appl
17975, A
24059, A
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	55	55	55	55.5	55.5	56	56	56
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US-09-392-277-27	US-09-031-563-27	US-09-258-000-5	US-09-392-277-5	US-09-031-563-5	US-09-258-000-7	US-09-392-277-7	US-09-031-563-7	US-09-252-991A-26578	US-09-252-991A-20600	US-09-369-364A-13	US-09-252-991A-31707	US-09-252-991A-24066	US-09-252-991A-30367	US-09-252-991A-23002	US-09-252-991A-17304	US-09-252-991A-17206	US-09-252-991A-23495
Sequence 27, Appl	Sequence 27, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 26578, A	Sequence 20600, A	Sequence 13, Appl	Sequence 31707, A	Sequence 24066, A	Seguence 30367, A	Sequence 23002, A	Sequence 17304, A	Sequence 17206, A	Sequence 23495, A

ALIGNMENTS

ID NO: 31: RISTICS: No acids	TELEX: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 49 amino acids	
847/935-1729 7/938-2623	TELEPHONE: 847/935-17 TELEFAX: 847/938-2623	
، ت	REFERENCE/DOCKET NUMBER:	
neryl L. 3ER: 35,441	NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35.	
INFORMATION:	۲	٠
MBER: U8/842,385 23-APR-1997	APPLICATION NUMBER: 23-AP	
70.10	PRIOR APPLICATION DATA:	
	CLASSIFICATION:	
3R: US/09/065,383	APPLICATION NUMBER:	
SQ FOR WINDOWS VERBION 2:0	CURRENT APPLICATION DATA:	
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FOR DETECTING DISEASE	TITLE OF INVENTION:	٠.
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RUSSELL, JOHN C.	APPLICANT: RUSSELL.	
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MICHAEL R.		٠.
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OS, EDWARD N.	••	٠
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IS, TRACER L.	APPLICANT: COLFITTS,	
ORICE	••	٠.
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: N
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Best Local Similarity
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                                                                                                                                   SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: R
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
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APPLICANT:
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                                                                                                                                                                                               NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/8
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 100.0%; Score 260; DB 4; Local Similarity 100.0%; Pred. No. 6.5e-30;
                                                                                                                                                                                   TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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T: 100 Abbott Park Road
Abbott Park
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RUSSELL, JOHN C.
STROUPE, STEPHEN D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BILLING-MEDEL, PATRICIA
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KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
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                                                                             linear
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                                                          No. 6391543e
                                                                                     single
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100.0%;
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Score 260; DB 4;
Pred. No. 1.1e-28;
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              Length 518;
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; Sequence 17975, Application US/09252991A
; Patent No. 6551795
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FELLORION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US/60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17975

LENGTH: 309

TYPES: USF
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LENGTH: 693
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Best Local Similarity
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                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa -09-252-991A-24059
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FAPPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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NUMBER OF SEQ ID NOS:
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370 HRPPS 374
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                                         KRPRS 44
                                                                                  PLASRGOREGULORARTLAAEGRRAHSRPTLESAPETADVTVSHFLGDTFDGHPRVAQQA 369
                                                                                                                       PLGPRGQDSPLLQRPQHLMDQGQMRHS-----
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nilarity 29.2%;
Conservative
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RESULT 7
US-09-252-991A-28435
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US-09-252-991A-21596
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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GENERAL INFORMATION:
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LENGTH: 501
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Patent No. 6551795
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                                                                                                                         GENERAL INFORMATION:
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 504
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48.3%;
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BER: US 60/074,788
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Pred. No. 0.55;
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Pred. No.
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US-09-252-991A-18380
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18380
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LENGTH: 567
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                     NUMBER OF SEQ ID NOS:
SEQ ID NO 28987
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       Sequence 28987, Ap
Patent No. 6551795
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                                                                             PRIOR FILING DATE: 1998-02-10
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION 1998-07-27
                                                                                                                                                                    FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                    PRIOR APPLICATION NUMBER:
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
                                       LENGTH:
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                        UMBER: US 60/074,788
1998-02-18
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64.7%;
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Pred. No. 0.
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RESULT 12
US-09-252-991A-28444
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LENGTH: 297
TYPE: PRT
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Matches
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GENERAL INFORMATION:
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Best Local Similarity
Matches 14; Conser
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LENGTH: 681
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                        Query Match
Best Local (
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PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEC
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND
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15; Conservative
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Pred. No. 0.52
8; Mismatches
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RESULT 14
US-09-252-991A-17299
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US-09-252-991A-26802
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS
FILE REFERENCE: 107196.136
CURRENT APPLICATION UNMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28444
TENETH: 140
                                                          GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                Sequence 17299, Application US/09252991A
Patent No. 6551795
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LENGTH: 148
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUCINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
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Local Similarity 36.4%;
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                                                                                                                                                                                                                               QAFRPRRNAPG 109
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J. Rubenfield et al.
M: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
N: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Pred. No. 1.2;
5; Mismatches
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Pred. No. 1.
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HALENL NO. 033173

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARBUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARBUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASSOCIATED AND THERAPEUTICS
THE REFERENCE: 107196.136
CURRENT FILING DATE: 1099-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
SEQ ID NO 28571
LENGTH: 565
TYPE: PRT
ORGANISM: PSEUdomonas aeruginosa
US-09-252-991A-28571
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17299
LENGTH: 351
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17299
Search completed: July 24, 2003, 12:16:25 Job time : 5.37628 secs
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US-09-252-991A-28571
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                                                                                                         243 LQAPREIVE--KYRGRYDAGPEALRQERLARLKELG 276
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                                                                                                                                                           13 LORPOHLMDQGQMRHSFSAGPELLRQDKRPRSGSTG 48
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
                  Published Applications AA:*

1: /cgn2 6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07_NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

9: /cgn2 6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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10: /cgn2 6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2 6/ptodata/2/pubpaa/US09EW PUB.pep:*

12: /cgn2 6/ptodata/2/pubpaa/US09EW PUB.pep:*

13: /cgn2 6/ptodata/2/pubpaa/US09EW PUB.pep:*

14: /cgn2 6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2 6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10B_PUB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10B_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Query Match Length DB	BB	ID	Description
_	63	24.2	70	و و	US-09-864-761-44434	Sequence 44434, A
2	56.5	21.7	1000	15	US-10-128-714-3305	Sequence 3305, Ap
ω	56	21.5	70	9	US-09-864-761-46074	Sequence 46074, A
4	56	21.5	432	15	US-10-156-761-10911	Sequence 10911, A
σ	55	21.2	32	ø	US-09-864-761-35805 ·	Sequence 35805, A
6	55	21.2	89	15	US-10-106-698-5596	Sequence 5596, Ap
7	55	21.2	1629	9	US-09-972-467-2	Sequence 2, Appli
8	55	21.2	1882	10	US-09-918-171A-13	Sequence 13, Appl
φ	55	21.2	1907	10	US-09-938-330-25	25,
10	54.5	21.0	1315	10	US-09-990-046-10	10,
11	54.5	21.0	1433	15	US-10-224-249-14	Sequence 14, Appl
12	54	20.8	623	14	US-10-108-605-125	125,
13	54	20.8	623	14	US-10-108-605-129	Sequence 129, App
14	54	20.8	638	15	US-10-059-585-8	Sequence 8, Appli
15	54	20.8	779	æ	US-08-817-832B-31	Sequence 31, Appl
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-10-063	116-10-339-565	US-10-104-	US-10-063-595	L5 US-10-063-599-164	US-10-233-873	US-10-090	US-10-063-538-	US-10-063-567	US-10-227-693	US-10-063-598	US-10-063-	US-10-063-502	US-10-063-616-	US-10-063-547-	US-10-006-867-1	10 US-09-912-672A-2	US-09-870-574	9 US-09-728-911-25	Sn	Sn	14 US-10-023-529-43	_	ڄ	US-09-867-550-1	US-09-734-329-	-09-734-	US-10-142-356-	US-09-919-585-	15 US-10-195-101-32
Sequence 4, Appri Sequence 164, App	۱ د	e 25		e 164	ത ഗ	e 25,	164	164,	164,	e 164,	o	e 164,	164,	164,	16,	e 2,	Ф 4.	25,		£ W	43	Sequence 43, Appl	e 8,	139	e 2,		9	12	Sequence 32, Appl

ALIGNMENTS

US-09-864-761-44434

Sequence 44434, Application US/09864761 Patent No. US20020048763A1

INFORMATION:

APPLICANT: Enn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aconica-x-1
CURRENT PILLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: BCT/US01/00666
PRIOR FILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665 APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00663 2001-01-30

APPLICATION NUMBER:

PCT/US01/00662

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; ORGANISM: Aspergillus fumigatus US-10-128-714-3305
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Query Match
Best Local Similarity
                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                             PRIOR FILING DATE:
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.85
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.84
                                                                                                              TYPE: PRT
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                                                                                                                                      ENGTH:
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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19; Conservative
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Tishkoff, Daniel
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Score 56.5;
Pred. No. 98
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0.78;
                     BB
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                     Length 1000;
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SEQ ID NO 46074
LENGTH: 70
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PRIOR FILIN
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PRIOR
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 4911
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/774,203
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PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR APPLICATION NUMBER:
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PRIOR APPLICATION NUMBER: PCT/US01/00665
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CURRENT FILING DATE: 2001-05-23
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APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                          FEATURE:
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-09-21
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                                                                         INFORMATION:
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MAP TO AC008752.3

EXPRESSED IN BRAIN, SIGNAL = 1.4

EXPRESSED IN PLACENTA, SIGNAL = 1.4

EXPRESSED IN PLACENTA, SIGNAL = 2

EXPRESSED IN ECTAL LIVER, SIGNAL = 1.6

EXPRESSED IN LUNG, SIGNAL = 3.4

EST_HUMAN HIT: BF314489.1, EVALUE 2.00e-28
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US-10-156-761-10911
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US-10-156-761-10911
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SEQ ID NO 10911
LENGTH: 432
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Best Local Similarity
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                           APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
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TYPE: PRT
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PRIOR APPLICATION NUMBER: JP 2001-272697
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                                                                                                                 PRIOR
                                                APPLICATION NUMBER: US 09/632,366
FILLING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILLING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
            FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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Pred. No. 6;
5; Mismatches
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Pred. No. 45;
4; Mismatches
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US-10-106-698-5596
Sequence 5596, Application US/10106698; Publication No. US20030109690A1; GENERAL INFORMATION:
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SOFTWARE: Annone
SEQ ID NO 35805
NUMBLE: Paces
SOFTWARE: Paces
SEQ ID NO 5596
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                                                                   APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR PPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
                                                        PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
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                                         PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN HBL100, SIGNAL = 3.9
IN LUNG, SIGNAL = 31
IN BONE MARROW, SIGNAL = 1.5
IN ADULT LIVER, SIGNAL = 1.2
IN FETAL LIVER, SIGNAL = 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IN HEART, SIGNAL = 1.2
IN BRAIN, SIGNAL = 1.8
IN BT474, SIGNAL = 1.8
IN HBL100, SIGNAL = 3.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55;
Pred. No.
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; LENGTH: 1629
; TYPE: PRT
; ORGANISM: Human
US-09-972-467-2
                                                                                 ; OTHER INFORMATION: Xaa = Tyr
US-09-918-171A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-918-171A-13
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Best Local Similarity 35.4
Query Match 21.2%;
Best Local Similarity 35.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
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Patent No. US20020090373A1
GENERAL INFORMATION:
APPLICANT: PFIZER INC.
                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                NAME/KEY: MOD RES
LOCATION: (468)
OTHER INFORMATION: X
NAME/KEY: MOD RES
LOCATION: (521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/972,467
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, TITLE OF INVENTION: USES THEREOF FILE REFERENCE: PC10850A
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/369,364
PRIOR FILING DATE: 1999-08-06
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/918,171A CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/04193
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Apte, Suneel APPLICANT: Hurskainen, Tiina L.
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                           ORGANISM: Homo sapiens ADAMTS-9
                                                                                                                                                                                                                                                              ENGTH: 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13, Application US/09918171A
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            ω,
           Score 55; DB 10; Length 1882; Pred. No. 3.1e+02; Indels 16; Indels
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Pred. No.
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Pred. No. 2.6e+02;
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APPLICANT: de Sauvage, Frederic
APPLICANT: Carpenter, David A.
TITLE OF INVENTION: Patched-2
FILE REFERENCE: P1405R1
CURRENT APPLICATION NUMBER: US/09/990,046
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 10
LENGTH: 1315
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-990-046-10
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TITLE OF INVENTION: No. US20020115838Alel Human Proteases and Polynucleotides Encoding File REFERENCE: LEX-0237-USA
CURRENT APPLICATION NUMBER: US/09/938,330
CURRENT FILING DATE: 2001-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Walke, D. Wade APPLICANT: Hilbun, Erin
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PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
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                                                                       y Match 21.0%; Score 54.5; DB 10; Local Similarity 26.8%; Pred. No. 2.4e+02; nes 15; Conservative 11; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 14; Conserv
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292
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                                    3 LGPRGQDSPLL-QRPQHLMDQGQMRHSFSAGPELLRQDKR------PRSGST 47
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US20020115838A1
LAPKGNOSRILTOAYKRMAEEAMOKKHONTGPALEQEDKTSKVAPGTAPLPRLGAT 347
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Scoville, John
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Pred. No. 3.1e+02;
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                                                                                                                 Length 1315;
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RESULT 11 US-10-224-249-14

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                                                                                                                                                          US-10-108-605-125
                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 125
                                                                                                                   Query Match
                                                                               Matches
                                                                                                 Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 125, Application US/10108605
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Publication No. US20030087867A1
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                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF FILE REFERENCE: 31133B
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
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PRIOR APPLICATION NUMBER: PCT/NL00/00482
PRIOR FILING DATE: 2000-07-07
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CURRENT FILING DATE: 2002-08-19
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                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/761,142 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Broadus, Julie APPLICANT: Stam, Lynn
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                                                                                                                                                                LENGTH: 623
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CHAIN
LOCATION: (1)..(1433)
OTHER INFORMATION: Human nitric oxide synthase
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ORGANISM: Homo sapiens
FEATURE:
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      110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 QD 39
                                    8 QDSPLLQRPQHL-----MDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
                                                                             17; Conservative
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                                                                                                 Similarity
QQSLLLQHPQQQQQHSHQSQQQQQHGYGSSAQL--PHHRLSGGSTGS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bachmann, Jane
Kamdar, Kim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PRGQDSPLL-----QRPQHLMDQGQMRHSF---SAGPELLR 37
                                                                                               20.8%;
                                                                                                                                                                                                                                                                                                                                                                       2002-03-27
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29.0%;
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                                                                             4; Mismatches
                                                                                             Score 54; DB 14;
Pred. No. 1.2e+02;
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Pred. No. 2
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                                                                                                                 DB 14; Length 623;
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US-10-108-605-129
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             PRIOR APPLICATION NUMBER: PCT/JP00/05060
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
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NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ota, APPLICANT: Iso
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                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
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TYPE: PRT
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APPLICATION NUMBER: JP 11-248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 QQSLLLQHPQQQQQQHSHQSQQQQQHGYGSSAQL--PHHRLSGGSTGS 155
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Bachmann, Jane
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Nezu, Jun-Ichi
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Otsuki, Tetsuji
Funahashi, Shin-Ichi
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Otsuka, Kaoru
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Wakamatsu, Ai
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Pred. No. 1.2e+02
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APPLICATION UNBER: US/08/817,832B
FILING DATE: 28-APR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: WO PCT/EP95/04258
FILING DATE: 30-OCT-1995
PRIOR APPLICATION UNBER: EP 94 11 7122.5
PRIOR APPLICATION UNBER: EP 94 11 7122.5
PRIOR APPLICATION UNBER: 31:
APPLICATION WHERE: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-817-832B-31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-817-832B-31
Sequence 31, Application US/08817832B; Publication No. US20030104516A1; GENERAL INFORMATION:
Search completed: July 24, 2003, 12:18:21 Job time : 6.86764 secs
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 638
TYPE: PRT
CRCANISM: Homo sapiens
US-10-059-585-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
COUNTRY: US
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MANDELKOW, Eckhard, et al.
TITLE OF INVENTION: No. US20030104516A1el Protein Kinase (NPK-110)
NUMBER OF SEQUENCES: 32
                                                                                                         388 LOSPAHLKVORTISANOKORRFSDHAGPSIPPAVSYTKRPOANSVES 434
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                                                                                                                                                        13 LORPOHL-----MDQGOMRHSFSAGPEL---LRQDKRPRSGSTGS 49
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length: 2000000000
       260
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28: /cgm2_6/ptcdata/1/paa/US09B_COMB.pep:*
29: /cgm2_6/ptcdata/1/paa/US09B_COMB.pep:*
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Match Length
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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49
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       25
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   US-08-842-385-10
US-09-991-681-31
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                                                                                                   Description
Sequence 10, Appl
Sequence 31, Appl
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61 61 61		1,600,0	: : : : : : : : : : : : : : : : : : : :	63.55 63.55 63.55 63	260 260 260 260 260 260 260 260 260 260
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250 250 250	407 407 833 171 179	504 210 87 87 407	70 70 70 70 70	195 693 501 132 132 70 70	3022873307716
31 31	30 31 31	31 32 33 33 33 33 33 33 33 33 33 33 33 33	1 28 2 28 2 28 2 28 2 8 2 8 2 8 2 8 2 8	1 30 22 23 23	12 25 27 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1-178	US-60-453-135-9 US-60-466-412-9 US-10-437-963-1 US-10-419-128-1 US-10-437-963-1	-10-419-128-233 -10-424-599-180 -09-644-265-116 -10-263-828-116 -10-419-128-284 -60-452-680-144	-10-203-134-3417 -10-203-135-3341 -10-203-136-3426 -10-203-137-3426 -10-203-139-3298 -US01-08631-5261	-US01-08656-9053 -10-419-128-2405 -10-419-128-2159 -09-758-446-1669 -10-212-759-1669 -US01-00663-3431 -09-864-761-4443	-08-842-385-6 -09-991-681-27 -US03-01943-44 -10-144-198-4 -US01-08631-400 -US01-42950-495 -10-416-993-495 -US03-04508-32 -US01-08631-400 -US01-08631-400 -US01-08631-400 -US01-08631-400 -US03-04508-32 -US03-04508-32 -US03-04508-32
326	equence equence equence equence equence equence	e 23374, e 180951 e 116, A e 116, A e 116, A e 28435, e 28435,	e 34171, e 33418, e 34264, e 34316, e 32981,	9053 e 240 e 215 e 166 e 166 e 166 e 444 e 444	e 427 e 427 e 495 307 117

ALIGNMENTS

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RESULT 1

US-08-942-385-10

(Sequence 10, Application US/08842385)

; GEMERAL INFORMATION:

APPLICANT: Russell, John

APPLICANT: Colpitts, Tracey

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

TITLE OF INVENTION: FOR DETECTING DISEASE OF THE PROSTATE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTYER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER TIBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASCEQ for Windows Version 2.0

CURRENT APPLICATION NUMBER: US/08/842,385

FILING DATE:

CLASSIFICATION: 435
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: None US-08-842-385-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
TELEPAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-NOV-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEB: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                   APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: IL
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRATOCHVIL, JON D.

ROBERTS-RAPP; LISA
OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09991681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRANADOS, EDWARD N. HODGES, STEVEN C. KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLPITTS, TRACEY L. FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 260; DB 12; 100.0%; Pred. No. 6.6e-25;
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; MOLECULE TYPE:
US-08-842-385-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/842 307 FILING DATA:

CURSSTEMT: DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/842 307 FILING DATE:

CLASSTETTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08842
GENERAL INFORMATION:
APPLICANT: Russell, John
APPLICANT: Colpitts, Tracey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 49; Conserva
                                                                         Matches
                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                           NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASE OF THE PROSTATE
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION NAME: Porembski, Priscil
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                        Local Similarity
                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                          TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 31:
342 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abbott Park
                    EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08842385
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TYPE: amino acid
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                                                                     100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                     linear
                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                          6
                                                                       <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                 6084.US.01
                                                                     Score 260; DB 12;
Pred. No. 1.1e-23;
D; Mismatches 0;
                                                                       Indels
                                                                                                       Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                   49
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                                                                     Gaps
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                                                                                                                    Sequence 44, Application PC/TUS0301943 GENERAL INFORMATION:
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Sequence 27, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                APPLICANT: ORIGENE TECHNOLOGIES INC
TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 10/054,935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-Nov-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                             393 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 441
                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                               1 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/065,383 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09991681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 518 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRANADOS,
                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDWARD N.
                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                        Score 260; DB 25;
Pred. No. 1.2e-23;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6084.US.P1
                                                                                                                                                                                                                                                                                                                                                                  DB 25;
                                                                                                                                                                                                                                                                                                                                                              Length 518;
                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens PCT-US03-01943-44
                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: Custom
SEQ ID NO 40087
                                                                                                                                                                                                                                                                                         Sequence 40087, Application PC/TUS0108631 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/10144198 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
                                                                                            PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
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SOFTWARE: PatentIn ver
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PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/197,824
PRIOR FILING DATE: 2002-07-19
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
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ORGANISM: Homo sapiens
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                                  ENGTH: 1807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/356,130 FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2002-01-25
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Pred. No. 5.8e-23;
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Pred. No. 5.8e-23
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US-10-416-993-495
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: PCT/US01/42950
CURRENT FILLING DATE: 2001-11-16
                                                                      Query Match
Best Local Similarity
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Best Local Similarity
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 495
LENGTH: 1839
                                                            Matches
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Best Local Similarity
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: US/10/416,993
CURRENT FILING DATE: 2003-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR PEPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                     LENGTH: 1839
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Pred. No. 6.1e-23;
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Pred. No. 6.1e-23;
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GENERAL INFORMATION
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CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
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PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 93
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CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Custom
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TYPE: PF
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                                                                                                                                                      NAME/KEY: DOMAIN
LOCATION: (1065)..(1074)
OTHER INFORMATION: Helper component proteinase domain identified by PFam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
                                                                                                                                                                                                                                                 OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX, OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw score
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LOCATION: (11)..(25)
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
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                                                               Score 260; DB 1;
Pred. No. 6.7e-23;
; Mismatches 0;
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Pred. No. 6.2e-23;
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1796 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 1844

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RESULT 14
US-10-419-128-17975
; Sequence 17975, Appl
; GENERAL INFORMATION:
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US-10-144-198-30
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APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prosta
FILE REFERENCE: 9U 105 R1
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Best Local Similarity
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CURRENT FILING DATE: 2002-05-14
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 10/054,935 PRIOR FILING DATE: 2002-01-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 10/197,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2002-02-14
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PRIOR APPLICATION NUMBER: US 60/356,130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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ENGTH: 2221
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FILING DATE: 2002-04-08
APPLICATION NUMBER: US 10/144,198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2002-05-14
                                                                                                                                                                         2096 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 2144
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                                                                 Application US/10419128
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Search completed: July 24, 2003, 12:15:15
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CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-19
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 135832
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GENERAL INFORMATION:
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SEQ ID NO 17975
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                        22 QGQMRHSFSAGP--ELLRQDKRPRSGSTGS 49
                                                                                                                                           40 PLAPRGQDHFRPRQTPPSAPQTASPLPTPPGPISRSFSIPSRGMRTSGISDGKETEDLQD 99
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                                                                      KGPARMSLSSLPSAQTSLEDHRPLSGATES 129
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Barbazuk, Brad
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Match Length
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US-10-273-573-9693

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US-09-291-417D-89

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US-10-273-573-8445
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PCT-US02-18638A-186
US-10-273-573-877-29
US-10-464-368-49
US-10-273-573-73-65
US-10-294-433-740
US-10-294-433-79
US-10-294-433-79
US-10-294-433-79
US-10-273-573-10953
US-60-478-196-3004
US-10-373-573-10697
PCT-US03-18787-101
PCT-US03-1976-3004
US-10-273-573-7584
US-60-478-196-3004
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9053, Ap
8476, Ap
9052, Ap
13, Appl
13, Appl
7947, Ap
89, Appl
1707, Ap
17748, Ap
17748, Ap
186, App
49, App
49, App
49, App
7365, Ap
7365, Ap
7597, Ap
740, Ap
740, Ap
740, Ap
106, Ap
106, Ap
101, App
10
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ALIGNMENTS

RESULT 1 US-10-367-978-32

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Sequence 9053, Application US/10273573

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTMARE: CUStom
SOFTMARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/10367978
GENERAL INFORMATION:
APPLICANT: GRATELY, DENNIS
TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND
TITLE OF INVENTION: OR THERAPEUTICS
FILE REFERENCE: 037003-0301988
CURRENT APPLICATION NUMBER: US/10/367,978
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
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                                                                                                                                                                                                                                                                                                                                 US-10-273-573-9053
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                        1747 EPIGPRGQDSPLLQRPQHIMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 1795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
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ilarity 100.0%;
Conservative 0
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Pred. No. 2.1e-27;
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                                                                                                                                                                                                                                       AND POLYPEPTIDES
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APPLICANT: HYSEG, Inc
APPLICANT: HYSEG, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
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Best Local Similarity
                                                                                  SOFTWARE: Custom
SEQ ID NO 9052
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LOCATION: (33)...(48)
LOCATION: (33)...(48)
OTHER INFORMATION: ww/rsp5/wwP domain proteins domain identified by eMATRIX,
OTHER INFORMATION: accession number BL01159, p-value=3.077e-15, raw score of 13.85
-10-273-573-9053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
CURRENT FILING DATE: 2002-10-18
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PRIOR APPLICATION NUMBER: 09/770,160
                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/522,929
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PRIOR FILING DATE: 2000-04-18
                                                                                                                                NUMBER OF SEQ ID NOS: 10994
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LOCATION: (1)...(149)
                                           TYPE: PRT
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OTHER INFORMATION: Xaa = X or * as defined in Table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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FEATURE:
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                                                                ENGTH:
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                                                                205
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                                                                                                                                                       2001-01-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 6; Length 149, Pred. No. 0.49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
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                                                         US-10-273-573-7947
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                                                                                                                                                                                                      SOFTWARE: Custom SEQ ID NO 7947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: P
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                                                                                                                                                                                                                                            APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7947, Application US/10273573 GENERAL INFORMATION:
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APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 10994
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LOCATION: (176)..(202)
OTHER INFORMATION: PpiC-type peptidyl-prolyl cis-trans isomerase proteins domain
OTHER INFORMATION: identified by eMATRIX, accession number BL01096C, p-value=6.063e-
                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(139)
OTHER INFORMATION: Xaa = X or *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                     LENGTH: 139
TYPE: PRT
                                                                                                                                   FEATURE:
                                                                                                                                              ORGANISM: Homo sapiens
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les 15; Conserv
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 19.6%;
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Pred. No. 0.72
5; Mismatches
 Score 51;
Pred. No.
                                                                           as defined in Table 2
 ; DB 6;
. 2.1;
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                   Length 139;
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APPLICANT: MARTINEZ, RICARDO

APPLICANT: WHYTE, DAVID

TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES

FILE REPERENCE: 038602/0329

CURRENT APPLICATION NUMBER: US/09/291,417D

CURRENT FILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: 60/081,784

PRIOR PILING DATE: 1998-04-14

PRIOR FILING DATE: 1998-04-14

PRIOR FILING DATE: 1998-04-14

PRIOR FILING DATE: 1998-04-14
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RESULT 9
US-10-273-573-7079
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                                                                                                                              Query Match
Best Local Similarity 40.0
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 89, Application US/09291417D GENERAL INFORMATION: APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
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GENERAL INFORMATION:
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                                                                                                                                                                                                                     LENGTH: 1233
TYPE: PRT
ORGANISM: Murine sp.
-09-291-417D-89
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
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PRIOR FILING DATE: 2001-01-26
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NUMBER OF SEQ ID NOS: 10994
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CURRENT FILING DATE: 2002-10-18
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PRIOR FILING DATE: 2000-04-18
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NAME/KEY: misc_feature

LOCATION: (1)...(167)

OTHER INFORMATION: Xaa = X or * as defined in Table 2
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 167
                                                                       627 RDSPLOGGGOONSOAGORNSTSSIEPRLLWERVEKLVPRPGSGSS 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 PRGPGGEEAPLLR----
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l Similarity 31.7%;
l3; Conservative
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Pred. No. 35;
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                                                                                                                                                                               Length 1233;
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LENGTH: 501
TYPE: PRT
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SOFTWARE: Custom
SEQ ID NO 7748
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Best Local Similarity
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                         NAME/KEY: DOMAIN
LOCATION: (463)..(486)
OTHER INFORMATION: TRAN
OTHER INFORMATION: eMAT
OTHER INFORMATION: 13.5
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PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
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CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
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                                                                                  LOCATION: (287)..(501)
OTHER INFORMATION: Ras family domain identified
OTHER INFORMATION: value=0.0015, PFam score of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (287)..(501)
OTHER INFORMATION: Ras family domain identified by PFam, accession name ras,
OTHER INFORMATION: value=0.0015, PFam score of -96.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: TRANSFORMING PROTEIN P21 RAS SIGNATURE domain identified by OTHER INFORMATION: eMATRIX, accession number PR00449E, p-value=8.714e-13, raw
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Pred. No. 14;
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; ORGANISM: Homo sapiens PCT-US02-18638A-186
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US-10-273-573-8445
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Best Local Similarity
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LENGTH: 501
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                                                                                   SEQ ID NO 186
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: OF CERVICAL CANCER
                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: PCT/US02/18638A CURRENT FILING DATE: 2002-06-12
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PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
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CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                    PRIOR FILING DATE: 2001-11-14
                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/335,936
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                                            TYPE: PRT
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Pred. No.
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Matches
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SEQ ID NO 49
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CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 40716-IP-017
CURRENT APPLICATION NUMBER: US/10/464,368
CURRENT FILING DATE: 2003-06-16
                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/388,970 PRIOR FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Krumlauf, Robb APPLICANT: Ellies, Debra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 10994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ellies, Debra
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Custom
                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(87)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                               ORGANISM: MOUSE
                                                                                                                                                                                  LENGTH: 205
TYPE: PRT
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                                                                     ch 18.8%; 1 Similarity 28.8%; 15; Conservative 1
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PRSRKVRLVASCKCKRPTRFHNOSELK---DFGPETARPOKGRKPRPGARGA 200
                                  PRGQDSPLL----QRPQHLMDQGQMRHSFSAGPELLRQDK--RPRSGSTGS 49
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Pred. No. 17;
9; Mismatches
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1: pir1:*
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-462 <STO>

A;Cross-references: GB:AE004929; GB:AE004091; NID:g9951462; PIDN:AAG08551.1; GSPDB:GN001 A;Experimental source: strain PAO1 C;Genetics:

A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: G83000

PAO1,

an

opportunistic patho

M.J.; Br K.; Lim,

98

Nature 406, 959-964, 2000

probable two-component response regulator PA5166 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 17-Mar-2003 C;Accession: G83000 C;Accession: G83000 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Larbig, K.; Larbig, S.; Olson, M.V.

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gene pointed prote calcium channel pr replication protei probable histone a clathrin heavy cha genome polyprotein hypothetical prote hypothetical prote glutamate synthase eyelid - fruit fly hypothetical prote	hypothetical prote nitric-oxide synth peptidylprolyl iso cobalt transport s hypothetical prote

ALIGNMENTS

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gene mastermind protein - fruit fly (Drosophila virilis)
(;Species: Drosophila virilis
(;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
(;Accession: T13998
R;Newfeld, S.J.; Tachida, H.; Yedvobnick, B.
J. Mol. Bvol. 38, 637-641, 1994
A;Reference number: Z17850; MUID:94365848; PMID:8083889
A;Accession: T13998
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                                                                          A;Cross-references: EMBL:M92914; NID:g157833; PID:g157834; PIDN:AAC37201.1
C;Genetics:
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C;Superfamily: response regulator of the NtrC type; response regulator homology; RNA
                                                             A;Cross-references: FlyBase:FBgn0013119
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Pred. No. 3.6;
3; Mismatches 1
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C;Accession: E75332
C;Accession: E75332
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein APE1577 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D72536
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Science 286, 1571-157, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus
A;Reference number: A75250; MUID:20038896; PMID:10567266
A;Accession: E75332
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A; Residues: 1-333 <WHI>
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    protein
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8; Mismatches
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C;Accession: S54830
R;Pehu, T.; Maki-Valkama, T.; Valkonen, J.P.T.; Koivu, K.; Lehto, K.; Pehu, R;Pehu, T.; Maki-Valkama, T.; Valkonen, J.P.T.; Koivu, K.; Lehto, K.; Pehu, R;Pescription: Potato plants transformed with a potato virus Y P1 gene sequent, Reference number: S54830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                   C;Accession: 11000
R;Kraemer, C.; Schmidt, E.R.
submitted to the EMBL Data Library, April 1996
submitted to the EMBL Data Library, April 1996
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A;Title: HEX: a novel homeobox gene expressed during haematopoiesis A;Reference number: S30230; MUID:93219088; PMID:8096636
A;Accession: S30230
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: S30230
                                                                                                                                                                                                                                                                                                                 A;Description: A novel gene, A;Reference number: Z17797
                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein X - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: tobacco etch virus genome polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-276 < PEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P1 protein - potato virus Y (fragment)
C;Species: potato virus Y, PVY
C;Dato: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z21524; NID:g288500; PIDN:CAA79729.1; PID:g288501 C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;139-195/Domain: homeobox homology <HOX>
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A; Residues: 1-271 <BED>
                                                                                                                   A;Cross-references: FlyBase:FBgn0023458
                                                                                                                                                                                              A;Cross-references: EMBL:X97196; NID:g1279383;
                                                                                                                                                                                                                  A; Residues: 1-3429 < KRA>
                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                        A;Accession: T13853
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Best Local
Query Match
Best Local Similarity
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Local Similarity 45.7%;
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                                                                           29/3;
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                                                                      102/2; 152/1; 2478/1; 2838/1; 2913/1; 3032/1; 3120/2; 3149/3; 3239/3;
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22.5%;
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Score 58.5;
Pred. No. 1.
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  5; DB 2;
1.3e+02;
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6.2;
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                                                                                                                                                                                                                                                                                                                                          X-chromosome;
                      Length 3429
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 24-Sep-1999
C;Accession: JN0767; S26799; S78048; S30231
R;Hromas, R.; Radich, J.; Collins, S.
Biochem. Biophys. Res. Commun. 195, 976-983, 1993
A;Title: PCR cloning of an orphan homeobox gene (PRH) preferentially expressed A;Reference number: JN0767; MUID:93384629; PMID:8103988
A;Accession: JN0767
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87433
                                                                                                                                                               transcription regulator, LacI family [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Decies: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: H87433
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A; Residues: 136-195 <BEW>
A; Cross-references: EMBL: Z21533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z21533; NID:g32068; PIDN:CAA79730.1; PID:g32069
R;Bedford, F.K.; Ashworth, A.; Enver, T.; Wiedemann, L.M.
Nucleic Acids Res. 21, 1245-1249, 1993
A;Title: HEX: a novel homeobox gene expressed during haematopoiesis and conserved A;Reference number: S30230; MUID:93219088; PMID:8096636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bedford, F.K.
submitted to the EMBL Data Library, February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L16499; NID:g292404; PIDN:AAA02988.1; PID:g292405
R;Crompton, M.R.; Bartlett, T.J.; MacGregor, A.D.; Manfioletti, G.; Buratti, E.; Giancot Nucleic Acids Res. 20, 5661-5667, 1992
A;Title: Identification of a novel vertebrate homeobox gene expressed in haematopoietic A;Reference number: S26799; MUID:93087175; PMID:1360645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                 RESULT 9
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A; Residues: 122-270 <BED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                EPLGPRGQDSPLLQRPQHLMDQGQMRHS
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Pred. No.
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Science 294, 2317-2323,
A;Authors: Yoo, H.; Tao,
                                         A; Map position:
C; Superfamily:
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C;Superfamily: lac repressor
                                                                                         A;Gene:
                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-405 < KUR>
                                                                                                                                                                                                           A;Status:
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A; Reference number: AB2577;
A; Accession: AD2784
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nes 11; Conserv
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                                                                                         AGR_C_3105
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                                           molybdenum
22.1%;
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A;Residues: 1-405 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42690.1; PID:g17740125; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                  A;Cross-references: GB:AE007869; PIDN:AAK87461.1; PID:g15156781; GSPDB:GN00169
C;Genetics:
                                                                                                                                                                                                                                                   A; Title: Genome Sequence of the Plant Pathogen and Biotechnology A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                      R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Blotechnology Agent Agrob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: circular chromosome C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Wood, D.W.; Setubal, J.C.; Kaul, erage, G.; Gillet, W.; Grant, C.;
                                                                                                                                                                                                                                                                                                                                                                   C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: D97563
                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AGR_C_3105 {imported} - Agrobacterium tumefaciens (strain C_iSpecies: Agrobacterium tumefaciens
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A;Residues: 1-357 <STO>
A;Cross-references: GB:AE005673; NID:g13422862; PIDN:AAK23468.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.; Romero, P.; Zhang, S.
294, 2317-2323, 2001
rs: Yoo, H.; Tao, Y.; Biddle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 QRPQHLMDQGQMRHSFSAGPELLRQDKRPRSG
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                                                                     circular chromosome
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Pred. No. 11;
Score 57.5;
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                                          biosynthesis protein moeA-2
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D.; Kutyavin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W.; Perry, M.; Gordon-Kamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
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Markelz,
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ckelz, B.;
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Length 405;

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C;Accession: D83622
R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; (
'Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 2-27;95-101;131-155;159-169;188-195;245-263;297-302;340-350;383-388;407-419;
R;Dierks, T.; Miech, C.; Hummerjohann, J.; Schmidt, B.; Kertesz, M.A.; von Figura, K.
J. Biol. Chem. 273, 25560-25564, 1998
A;Title: Posttranslational formation of formylglycine in prokaryotic sulfatases by modif.
A;Reference number: A59074; MUID:98421466; PMID:9748219
A;Contents: annotation; post-translational modification
A;Note: confirmation of 3-oxoalanine active site, referred to as formylglycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pseudomonas aeruginosa (;Date: 17-Jul-1998 #text_change 17-Mar-2000 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Mar-2000 C;Accession: S69336; S69359 C;Accession: S69336; S69359 R;Beil, S.; Kehrli, H.; James, P.; Staudenmann, W.; Cook, A.M.; Leisinger, T.; Bur. J. Biochem. 229, 385-394, 1995 Fur. J. Biochem. 229, 385-394, 1995 A;Title: Purification and characterization of the arylsulfatase synthesized by A;Reference number: S69336; MUID:95262702; PMID:7744061
                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-536 <STO>
A;Cross-references: GB:AE004456; GB:AE004091; NID:g9946013; PIDN:AAG03573.1; GSPDB:GN001
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                                                                                                                                                                                                                                                                                                                                                                 .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arylsulfatase PA0183 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                A; Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-533 <BEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Superfamily: animal sulfatase
;Keywords: sulfuric ester hydrolase
;51/Modified site: 3-oxoalanine (Cys)
                                                                                                                                                                                                                                                                                               Reference number: A82950; Accession: D83622
                                                                                                                                                                                                                                                                                                                      ;Title: Complete genome sequence of Pseudomonas aeruginosa;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                        ;Gene: atsA; PA0183
                                                                                                                                                                                                                                                                       Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Cross-references: EMBL:Z48540; NID:g2440146; PIDN:CAA88421.1; PID:g695684
;Experimental source: strain PAO1
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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Best Local
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                                            Local Similarity
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36.1%;
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Pred. No. 24;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                           , A.L.; Mizoguchi, S.D.; Warrener, Coulter, S.N.; Folger, K.R.; Kas,
                                            Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 15;
                         Mismatches
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24;
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                                                                 Length 536;
                       Indels
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A.; Larbig,
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K.; Lim,
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C;Accession: A23047; I55318; JU0120; A22393; A33842
R;Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, O.; Seno, T.
Nucleic Acids Res. 13, 2035-2043, 1985
A;Title: Nucleotide sequence of a functional cDNA for human thymidylate synthase.
A;Reference number: A23047; MUID:85215597; PMID:2987839
A;Accession: A23047
                                                                                                                                                                                                                                  A;Cross-references: GDB:120465; OMIM:188350
A;Map position: 18p11.32-18p11.32
A;Introns: 69/1; 93/3; 152/1; 186/1; 244/3; 268/3
A;Introns: 69/1; 93/3; 152/1; 186/1; 244/3; 268/3
C;Superfamily: thymidylate synthase; thymidylate synthase homology C;Keywords: deoxyribonuclectide biosynthesis; methyltransferase F;30-313/Domain: thymidylate synthase homology <TDS>
F;199/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 2-25 <SHI>
R;Davisson, V.J.; Sirawaraporn, W.; Santi, D.V.
J. Biol. Chem. 264, 9145-9148, 1989
A;Title: Expression of human thymidylate synthase in Escherichia coli.
A;Reference number: A33842; MUID:89255401; PMID:2656695
A;Accession: A33842
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: TYMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 2-10 < DAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Purification and NH2-terminal amino acid sequence A;Reference number: A22393; MUID:85261174; PMID:3839505 A;Accession: A22393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:D00517; NID:g220133; PIDN:BAA00404.1; PID:g2160415 R;Shimizu, K.; Ayusawa, D.; Takeishi, K.; Seno, T. J. Biochem. 97, 845-850, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-68 < TA2 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Human thymidylate synthase gene: isolation of phage clones which cover a A;Reference number: JU0120; MUID:90110051; PMID:2532645 A;Accession: JU0120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:D00596; NID:g220135; PIDN:BAA00472.1; R;Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, J. Biochem. 106, 575-583, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-313 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: I55318; MUID:91056070; A;Accession: I55318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Shimizu, K.; Gotoh, O.; Seno, T.; Ayu
J. Biol. Chem. 265, 20277-20284, 1990
A;Tille: Structural and Functional Analysis of the Human Thymidylate Synthase Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X02308; NID:g37478; PIDN:CAA26178.1; PID:g37479 R;Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Shimizu, K.; Gotoh, O.; Seno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-313 < TAK>
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Date: 31-Mar-1993 #sequence
                                                                                                                                                                                    Query Match
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                                                       PLGPRGQDSPLLQRPQH--LMDQGQMRHSFSAGPELLRQDKRPRSGS 46
PLPPAAQERDAEPRPPHGELQYLGQIQHILRCG---VRKDDRTGTGT
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Pred. No. 15;
7; Mismatches
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O.; Seno, T.
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protein

Arabidopsis thaliana

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Daces 102-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C;Daces 102-Mar-2001 #sequence_revision 02-Mar-2001 #sext_change 09-Nov-2001
C;Daces 102-Mar-2001 #sequence_revision or change of the plant Arabidopsis.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: AB6141; MUID:21016719; PMID:11130712
A;Accession: D#6350
A;Accession: D#6350
A;Accession: D#6350
A;Cross-references: GB:AE005172; NID:95263321; PIDN:AAD41423.1; GSPDB:GN00141
C;Generics
A;Map position: 1

Query Match
Best Local Similarity 29.6%; Pred. No. 44;
Pred.
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.
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HXB9 HUMAN
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HNEH MOUSE
HMPH-HUMAN
NECZ HUMAN
ONCZ HUMAN
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ARS PSEAE
TYSY HUMAN
SP7 HUMAN
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CLH RAT
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               O9ujv9 homo sapien
P07279 saccharomyc
O9p274 homo sapien
P15458 arabidopsis
O9qu77 mus musculu
P1675 human cytom
P51022 drosophila
P54282 rattus norv
O8vi67 mos sapien
P49951 bos taurus
P11442 rattus norv
P18247 p genome po
O9s777 arabidopsis
P49805 rattus norv
O9c0j8 homo sapien
O9c0j8 homo sapien
O9c0j8 mus musculu
O91zi0 mus musculu
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P04818
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Q92794
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4 homo sapien
8 homo sapien
1 pseudomonas
8 homo sapien
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6 homo sapien
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8 sallus gall
9 salmonella
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homo sapien
mus musculu
  pseudomonas
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						RESIT.T 1
	ALIGNMENTS					
015481 homo sapien	MGB4_HUMAN	_		19.6	51	45
P20471 rhizobium m	NDVB_RHIME	_		19.8	51.5	44
P76558 escherichia	MAO2 ECOLI	_	759	19.8	51.5	43
	VINT_FRG3V	_		19.8	51.5	42
P15459 arabidopsis	2SS3 ARATH	_		19.8	51.5	41
P53675 homo gapien	CLH2_HUMAN	۳.		20.0	52	40
O95819 homo sapien	M4K4_HUMAN	_		20.0	52	39
	PBPA_XYLFA	_		20.0	52	38
P17599 bos taurus	SYN1_BOVIN	_		20.0	52	37
P09951 r	SYN1_RAT	ш		20.0	52	36
O54828 mus musculu	RGS9_MOUSE	_		20.0	52	35
Q59711 pseudomonas	PYRB_PSEPU	_		20.0	52	34

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MOZ HUMDA
ID MOZ NOZ
AC 0927
DT 15-J
DT 15-J
DT 15-S
DE Runt
DE leukh
GN RUNY
OS Home
OC Euke
OC Euke
OC Euke
OC Mamm
OX NCBJ
RN [1]
RN [1]
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R GO; GO:0003700; F:transcription factor activity; NAS.
R GO; GO:0003705; P:development; NAS.
R GO; GO:00003275; P:development; NAS.
R GO; GO:0006455; P:regulation of transcription, DNA-dependent; NAS.
R InterPro; IPR001356; Homeobox.
R InterPro; IPR001356; Homeobox;
InterPro; IPR00047; HTH lambrepressr.
R Pfam; PF004617; Hox9 act; 1.
R Pfam; PF04617; Hox9 act; 1.
R PFINTS; PR00024; HOMEOBOX.
R PRINTS; PR000010; HOMEOBOX; 1.
R PRINTS; PR00031; HTHREPRESSR.
R PRODON; PD000010; Homeobox; 1.
R PROSITE; PS00027; HOMEOBOX 1; 1.
R PROSITE; PS00027; HOMEOBOX 1; 1.
R PROSITE; PS00027; HOMEOBOX 1; 1.
R PROSITE; PS50071; HOMEOBOX 1; 1.
R PROSITE; PS
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 142964; -. GO; GO:0005634; GO; GO:0003700; GO:0007275; GO; GO:0006355;
                                                                                                                                                                                                                                                                                         MOZ HUMAN
Q92794;
15-JUL-1998
15-JUL-1998
15-SEP-2003
                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Runt-related transcription factor binding protein 2
leukemia zinc finger protein) (Zinc finger protein RUNXBP2 OR ZNF220 OR MOZ.
      SEQUENCE FROM N.A
                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation.
DNA_BIND 185 244
CONFLICT 173 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY014296; AAG42144.1; -.
EMBL; AY014295; AAG42144.1; JOINED.
EMBL; BC015566; AAH15565.1; -.
EMBL; X16172; CAA34294.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., "Organization of human class I homeobox genes."; Genome 31:745-756(1989).
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                                                                                                                                                             Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homeobox;
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SIMILARITY: BELONGS TO THE ABD-B HOMEOBOX FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS AND FETUSES AT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EPLGPRGQDS------PLLQRPQHLMDQGQMRHSF--SAGPELLRQDKRPRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÉP-APRGEAAPGQGQAAVKAEPLLGAPGELLKQGTPEYSLETSAGREAVLSNQRPGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Developmental protein; Nuclear protein;
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                                                                                                 Chordata;
Primates;
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Pred. No.
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T -> A (IN REF. 3).
; F06ECBC08FBBED2C CRC64;
                                                                                                 Craniata; V
Catarrhini;
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                                                                                                 Vertebrata; Euteleostomi; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96376968; PubMed=8782817;
Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G.,
Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M.,
Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M.,
Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.;
"The translocation t(8;16)[p1];p13) of acute myeloid leukaemia fuses
a putative acetyltransferase to the CREB-binding protein.";
Nat. Genet. 14:33-41(1996).
                                                                                                                                                                                                                                                                                                                                                                                 MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                      PROSITE; PS01359; ZF_PHD_1; PROSITE; PS50016; ZF_PHD_2; Proto-oncogene; Chromosomal
                                                                                                                                                                                                                                                                                                                                          GO; GO:0006323; P:DNA packaging; TA
InterPro; IPR005818; Histone H1/H5.
InterPro; IPR002717; WOZ SAS.
InterPro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U47742; AAC50662.1; -. Genew; HGNC:13013; RUNXBP2.
 1679
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                                      l Similarity
17; Conserv
                   Ç,
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206
259
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371
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PQQQPQPQPQPPPPPPPPQQQPPLSQCSMNNSFTPAPMIM---EIPESGSTGN
                   PRGQDSPLLQRP-----
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1019
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                                       Conservative
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                                                                                                                                                                                                                                                                        translocation; Zinc-finger; Repeat;
                                                                                                                              POLY-GLU.
POLY-SER.
                                                                                                                                                  GLU-RICH.
GLU-RICH.
                                                                                                                                                                                                                                          PHD-TYPE
                                                 Score 59.5;
Pred. No. 41
                  QHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                        MOZ-CBP
                                                                                                 BREAKPOINT FOR TRANSLOCATION
                                                                                                          GLN/PRO-RICH.
MET-RICH.
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                                      ed. No. 41;
Mismatches
                                                                              9FFBBAC3792854BA CRC64;
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                                                         DB 1;
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Best Local
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Q03014;
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Embryo;

MEDLINE=93219088; PubMed=8096636;

Bedford F.K., Ashworth A., Enver T., Wiedemann L.M.;

"HEX: a novel homeobox gene expressed during haematopoi.

conserved between mouse and human.";

Nucleic Acids Res. 21:1245-1249(1993).

-!- FUNCTION: RECONIZES THE DNA SEQUENCE 5'-ATTAA-3'.

IN HEMATOPOLETIC DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                              NAMUH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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  SEQUENCE FROM N.A. MEDLINE=93087175;
                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                            HOMO
                                                                                                                                                            protein HEX).
HHEX OR PRHX
                                                                                                                                                                                                            Homeobox
                                                                                                                                                                                                                                                      01-JUN-1994
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PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein.
DOMAIN 1 134 PRO-RICH.
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Mammalia; Eutheria; Rodentia;
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HHEX OR PRHX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MGI:96086; Hhex.
GO:0005634; C:nucleus; IDA.
GO:0007420; P:brain development;
erPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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DEVELOPMENTAL STAGE: EXPRESSED DURING HEMATOPOIESIS.
                                                                                                                                         Bapiens
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2003 (Rel. 42,
protein PRH
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271 I
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llarity 45.7%;
Conservative
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    PubMed=1360645;
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                                                                                          Chordata;
Primates;
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2; Mismatches
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TRANSFAC

HGNC:4901; HHEX

HSSP; P22808; INK3. PIR; JN0767; JN0767.

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RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R. D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 345:93-98(1994).

-i- FUNCTION: RECOGNIZES THE DNA SEQUENCE 5'-ATTAA-3'.
IN HEMATOPOIETIC DIFFERENTIATION.

-i- SUBCELLULAR LOCATION: Nuclear (Probable).
-i- TISSUE SPECIFICITY: LIVER AND PROMYELOCYTIC LEUKEM.
                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved between mouse and human."; Nucleic Acids Res. 21:1245-1249(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hromas R.A., Collins S.J., Radich J.;
"PCR cloning of an orphan homeobox gene (PRH) preferentially expressed in myeloid and liver cells.";
Biochem. Biophys. Res. Commun. 195:976-983(1993).
                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced throubetween the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93219088; PubMed=8096636;
Bedford F.K., Ashworth A., Enver T., Wiedemann L.M.;
"HEX: a novel homeobox gene expressed during haematopoiesis and
conserved between mouse and human.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A homology-based molecular model of the proline-rich homeodomain protein Prh, from haematopoietic cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94259190; PubMed=7911091; Neidle S., Goodwin G.H.;
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X67235; CAA47661.1; -. 
L16499; AAA02988.1; -. 
BC015110; AAH15110.1; 
Z21533; CAA79730.1; -.
                                                                                                                                                                                   an email to license@isb-sib.ch)
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PROMYELOCYTIC LEUKEMIA
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J. Biol.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Nuclear factor of activated T-cells, cytoplasmic 1 (NFAT transcription complex cytosolic component) (NF-ATC1) (NF-ATC).
NFATC1 OR NFATC OR NFATC2.
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                                                                   Chuvpilo S., Zimmer M., Kerstan A., Fischer C., Inashkina I., Jankevics Schmitt E., Serfling E.; "Alternative polyadenylation events NF-ATC in effector T cells.";
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SMART; SM00389; HOX; 1.
MUTAGENESIS
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MEDLINE=99170294; PubMed=10072078;
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"NF-AT components define a family of transcription factors targeted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Peripheral blood lymphocytes, and MEDLINE=94261186; PubMed=8202141; Northrop J.P., Ho S.N., Chen L., Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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DOMAIN
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CONFLICT 115 115 L -> V (IN REF. 2).
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PROSITE; PS50071; HOMEOBOX_2; 1.
                                            Immunity 10:261-269(1999)
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TISSUE=B-cell;
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                                                                                                                                                                                                                                                                                                                                                                                  Park J. Takeuchi A., Sharma S.;
"Characterization of a new isoform of the NFAT (nuclear factor activated T cells) gene family member NFATc.";
J. Biol. Chem. 271:20914-20921(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 369:497-502(1994).
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Chem. 271:33705-33705(1996).
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Berberich-Siebelt F
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cardiac cells. Could regulate not only the activation and proliferation but also the differentiation and proliferation but also the differentiation and programmed death of T-lymphocytes as well as lymphoid and non-lymphoid cells. SUBUNIT: Member of the multicomponent NFATC transcription complex that consists of at least two components, a pre-existing cytoplasmic component NFATC2 and an inducible nuclear component NFATC1. Other members such as NFATC4, NFATC3 or members of the activating protein-1 family, MAF, GATA4 and Cbp/p300 can also bind the complex. NFATC proteins bind to DNA as monomers.

-!- SUBCELLULAR LOCATION: Cytoplasmic for the phosphorylated form and nuclear after activation that is controlled by calcineurin-mediated dephosphorylation. Rapid nuclear exit of NFATC is thought to be one mechanism by which cells distinguish between sustained and transient calcium signals. The subcellular localization of NFATC play a key role in the gene transcription.
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Cell 96:611-614(1999)
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J. Immunol. 162:7294-7301(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brabletz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chuvpilo S., Avots A., Berberich-Siebelt F., Gloeckner J., Kerstan A., Escher C., Inashkina I., Hlubek F., Jankevics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20119316; PubMed=10652349;
POTTET C.M., Havens M.A., Clipstone N.A.;
Potter C.M., Havens M.A., Clipstone N.A.;
"Identification of amino acid residues and protein kinases involved the regulation of NFATC subcellular localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Generic signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crabtree G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99189746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brabletz T., Serfling E.; "Multiple NF-ATC isoforms with individual transcriptional properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99288090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 275:3543-3551(2000).
                     Comment=6 isoforms may be produced by alternative initiating Met-1 and Met-37 of alpha-type isoforms;
TISSUE SPECIFICITY: Expressed in thymus, peripheral leukocyt T-cells and spleen. Isoforms A are preferentially expressed effector T-cells (thymus and peripheral leukocytes) whereas isoforms B and isoforms C are preferentially expressed in name of the communication of the communication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event-Alternative splicing; Named isoforms=6;
Comment=Isoform C-alpha and isoform C-beta are the strongest
activator of gene transcription, followed by isoform A-alpha ar
isoform A-beta, whereas isoform B-alpha and isoform B-beta are
the weakest. Isoform B-alpha, isoform B-beta, isoform C-alpha
and isoform C-beta, both present in T-cells, can modulate their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION:
                                                                                                                                                                                                     IsoId=095644-6; Sequence=VSP_005590;
Event=Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=B-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=A-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=A-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=C-alpha;
                                                                                                                                                                                                                                                                                                                                              Note=An additional isoform may be produced initiation at Met-37 of isoform B-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=095644-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=095644-2; Sequence=VSP_005591, VSP_005592; Note=An additional isoform may be produced by al initiation at Met-37 of isoform A-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note=An additional in
initiation at Met-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=095644-1; Sequence=Displayed;
Note=An additional isoform may be produced by alternative
initiation at Met-37 of isoform C-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcriptional activity;
                                                                                                                                                                                                                                                                                             IsoId=095644-5;
                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=095644-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plays a role in the inducible expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NF-AT.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10358178,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10089876
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=VSP_005593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence=VSP_005590, VSP_005591,
                                                                                                                                                                                                                                                                                       Sequence=VSP_005590, VSP_005593
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                                                                                                                                                                                                                                                                                                                                                                                   by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSP_005592;
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he IL-2 or IL-4
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InterPro; IPR000451; NF Rel_dor_fam.
Pfam; PF00554; RHD; 1.
Pfam; PF01833; TIG; 1.
SMART; SM00429; IPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U08015; AAA19601.1; --
EMBL; U59736; AAC50869.1; --
EMBL; U80917; AAD00450.1; --
EMBL; U80918; AAD00451.1; --
EMBL; U80919; AAD00452.1; --
                                                                                                                                         REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T01945; -. Genew; HGNC:7775; NFATC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1A66; 17-JUN-98.
PDB; 1NFA; 01-APR-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified
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                                                                                                                                                                                                                                                                                                                   DNA-binding;
                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                  Phosphorylation;
                                                                                                                                                                                                                                                                                                                              Transcription regulation; Activator; Repressor; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0005737; C:cytoplasm; TAS.
GO:0005528; F:FK506 binding activity; TAS.
GO:0003700; F:transcription factor activity; TAS.
GO:0003766; P:transcription from Pol II promoter; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ween the Swiss Institute of Bioinformatics and the EMBL outs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             calcineurin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: Only isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDUCTION: Only isoforms A are inducibly expressed lymphocytes upon activation of the T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                               PS01204; REL_1; FA
PS50254; REL_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen
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                                                                                                                                                                                                                                                                                               Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exposure and isoforms A are expressed in effector
                                                                                                                                                                                                                                                    943
                                                                                                                                                                                                                                                                                               initiation; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                            FALSE_NEG
                           DNA-BINDING.
NUCLEAR LOCALIZATION SIGNAL
TRANS-ACTIVATION DOMAIN B ('
NUCLEAR EXPORT SIGNAL.
                                                                                          NUCLEAR LOCALIZATION SIGNAL. NUCLEAR EXPORT SIGNAL.
                                                                                                                                                                                                                     CYTOPLASMIC 1, FOR ALPHA-TYPE
                                                                                                                                                                                                                                                   CYTOPLASMIC 1. NUCLEAR FACTOR
MPSTSFPVPSKFPLGPAAAVFGRGETLGPAPRAGGTMKSAE
                                                                                                                                                                                      TRANS-ACTIVATION DOM
                                                                                                                                                                                                                                                                                NUCLEAR FACTOR OF ACTIVATED T-CELLS
                                                                                                                                                                       X SP REPEATS.
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                                                                                                                                                                                                                   ALPHA-TYPE ISOFORMS.
                                                                                                                                                                                                                                                    OF ACTIVATED T-CELLS
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                                             (TAD-B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            095948;
16-OCT-2001
16-OCT-2001
28-FEB-2003
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                               transcription factors whose function in liver partially that of hepatocyte nuclear factor-6.";
J. Biol. Chem. 274:2665-2671(1999).

-i- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. ACTIVATES THE TOP A NUMBER OF LIVER GENERAL ACTIVATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONC2
                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produce between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
One cut domain family
                                                     PROSITE; PS00027; HOMEOBOX 1; FALSE NEG PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                       Pfam; PF00376; CUT; 1.
Pfam; PF00046; homeobox; 1.
                                                                                                                              InterPro; IPR007108;
InterPro; IPR003350;
InterPro; IPR001356;
                                                                                                                                                        GO; GO:0003702; F:RNA polymerase II transcription factor acti. . GO; GO:0007397; P:histogenesis and organogenesis; TAS. InterPro; IPR007108; Cut_homeo.
                                                                                                                                                                                                                                       EMBL; Y18198; CAB38253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacquemin P., Lannoy V., Rousseau G.G., "OC-2, a novel mammalian member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONECUT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
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                           Activator.
                                      Transcription
                                                                             SMART; SM00389; HOX;
                                                                                         ProDom;
                                                                                                                                                                                                  MIM; 604894;
                                                                                                                                                                                                             Genew; HGNC:8139; ONECUT2.
                                                                                                                                                                                                                           TRANSFAC; T03259;
                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: Contains 1 CUT domain.
-1- SIMILARITY: BELONGS TO THE CUT HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99115605; PubMed=9915796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                   OF A NUMBER OF LIVER GENES SUCH AS SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
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                                                                                          PD000010; Homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLGPRGQDSPLLQ-----RPQHLMDQGQMRHSFSAGPELL---RQDKRP
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(Rel.
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                                      regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
 391
466
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                                                                                                                                 Homeobox.
                                                                                                                                               Hmoeo CUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
member 2 (ONECUT-2 transcription factor) (OC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                       Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoform A-beta,
isoform C-beta).
/FTId=VSP_005590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58;
Pred. No.
  HOMEOBOX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPIIKTEPTDDYEPAPTCG ->
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP_005591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G.G.,
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                                                                                                                                                                                                                                                                                                                                             It is produced through
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                                                                                                                                                                                                                                                                                                     There are no restrictions in as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lemaigre F.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATES THE TRANSCRIPTION
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Best Local S
Matches 16
                                                                                                                                                                                                                                             STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; pubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSEAE
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EMBL;
                                        the European Bioinformatics Institute. There are no rest
use by non-profit institutions as los content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by Pseudomonas aeruginosa PAO during and cloning of the arylsulfatase gene Eur. J. Biochem. 229:385-394(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL S
STRAIN=ATCC 15692 / PAO1;
MEDLINE=95262702; PubMed=7744061;
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p51691;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ATSIANTATASE (EC 3.1.6.1) (Aryl-sulfate sulphohydrolase)
ATSA OR PA0183.
                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Purification and characterization of the arylsulfatase synthesized by Pseudomonas aeruginosa PAO during growth in sulfate-free medium and cloning of the arylsulfatase gene (atsA).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beil S., Kehrli H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kertesz M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kertesz M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                          FUNCTION: SHOWS MAXIMAL ACTIVITY AT INCUBATION THAT OVERSTEPS 20 MINUTES LEADS TO ENZYME INACTIVATION.
                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic (Potential SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
                                                                                                                                                                               SUBUNIT: Monomer.
                                                                                                                                                                                        CATALYTIC ACTIVITY: A phenol sulfate + H(2)0 =
                                                                                SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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248540;
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66 P
82 P
165 P
303 P
52482 MW;
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POLY-PRO.
POLY-ALA.
POLY-HIS.
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AF21E052EFBE5DA1 CRC64;
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                                        (See http://www.isb-sib.
                                                                                                                                                              (Potential).
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S ABOVE 50 I
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RX MEDLINE=2238257; Numbed=1247792;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wasan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
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P04818;
13-AUG-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=85215597; PubMed=2987839; Takeishi K., Kaneda S., Ayusawa D., Sunucleotide sequence of a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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TYMS OR TS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Bone
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Kaneda S., Nalbantoglu J., Takeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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ACT SITE 114 114 POTENTIAL.
CONFLICT 1 1 8 -> D (IN RE)
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PDB; 1HDH; 22-NOV-01.
InterPro; IPR000917; Sulfatase.
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LQAPREIVE--KYRGRYDAGPEALRQERLARLKELG 246
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, Kaneda S., r
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Last annotation update)
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S -> D (IN REF. 1;
; 7404F3749E14EA77
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l cDNA for human
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CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goton
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MEDLINE-90110051; PubMed-2532645; Takeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno Takeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno Tenkeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno Tenkeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno Tekeishi K., Gotoh O.,
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                                                                                        PIR; A2
PDB; 11
PDB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X02308; CAA26178.1; --
EMBL; D00596; BAA00472.1; --
EMBL; BC002567; AAH02567.1;
EMBL; BC013919; AAH13919.1;
EMBL; D00517; BAA00404.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of human thymidylate synthase suggests advar chemotherapy with noncompetitive inhibitors.";
J. Biol. Chem. 276:14170-14177(2001).
-!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=21229106; PubMed=11329255;
Phan J., KOli S., Minor W., Dunlap R.B., Berger S.H., Lebioda I "Human thymidylate synthase is in the closed conformation when complexed with dUMP and rallitrexed, an antifolate drug.";
                      GO; GO:0009157; P:deoxyribonucleoside monophosphate biosynthesis; TAS. GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. . .; The InterPro; IPR000398; Thymidylat_synt. Pfam; PF00303; thymidylat_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions a modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phan J., Steadman D.J.,
Berger S.H., Lebioda L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=21216721; PubMed=11278511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 40:1897-1902(2001).
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MEDLINE=96110704; PubMed=8845352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=85261174; PubMed=3839505; Shimizu K., Ayusawa D., Takeishi K., Purification and NH2-terminal amino thymidylate synthase in an overproduc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-24.
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                                                                                                                                                                                ;; A23047; YXHUT.
;; 1HVY; 31-JAN-01.
;; 1HW3; 09-MAY-01.
;; 1HW4; 09-MAY-01.
;; 1HO; 09-MAY-01.
;; 1100; 09-MAY-01.
;; 1100; 14-NOY-01.
;; 1JUU; 14-NOY-01.
;; JUU; 19-SEP-01.
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                                                                                                                                                         188350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    BC002567; AAH02567.1; -.
BC013919; AAH13919.1; -.
D00517; BAA00404.1; -.
A23047; YXHUT.
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of mouse
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RESULT
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Best Local S
Matches 16
          P7 HUMAN

SP7 HUMAN

SP7 HUMAN

OBTDD2;

15-SEP-2003 (I

15-SEP-2003 (R)

Transcription 1

SP7 OR OSX.

Homo
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INIT_MET
ACT_SITE 1
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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HELIX
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STRAND
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STRAND
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                                                                                 16;
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                  PD001180;
                                                                PLPPAAQERDAEPRPPHGELQYLGQIQHILRCG---VRKDDRTGTGT
                                                                      PLGPRGQDSPLLQRPQH--IMDQGQMRHSFSAGPELLRQDKRPRSGS
                                                                                                                                                                                                                                                                                                                              PS00091;
                     (Rel.
(Rel.
(Rel.
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120
123
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                                                                                 Conservative
                                                                                                                                                                                                                                                           102
                                                                                                                                                                                                                                                                                                                        1180; Thymidylat synt; 1.
0091; THYMIDYLATE SYNTHASE; 1.
Methyltransferase; Nucleotide biosynthesis;
                  factor
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                                         STANDARD;
                      442,
                                                                                                            298
35584 MW;
                                                                                     21.7%;
                  , Last sequence update)
, Last annotation update)
Sp7 (Zinc finger protein
                                                                                 7;
                                                                                 Score 56.5; D
Pred. No. 11;
7; Mismatches
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                   A66F0E6D1973AB41 CRC64;
                                         431
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                                                                                          BB
                                                                                 19;
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                   osterix)
                                                                                          Length
                                                                                 Indels
                                                                                          312;
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                                                                                 Gaps
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RESULT 10
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Best Local S
Matches 21
                                                                                                                                         Q13526;
15-JUL-1998
15-JUL-1998
15-SEP-2003
. #E
     SEQUENCE FROM N.A.
MEDLINE=96195064; PubMed=8606777;
Lu K.P., Hanes S.D., Hunter T.;
"A human peptidyl-prolyl isomeras:
                                                                      Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                    Peptidyl-prolyl (Rotamase Pin1)
                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00028; ZĪNC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription_regulation; Zinc-finger; M
                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD00006; zf-C2H2; 3
ProDom; PD000003; Znf C2H2
SWART; SW00355; ZnF C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF477981; AAL84281.1; -. EMBL; AF466179; AAO33377.1; -. Genew; HGNC:17321; SP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Nakashima K., Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "cDNA sequence,
human osterix (
Submitted (JAN-:
                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein; Repeat; Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 606633;
                                                                                                                                                                                      NAMUH_LINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
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                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007087; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ashima K., Zhou X., de Crombrugghe B.;
mitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Transcriptional activator essential for os
differentiation. Binds to Sp1 and EKLF consensus seq
other G/C-rich sequences (By similarity).
SUBCELLULAR IOCATION: Nuclear (By similarity).
SUBCELLULAR IOCATION: SP1 FAMILY OF C2H2-TYPE Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 3 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                             PLNPAPYPAPHLLQPGPQHVLPQDVYKPKAVGNSGQLEGSGGAKP-----PRGASTG
                                                                                                                                                                                                                                                                PLGPRGQDSP-LLQ-RPQHLMDQ------GQMRHSFSAGPELLRQDKRPRSGSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Swiss
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                                                                                                                   (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 42, Last annotation update)
olyl cis-trans isomerase NIMA-Interacting
inl) (PPlase Pinl).
                                                                                                                                                                                                                                                                                                                                 431 AA;
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                              354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , gene structure and chromosomal localization of
(OSX) gene.";
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                        348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Institute
                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                 44994 MW; 454A6FEA84309FF9 CRC64;
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                                                                                                                                                                                                                                                                                                 21.7%;
35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   _C2H2; 1.
        isomerase
                                                                                                                                                                                                                                                                                                                                            C2H2-TYPE 1.
C2H2-TYPE 2.
C2H2-TYPE 3.
                                                                                                                                                                                                                                                                                        4.
                                                                                                                                                                                                                                                                                                Score 56.5;
Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Bioinformatics
                                                                                                                                                                                    PRT;
                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        Mismatches
      essential
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Haley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U49070; AAC50492.1; -.
EMBL; BC002899; AAH02899.1; -.
FIR; S68520; S68520.
PDB; 1FFN; 25.NOV-98.
PDB; 1F8A; 23-AUG-00.
PDB; 118C; 18-JUL-01.
PDB; 118G; 18-JUL-01.
PDB; 118H; 18-JUL-01.
Genew; HGNC:8988; PIN1.
                                                                                                                                                                                                                                                       GK; Q13526; ...
MIM; 601052; ...
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005515; F:protein binding activit
GO; GO:0007088; P:regulation of mitosis;
InterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW Rsp5_WWP.
                                                                                                       Pfam; PF00639; Rotamase; Pfam; PF00397; WW; 1. SMART; SM00456; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institutions as long as its content is in the content of the co
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MEDLINE=22388257;
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CATALYTIC ACTIVITY: Peptidylproline (omega=180) =
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PS01096;
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PPIC_PPIASE_1;
PPIC_PPIASE_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity;
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Matches 15; Conser
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HMPH_CHICK
Q05502;
Q01-JUN-1994
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                                                                                                  This
                                                                                                                                                                                                                                 Crompton M.R., Bartlett T.J., Macgregor A.D., Manfioletti
Buratti E., Giancotti V., Goodwin G.H.;
"Identification of a novel vertebrate homeobox gene expres
haematopoietic cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
01-NOV-1995 (Rel.
                               modified
                                                                                  between
                                                                                                                                                                                                                      Nucleic
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Archosauria; Aves; N
                                                                                                                                                                                                                                                                                                                                                                                                                       Homeobox protein PRH.
Gallus gallus (Chicken).
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                                        s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                IN HEMATOPOIETIC DIFFERENTIATION.
SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: IN ALL HEMATOPOIETIC
                                                                                                                                                                                             FUNCTION: RECOGNIZES THE DNA SEQUENCE 5'-ATTAA-3'.
                                                                                                                              PERIPHERAL BLOOD ERYTHROCYTES AND IN THE LIVER AND LUNG.
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PS50020;
               non-profit institutions as long and this statement is not removed. requires a license agreement (See
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to license@isb-sib.ch).
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32,
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WW_DOMAIN_2; 1.
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Veognathae; Galliformes; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18243 MW;
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Last annotation update)
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Pred. No.
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277
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P37418;
01-OCT-1994
                                                                                                                                                                                                                MEDLINE=94266/12; runneu-valled J.K.; Roland K.L., Esther C.R., Spitznagel J.K.; "Isolation and characterization of a gene, pmrD," Isolation and characterization of a gene, pmrD, where confers resistance to polymyxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA BIND
                                                    -!- CATALYTIC ACTIVITY: ATP + O-succinylbenzoate diphosphate + O-succinylbenzoyl-COA.
-!- PATHWAY: Menaquinone biosynthesis.
-!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
0-succinylbenzoic acid--CoA ligase (EC 6.2.1.26)
                                                                                                                                                               J. Bacteriol. 176:3589-3597(1994
                                                                                                                                                                                                      multiple copies.";
                                                                                                                                                                                                                                                                                                                                                                                                                          McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Le
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S.
Ceonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul
Leonard S., Sun H., Florea L., Miller W., Stoneking T., Nhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homeobox; DNA-binding; Developmental DOMAIN 1 140 PRO-RIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X64711; CAA459
PIR; S78063; S78063.
HSSP; P22808; 1NK3.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                          Ryan E., Sun H., Florea L. Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (O-succinylbenzoate-CoA synthase).
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                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome
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13; Conserv
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277 AA;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UTV9; Q96BK6; Q96K05; Q9NW04;
16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
DEAD-box protein abstrakt homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE008803; AAL21206.1; -.
EMBL; U02281; AAA21323.1; -.
StyGene; SG10221; menE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto J., Wakamatsu A., Nakamura
Ninomiya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00501; AMP-binding; 1. PROSITE; PS00455; AMP_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Irion U., Leptin M.;
"Developmental and cell biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20076860; PubMed=10607561;
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9:1373-1381(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing project.";
001) to the EMBL/GenBank/DDBJ databases.
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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InterPro; IPR001650; Helicase_C.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00939; Zf-CCHC; 1.
PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00480; HELICC; 1.
SMART; SM00480; HELICC; 1.
SMART; SM00480; HELICC; 1.
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RL18 YEAST
P07279;
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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,00
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: PROBABLE ATP-DEPENDENT RNA HELICASE.
POST-TRANSCRIPTIONAL GENE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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EMBL; AK001255; BAA91585.1; -.
EMBL; AK027768; BAB55355.1; -.
                                     Saccharomyces cerevisiae (Baker's yeast).
                                                           N0425)
                                                                              60S ribosomal protein L18 (RPL18A OR RP28A OR YOL120C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0006915; P:apoptosis; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0006396; P:RNA processing; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no rest
                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00039; DEAD_ATP_HELICASE; FALSE_NEG.
ATP-binding; RNA-binding; Helicase; Nuclear protein.
NP_BIND 225 232 ATP (BY SIMILARITY).
SITE 344 347 DEAD BOX.
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an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     PLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTG
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Ascomycota; Saccharo; Saccharomycetaceae;
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Q9P2N4; Q9NR29;

16-OCT-2001 (Rel. 40, (

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28-FEB-2003 (Rel. 41, )
                                                                                                                                                                                                                                                                                                                                     Pfam; PF00828; PROSITE; PS0110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lafuente M.J., Gamo F.J., Gancedo C.;
"DNA sequence analysis of a 10 624 bp fragment of the left arm of chromosome XV from Saccharomyces cerevisiae reveals a RNA binding protein, a mitochondrial protein, two ribosomal proteins and two ropen reading frames.";
Yeast 12:1041-1045(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96132033; PubMed=8553702;
Maurer K.C.T., Urbanus J.H.M., Planta R.J.;
"Sequence analysis of a 30 kb DNA segment from yeast che carrying a ribosomal protein gene cluster, the genes er plasma membrane protein and a subunit of replication for novel putative serine/threonine protein kinase gene.";
Yeast 11:1303-1310(1995).
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                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                      InterPro; IPR000039; Ribosomal_L18e.
Pfam; PF00828; Ribosomal_L18e; 1.
PROSITE; PS01106; RIBOSOMAL_L18E; 1.
Ribosomal protein; Multigene family; 3D-structure.
SEQUENCE 186 AA; 20563 MW; D097B187F369EACD CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97051591; PubMed=8896268;
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SIMILARITY: BELONGS TO THE
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                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                          PRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTG 48
                                                                                                                                                                                                                                                Conservative
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                                                                             STANDARD;
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OF RIBOSOMAL PROTEINS
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     InterPro;
InterPro;
                                                GO; GO:0008191; F:tumor suppressor; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0006516; P:glycoprotein catabolism;
InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep M12B propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR001894; TSP1.
   Pfam;
Pfam;
                                                                                                                                                                                                                                          EMBL; AF261918; AAF89106.1;
EMBL; AB037733; BAA92550.1;
HSSP; P15167; 1ATL.
                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADAMTS-9 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 9) (ADAM-TS 9) (ADAM-TS9). ADAMTS9 OR KIAA1312.
                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
The complete sequences of 150 new cDNA clones from brain which c
                                                                                                                                                                                      MIM; 605421; -.
                                                                                                                                                                                                        Genew; HGNC:13202; ADAMTS9.
                                                                                                                                                                                                                           MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: Binds 1 zinc ion per subunit (By -!- SUBCELLULAR LOCATION: Secreted. Associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENI
SIMILARITY).
SIMILARITY: Belongs to peptidase family M121
SIMILARITY: Contains 1 disintegrin-like doma
SIMILARITY: Contains 12 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9P2N4-2; Sequence=VSP_005499, VSP_005500;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ALL FETAL TISSUES.
EXPRESSED SLIGHTLY IN ADULT OVARY, PANCREAS, HEART, KIDNEY, LUN PLACENTA. ALSO DETECTED IN SPINAL CORD AND BRAIN. NOT DETECTED COLON, SMALL INTESTINE, TESTIS, LIVER, SKELETAL MUSCLE, SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THYMUS.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX
SIMILARITY).
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ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  large proteins in vitro."; Res. 7:65-73(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative
                     Pro; IPR006025;
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                                                                                                                                                                                                                               M12.021;
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 Reprolysin;
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                   5; Zn_MTpeptdse.
_M12B_propep; 1.
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SMART; SM00209; TSP1; 12.
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SIGNAL 1
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PS00546; CYSTEINE SWITCH; FALSE NEG.
PS00427; DISINTEGRIN 1; FALSE NEG.
PS50214; DISINTEGRIN 2; FALSE NEG.
PS50092; TSP1; 12.
                                                                         QDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGS
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                                                                                                       Conservative
                                                                                                                                                              A,
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loprotease; Zinc; Signal; Glycoprotein; Zymogen; lular matrix; Alternative splicing.
                                                                                                                                                                                                     1629
                                                                                                                                                                                                                                                                                                                                                                                                                       1494
1555
1613
96
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1054
1104
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1240
1296
1379
1440
                                                                                                                                                             367 F -
; 182649 MW;
                                                                                                                                                                                                                                                                                                 223
434
438
438
444
112
1135
749
                                                                                                                       21.2%;
35.9%;
                                                                                                                                                          Short).
/FTId=VSP 005499.
/FSId=VSP 005500.
/FSId=VSP 005500.
/F -> L (IN REF. 1).
F -> L (IN REF. 1).
                                                                                                         ω
••
                                                                                                                       Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                              CYSTEINE SWITCH (
ZINC (CATALYTIC)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                              TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 7.
TSP TYPE-1 10.
TSP TYPE-1 10.
TSP TYPE-1 11.
TSP TYPE-1 11.
TSP TYPE-1 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISINTEGRIN-LIKE.
TSP TYPE-1 1.
TSP TYPE-1 2.
CYS-RICH.
                                                                                                                                                                                                                                                                                 N-LINKED
N-LINKED
                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
CLVTCGKGH -> VRWEGCYFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                   ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPACER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METALLOPROTEASE
                                                                                                         Mismatches
                                                                                                                                                                                                                                                     ATALYTIC) (BY SIMILARITY).

ATALYTIC) (BY SIMILARITY).

D (GLCNAC. . . ) (POTENTIAL).

D (GLCNAC. . . ) (POTENTIAL).
                                                                                                                       DB 1; ; . 1.1e+02;
                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
(BY SIMILARITY).
                                                                                                                                 Length 1629;
                                                                              46
                                                                                                         Indels
                                                                                                                                                                                                                                              (in isoform
                                                                                                         6
                                                                                                         Gaps
                                                                                                         1;
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Result
No.
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Maximum Match 100%
Listing first 45 sv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                      Score
      seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPTREMBL 23:*

1: sp archea:*
2: sp bacteria
3: sp fungi:*
4: sp human:*
5: sp inverteb
6: sp mammal:*
7: sp mhc:*
8: sp organel:
9: sp phage:*
10: sp plant:*
11: sp rodent:
12: sp virus:*
13: sp vertebr
14: sp urclase
15: sp archea!
16: sp bacteri
17: sp_archea!
                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        July 24, 2003, 11:47:53 ; Search time 10.9048 Seconds (without alignments) 1159.539 Million cell updates/sec
      US-09-991-681-31
260
1 EPLGPRGQDSPLLQRPQHLM.....SAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_invertebrate:*
sp_mammal:*
      589
1770
4625
1655
384
293
345
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281
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277
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                                                                                                                                                                                                                                                                                                                                                                                      BB
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17
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2
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  08N4Y4
09ULH6
99ULH6
6 09HU19
024754
6 08DL53
6 09X6T3
6 09X6T3
7 09YBM1
7 09YBM1
7 09YBM1
7 09R1X2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830525
Q9hu19 pseudomonas
Q24754 drosophila
Q84153 synechococc
Q9x6t3 streptomyce
Q9rt11 deinococcus
Q9ybm1 aeropyrum p
Q9r1x2 mus musculu
Q9crv1 mus musculu
Q9crv1 mus musculu
Q9act4 streptomyce
Q9nrx6 homo sapien
Q85275 potato viru
Q9c2e4 neurospora
Q96wj2 kluyveromyc
                                                                                                                                                                                                                                                                                       Q8n4y4 homo sapien
Q96ch9 homo sapien
Q9ulh6 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                    Description
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ď	n 4	4	3	42	41	40	9	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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			•	٠	21.7	•	•	21.7	٠		21.9		22.1	22.1		22.1	22.1	22.1	22.1	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.5	22.5
0	0 1	714	561	480	431	279	230	165	119	159	101	1675	1451	1451	1451	1207	511	500	405	743	726	628	523	357	270	221	172	3429	3419.
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K V X Y X	CONTO	OBWZY7	08G4W0	Q91046	Q8TDD2	Q8WYK3	QBWYK4	Q9CUI9	Q9CTL8	Q9I9K6	Q8BYT7	Q8UUR1	049142	049140	049143	Q8I174	Q8PIW9	QBUUQ9	Q8UER5	Q9N313	Q8MXS5	056253	Q9N310	Q9A875	Q96CE9	Q95KQ8	Q9CUI2	Q24593	Q9W425
βρχιο, αιαριασβαια	Control out to be control	3		6 gob:	homo	homo	Q8wyk4 homo sapien	Q9cui9 mus musculu		xen			O49142 arabidopsis		O49143 arabidopsis	Q8i174 drosophila			Q8uer5 agrobacteri	Q9n3l3 caenorhabdi	Q8mxs5 caenorhabdi	w	Q9n310 caenorhabdi	Q9a875 caulobacter	Q96ce9 homo sapien	Q95kq8 sus scrofa		Q24593 drosophila	Q9w425 drosophila

ALIGNMENTS

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RESULT 2
Q96CH9
ID Q96CC
AC Q96CC
DT 01-D
DT 01-D
DT 01-O
DE Hypo
OS Homo
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Q8N4Y4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 260; DB 4; Length 589; Best Local Similarity 100.0%; Pred. No. 6.5e-26; Matches 49; Conservative 0; Mismatches 0; Indels
                               Q96CH9 PRELIMINARY; PRT; 592 AA.
Q96CH9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8N4Y4
Q8N4Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC033191; AAH33191.1; -.
NON TER 1 1
SEQÜENCE 589 AA; 66086 MW; 8041EEA348DE65F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similar to KIAA1244 protein (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
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    (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
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RESULT 4
Q9HU19
ID Q9HU19
AC Q9HU1
AC Q9HU
DT 01.-M
DT 01.-C
DE Prob
GN PASI
OS PBeu
OC Bact
OC Bact
OC Bact
RN ([1]
RN [1]
RN [1]
RN SEOU
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Q9ULH6
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Best Local S
Matches 49
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Best Local S
Matches 49
   SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / 1
MEDLINE=20437337; Pul
Stover C.K., Pham X.
                                                                                                                                                               Q9HU19;
                                                                                                                            01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                       Hypothetical SEQUENCE 17
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000904; Sec7. SMART; SM00222; Sec7; 1.
                                                                                                                                                                                                                                                                                                                                                                  "KIAA1244 as a novel distantly related member (BIG3) of subfamily of ARF GEFs.", Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF413080; AAL04174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ULH6; Q96P46;
01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                  Probable two-component response
                                                                                                                                                                                                                                                                                                                                                                                                               Hong W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9HTIN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC014227; AAH14227.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                         NCBI_TaxID=287;
                                                                     Pseudomonadaceae; Pseudomonas
                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                             Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467
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                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                            EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
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                                                                                                                                                                                                                                EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                       al protein.
1770 AA;
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                                                                                                                                                                                                                                                                            100.0%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
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                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
/ PAO1;
pubMed=10984043;
n X.-Q.T., Erwin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
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Primates;
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                                                                                                                                                                                                                                                                                                                       195845 MW;
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22,
22,
                                                                                                                 Last sequence update)
Last annotation update)
onse regulator.
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Last annotation update)
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                                                                                                                                                                                                                                                                            Score 260; D
Pred. No. 2.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 260; DB 4;
Pred. No. 6.5e-26;
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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   A.L.,
                                                                                                                                                                                                                                                                                                                         5E996E36A6F92AB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1770
                                                                                                                                                                           462
  Mizoguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                           B
                                                                                                                                                                                                                                                                         DB 4;
.2e-25;
.8 0;
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   S.D.,
                                                                                                                                                                                                                                                                                                Length 1770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 592;
                                                                                                                                                                                                                                                                          Indels
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PRODOM; PRO100039; Response reg; 1.

SMART; SM00382; AAA; 1.

TIGRFAMM; TIGRO1199; HTH fis; 1:

PROSITE; PS50110; RESPONSE REGULATORY; 1.

PROSITE; PS50675; SIGMA54 INTERACT 1; 1.

PROSITE; PS00676; SIGMA54 INTERACT 2; 1.

PROSITE; PS00688; SIGMA54 INTERACT 3; 1.

PROSITE; PS00688; SIGMA54 INTERACT 4; 1.

PROSITE; PS00688; SIGMA54 INTERACT 4; 1.

PROSITE; PS00688; SIGMA54 INTERACT 4; 1.
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Q24754;
01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                        Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7244;
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Nature 406.959-964(2000).
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                                          MEDLINE=94111143; PubMed=8283480;
Newfeld S.J., Schmid A.T., Yedvob
"Homopolymer length variation in
J. Mol. Evol. 37:483-495(1993).
                                                                                                                                                                                                                mastermind.
                                                                                                                                                                                                                                          SEQUENCE OF 260.762 FROM N.A.
MEDLINE=91251140; PubMed=1904096;
Newfeld S.J., Smoller D.A., Yedvobnick B.;
"Interspecific comparison of the unusually
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription SEQUENCE 462
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Pfam; PF00072; response_reg;
Pfam; PF00158; Sigma54_activ
SEQUENCE FROM N.A.
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InterPro;
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iPR002078; Sig54_interact.
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IPR002197; HTH_Fis.
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462 AA; 50864
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5.7;
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Submitted (MAY-1992) to the EMBL EMBL; M92914; AAC37201.1; -. FlyBase; FBgn0013119; Dvir\mam. SEQUENCE 1655 AA; 175048 MW;
                                                                                                                                                                                                                                                                                        Q9X6T3;
Q9X6T3;
01-NOV-1999
01-NOV-1999
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamot Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
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01-NOV-1999 (TrEMBLrel.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DevC-like ABC transporter permease protein.
SEQUENCE FROM N.A.
                                                    Streptomycineae; Streptomycetaceae;
NCBI_TaxID=68270;
                                                                                                                         Streptomyces spectabilis.
Bacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                          Glycosyltransferase
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01-MAR-2003
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Mewfeld S.J., Tachida H., Yedvobnick B.;
"Drive-selection equilibrium: homopolymer evolution
gene mastermind.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42660 MW;
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Last
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Pred. No. 8.6;
8; Mismatches
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Pred. No. 27;
9; Mismatches
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Nakazaki N.,
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RESULT 9
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  01-NOV-1999
01-NOV-1999
01-MAR-2002
                                                                       Q9YBM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., White O., Eisen J.A., Heidelberg J.F., Nelson W.C., Richardson D.L., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF145038; AAD28487.1; -.
InterPro; IPR001173; Glyco_trans_
Pfam; _PF00535; Glycos_transf_2; ]
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"Isolation of the genes for glycosyltransferase and N-
methyltransferase from Streptomyces spectabilis ATCC2774
spectinomycin producer.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005502; ADP_ribglychydro.
InterPro; IPR000209; Peptidase_S8.
Pfam; PF03747; ADP-ribosyl_GH; 1.
PROSITE; PS00136; SUBTILASE_ASP; 1.
Hydrolase; Complete proteome.
SEQUENCE 333 AA; 34881 MW; 47042A084B54D638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9RT11;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the radioresistant radiodurans R1."; Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Deinococcus-Thermus; Deinococcaceae; Deinococcus.
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01-MAR-2003
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l Similarity 41.7%;
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                                                                                                                                                                                                                                                            GPRGQDSPLLQRPQHLMDQGQMRHSFSAG----
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(TrEMBLrel. 23, Last and
glycohydrolase, putative.
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Created)
Last sequence update)
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MGD; MGI:96086; Hhex.
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeobox; 1.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
               PROSITE; PS00027; HÓMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 271 AA; 29952 MW; 4COAD438CCAAA6F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB017132; BAA76714.1; -.
EMBL; AB017130; BAA76714.1; JOINED.
EMBL; AB017131; BAA76714.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP000062; BAA80577.1; -. Hypothetical protein; Complete SEQUENCE 345 AA; 38129 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHEX OR HEX (PRH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein APE1577. APE1577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129;
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                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myint Z.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuriyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=129; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desulfurococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M., Inazu T., Tanaka T., Yamada K.,
M., Noguchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organization and promoter analysis of a
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38129 MW; CF1D95C2B17E92E8 CRC64;
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ba S.-I., Ankai A., Kosugi H.,
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Rackimann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Toruno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Radraferelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Lyons P., Raing B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashiraki Y., Storch
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Q9CRV1;
01-JUN-2001
01-JUN-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR EMBL; AK014111; BAB29163.1; -. HSSP; P22808; 1NK3.
                                                                                                                                                                                                                                                                                                               SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Embryo; MEDLINE=21085660; PubMed=11217851;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                 SEQUENCE
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Pfam; PF00046; homeobox; 1.
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                                                                                                                                                                                                                                                                                 DNA-binding; Homeobox; Nuclear protein
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l6; Conservative
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DPLGKPLLWSPFLQRPLHKRKGGQVRFSNDQTVEL
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nilarity 45.7%;
Conservative
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MBLrel. 17,
MBLrel. 20,
expressed
                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
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                                                                                                                                          Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
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                                                                                                                                                                  11;
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                                                                                                               17;
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                                                                                                                                                                  Length 280;
                                                                                                               Indels
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; Murinae; Mus
                                                                                                               0,
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                                                                                                               Gaps
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RESULT 12 Q9ACT4 ID Q9ACT

Q9ACT4

PRELIMINARY;

PRT;

381

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Q9ACT4;

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QONRE AC QONRE AC QONRE AC QONRE AC QONRE DT 01-00 DT 01-MD DE Phosp OS Homo OC Eukar OX NCBL RX NCBL TRN [1] - RN [1] -
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                                                                             Query Match
Best Local S
Matches 18
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Best Local
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                                                                                                                                                                                                                      MEDLINE=20347929; PubMed=10764818;
Kisseleva M.V., Wilson M.P., Majerus P.W.;
"The Isolation and Characterization of a cDNA Encoding specific Inositol Polyphosphate 5-Phosphatase.";
J. Biol. Chem. 275-20110-20116(2000).
EMBL; AF187891; AAF81404.1; -.
InterPro; IPR000310; IPPC.
InterPro; IPR000300; IPPC.
Plam: PF03372; Exo_endo_phos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation updat
Hypothetical protein SCP1.217.1c.
SCP1.217.1C OR SCP1.217AC.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphatidylinositol polyphosphate 5-phosphatase type IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model actinomycete Streptomyces coellcolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL590464; CAC36740.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens (Human).
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                               N
                                                                                                                                                                                                       SM00128; IPPc;
                                                                        . Similarity 18; Conserv
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PLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELL--RQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDSPLLQRPQHL--MDQGQMRHSF----SAGPELLRQ--DKRPRSGSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDDPLSPRPGHLFRIDAGVFRHTLLRLPAAGDPWLREVLENLPTYARTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; CAC36740.1; -. protein; Plasmid; 81 AA; 40037 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                                                                                                                                                                             AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.7%;
                                                                                                                                                                          70150 MW;
                                                                                                  22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
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Pred. No.
                                                                           Score 59; DB 4
Pred. No. 28;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                          1BB794522C94A49F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
45B3D68D962B7525 CRC64;
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                                                                           27;
                                                                                                                         Length 644;
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RESULT 15
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Best Local S
Matches 17
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Best Local S
Matches 19
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Q85275;
                                                                                                                     Interpro; IPRO01683; PX.
Pfam; PF00787; PX; 1.
PROSITE; PS50195; PX; 1.
SEQUENCE 580 AA; 64100 MW;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheise
Nyakatura G., Mewes H.W., Ma
Submitted (FEB-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1994) to the EEMBL; X82848; CAA58053.1; -
InterPro; IPR002540; Poty_P1.
Pfam; PF01577; Poty_P1; 1.
NON_TER 276 276
                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                     Submitted (NOV-2001) to the EMBL; AL513463; CAC28769.2;
                                                                                                                                                                                                                     German Neurospora genome Submitted (NOV-2001) to t
                                                                                                                                                                                                                                                                                                                                                                                                    Sordariales; Sor
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Related to vacuolar protein 9G6.210.
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01-DEC-2001
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01-MAR-2003
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potato virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potato plants transformed with esistant to PVY-O.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
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                                           l Similarity
17; Conserv
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  EPLGPRG-----QDSPLLQRPQHLMDQGQMRHSFSAGPELLRQD-KRPRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPQAPRGIIHTTPRVRKVKTRPIIKLTEGQMDH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 AA; 31269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 17, (TrEMBLrel. 19, (TrEMBLrel. 23,
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                           22.5%;
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                                                                                                                                                                                                                                            project;
                                                                                                                                                                                                                                                                                                      Mannhaupt G.;
he EMBL/GenBank/DDBJ
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,;
                                           7;
                                         Score 58.5; I
Pred. No. 29;
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Billing-Medel PA, Cohen Granados EN, Hodges SC,
                                                                                                                                        (BILL/)
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PN, Gordon J
Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordan J;
Roberts-Rapp
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RESULT 3
AAW85472
ID AAW8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising amino acids 332-371 of human prostate-specific PS118 polypeptide (see AAM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate tissue. PS118 polypeptides, polymucleotides, in non-prostate tissue. PS118 polypeptides, polymucleotides, admitibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polymucleotides in transfected host calls, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the prostate and may provide an early means of detecting diseases of the between the clinically important and unimportant prostate cancers without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
WPI; 1998-610000/51.
N-PSDB; AAV82812.
                                           Billing-medel PA,
Granados EN, Hod
Russell JC, Stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                      AAW85472;
                                                                                                                                                                                                                                                                                                                                                                                                                   AAW85472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 44; 57pp;
                                                                                                                                  23-APR-1997;
                                                                                                                                                                                             29-0CT-1998
                                                                                                                                                                                                                         WO9848054-A1
                                                                                                                                                                                                                                                                                                             PS118 protein encoded by consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-187683/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Russell JC,
                                                                                                     (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                  clone; PS118; prostate tumour tissue; prostatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is that of an immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK
                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 AA;
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Conservative 0;
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                                            Stroupe
                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                          Hodges
                                                                                                                                  97US-0842385
                                                                                                                                                                98WO-US08239.
                                            Cohen M, Colpitts TL, es SC, Klass MR, Krat pe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 23;
Pred. No. 1.6e-35;
                                                          g TL, Friedman
Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                          PN, Gordon 
Robertsrapp
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Best Local S
Matches 40
                    Billingel
Granados E
Russell JO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a cDNA library made from prostate tumour tissue. Recombinant PS18 protein is used to detect PS118 specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 protein or mucleic acid, which are prostate related, and altered or elevated in prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of prostatic disease, particularly cancer, and to identify subjects at
WPI; 2002-665429/71
                                                                                                                               (FRIE/)
(GORD/)
(GRAN/)
                                                                                                                                                               (COLP/)
                                                                                                                                                                                                          23-APR-1998;
23-APR-1997;
                                                                                                                                                                                                                                         26-NOV-2001; 2001US-0991681.
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                                                                                                                                                                                                                                                                                      US2002086316-A1.
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                             Human; prostate; prostate-specific sequence; prostate cancer; EST; expressed sequence tag; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                               Human prostate-specific PS118 protein fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                      27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                            AAO19165;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAO19165 standard; Protein; 518 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New
                                                                           (ROBE/)
                                                                                                                     (HODG/
                                                                                                 (KRAT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                           KLAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332
                                                                                                                  COHEN M.
COLPITTS T L.
FRIEDMAN P N.
GORDAN J.
GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
40; Conserv
                 JC,
                                                                ROBERTS-RAPP
RUSSELL J C.
STROUPE S D.
                                                                                                                                                                                    BILLINGEL P A.
                                                                                               KLASS M R.
KRATOCHVIL J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid and
t of prostatic dis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 371
                                          PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                     Stroupe
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                Cohen
Hodges
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                                                                                                                                                                                                          98US-0065383.
97US-0842385.
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                     SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                     F 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and proteins - used for diagnosis and disease, especially cancer, and also
                              Colpitts TL,
Klass MR, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB
Pred. No. 1.7
); Mismatches
                                Friedman
Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
1.7e-34;
                              JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 518;
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                                          Gordan J;
                              Roberts-Rapp
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RRESULT 5
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XX AAMSOS
XX AAMSOS
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Best Local
                                                                                                                                                                                                                       Billing-Medel PA,
Granados EN, Hodo
Russell JC, Stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                       preventing or treating or disease -
                                          Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                                                                                                                                                                       (GRAN/)
(HODG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COPL/)
(FRIE/)
(GORD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COHE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                        (KLAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1997;
                                                                                                                                                     2002-187683/24.
DB; ABA91651.
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                                                                                                                                                                                                                                                                                                                           FRIEDMAN P N.
GORDON J.
GRANADOS E N.
HODGES S C.
KLASS M R.
KRATOCHVIL J D.
ROBERTS-RAPP L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COPLPITTS T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COHEN M.
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                            Stroupe
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                                                                                                                                                                                                                            PA, Cohen I
Hodges SC,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0842385.
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                                                                                                                                                                                                                                                    M, Coplpitts TL, Friedman PN, Gordon C
Klass MR, Kratochvil JD, Roberts-Rapp
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Pred. No. 1.7
0; Mismatches
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                                                                         prognosticating,
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                                                                                                                                                                                                                                                                              Gordon J;
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CC polypeptide, as predicted from a partial consensus cDNA sequence
CC (see BAB31651), and lacking the N-terminal region. The PS118
CC consensus sequence is found at least 12 times more often in
CC prostate than in non-prostate tissue. PS318 polypeptides,
CC including derivatives of the present sequence, polynucleotides,
CC antibodies, agonists and inhibitors are useful for detecting,
CC diagnosing, staging, monitoring, prognosticating, preventing and
CC treating (including by genetic immunisation), or determining the
CC prostate, such as benign prostatic hyperplasia, prostatitis,
CC prostate, such as benign prostatic hyperplasia, prostatitis,
CC prostate, such as benign prostatic hyperplasia, prostatitis,
CC prostate such as benign prostatic cancer, tumours and
CC metastases. The PS118 polypeptides can be produced by expression
CC of PS118 polypucless in transfected host cells. The methods
CC and reagents of the invention may provide an early means of
CC detecting diseases of the prostate and may also provide new markers
CC which can differentiate between the clinically important and
CC unimportant prostate cancers without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences, orimers, oligomers, and for chromosome
                                                                          Claim 20;
                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                       Drmanac RT,
                                                                                                                                                                                                                                                                                                        31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001
                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                         2001-639362/73.
DB; AAS73915.
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                                                                         SEQ
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2000US-0649167
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                                                                     40087; 103pp;
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Pred. No.
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                                                                       English.
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                                                                                                                                                                                                                    WPI; 200
N-PSDB;
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                                                                                      New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders invaluerating the protein expression or biological activity -
                                                                                                                                                                                                                                                                                                                                                  Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
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DB; ABQ99421.
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                                                                                                                                                                                                                                                                                                                 Goodrich RW,
ue AJ, Yang
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                                                                                                                                                                                                                                                                                                                     Liu C, Zhou
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Pred. No. 5.2
0; Mismatches
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Claim 20; SEQ ID 495;

394pp; English

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RESULT 8
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CC (AB099268-AB099608) and proteins (AB04682-AB065022). The sequences are
CC useful in therapeutic, diagnostic and research methods. The
CC polynuclectides may be used in the field of molecular biology as
CC polynuclectides may be used in the field of molecular biology as
CC hybridisation probes, primers for PCR, for chromosome and gene mapping,
CC for the recombinant production of protein, or in generation of anti-sense
CC DNA or RNA. The polynuclectides are useful in diagnostics as expressed
CC sequence tags (ESTs) for identifying expressed genes or for physical
CC markers, or as nutritional sources or supplements. The proteins may be
CC used to maintain and expand cell population in a totipotential or
CC puripotential state useful for re-engineering damaged or diseased
CC tissues, transplantation, manufacture of bio-pharmaceuticals or the
CC development of bio-sensors. The polynucleotides and proteins are useful
CC protein expression or biological activity, e.g. haematopoietic disorders,
CC central/peripheral nervous system diseases, mechanical and traumatic
CC disorders, non-healing wounds, immune deficiencies and disorders,
CC infectious diseases caused by viral, bacterial or fungal infection,
CC authormune diseases caused by viral, bacterial or fungal infection.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                         WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
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40; Conserv
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RESULT 9
ABG16511
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Best Local Similarity
                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
Claim 20; SEQ ID No 46870; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                 N-PSDB; AAS80698.
                                                                                                                                                                                         WPI; 2001-639362/73
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Pred. No. 5.7e-3
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RESULT 10
ABG16512
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
Claim 20; SEQ ID No 46871; 103pp; English
                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                             N-PSDB;
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23-AUG-2000; 2000US-0649167.
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food supplement; medical imaging; diagnostic; genetic disorder.
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DB; AAS80699.
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                                                                                                                                                                                                                                                                                                                                                              HYSEQ INC.
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0; Mismatches
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o. 10;
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The invention relates to isolated polynucleotide (I)

and

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome

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CC Note: The sequence data for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed cast for this patent did not appear in the printed
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Best Local
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                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                       Claim
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #16501.
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                                                                                                                                 biodiversity
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                                                                                    20; SEQ ID No 46869;
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2000US-0649167.
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100.0%; Pred. No.
                                                                                  103pp; English.
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5. 21;
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RESULT 12
ABG17536
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CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO or internation of internation of internations.
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                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chrome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                       Claim 20; SEQ ID No 47895; 103pp; English.
                                                                                                                                                                                                                                   biodiversity
                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder.
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  polynucleotides
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DB; AAS81723.
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2000US-0649167
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  are also used in
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100.0%; Pred. No.
Live 0; Mismatch
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diagnostics as expressed sequence tags
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                                                     chromosome
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CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC diagnostice, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences of the invention.
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
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Best Local
                                                         30-APR-1999;
04-MAY-1999;
05-MAY-1999;
                                                                                                                                 21-APR-1999;
23-APR-1999;
23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 39388.
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               99US-0132486.
99US-0132487.
99US-0132863.
                                                         99US-0132407.
99US-0132484.
99US-0132485.
                                                                                                                   99US-0130449.
99US-0130510.
99US-0130891.
99US-0131449.
                                                                                                                                                                                                         99US-
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99US-0130077.
                                                                                                                                                                                                                                      99US-0126785.
99US-0127462.
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                                                                                                    99US-0132048
                                                                                                                                                                                                                          99US-0128234.
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                                                                                                                                                                                                                                                                                                               99US-0123180.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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20-JUL-1999; 99US-011 20-JUL-1999; 99US-012 20-JUL-1999; 99US-012 21-JUL-1999; 99US-012 21-JUL-1999; 99US-013 21-JUL-1999; 99US-013 22-JUL-1999; 99US-013 22-JUL-1999; 99US-013 22-JUL-1999; 99US-013 22-JUL-1999; 99US-013 22-JUL-1999; 99US-013 23-JUL-1999; 99US-013 23-JUL-1999; 99US-013	7-UN-1999 99US-011 8-UN-1999 99US-011 1-UN-1999 99U	14-MAY-1999; 99US-011 14-MAY-1999; 99US-011 14-MAY-1999; 99US-011 14-MAY-1999; 99US-011 14-MAY-1999; 99US-011 19-MAY-1999; 99US-011 20-MAY-1999; 99US-011 24-MAY-1999; 99US-011 25-MAY-1999; 99US-011 27-MAY-1999; 99US-011 27-MAY-1999; 99US-011 01-JUN-1999; 99US-011 11-JUN-1999; 99US-011 11-JUN-1999; 99US-011 11-JUN-1999; 99US-011 11-JUN-1999; 99US-011 11-JUN-1999; 99US-011

-0CT-199 -0CT-199 -0CT-199 -0CT-199 -0CT-199 -0CT-199 -0CT-199 -0CT-199	AUG-1999	<i>222222222222222222222222222222222222</i>
9005-015 9005-015 9005-016 9005-016 9005-016 9005-016	99US-014856 99US-014868 99US-014917 99US-014972 99US-014972 99US-014972 99US-015106 99US-015106 99US-015106 99US-015106 99US-015130 99US-0151330 99US-0151330 99US-0151330 99US-0155465 99US-015645 99US-015645 99US-015645 99US-015645 99US-015645 99US-015645 99US-015645 99US-015645 99US-015645	9US-014527 9US-014527 9US-014591 9US-014591 9US-014591 9US-014638 9US-014638 9US-014638 9US-014730 9US-014730 9US-014730 9US-014730 9US-014730 9US-014730 9US-014730 9US-014730 9US-014730

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RESULT 14
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Matches
25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
01-APR-1999
01-APR-1999
16-APR-1999
16-APR-1999
23-APR-1999
11-MAY-1999
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11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction hybridisation assay; genetic mapping; gene etermination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment
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- OCT - 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | DKTISKL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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99US-0161404.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161993.
99US-0161993.
99US-0161993.
  3-0121825

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3-0125788

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Pred. No. 25;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n pathway; metabolic pathway;
expression control; promoter;
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9908-0137528.
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9908-0138094.
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9908-0145518.
9908-0145513.
9908-0145513.
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02-AUG-1999 02-AUG-1999 03-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 10-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 13-AUG-1999

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RESULT 15
ABB2161
ID 82161
ID 82161
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ABB2262
XX ABB22
XX ABB22
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XX ABB22
XX ABB22
XX NOVX;
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Best Local S
Matches 7
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21-MAR-2001;
29-MAR-2001;
03-APR-2001;
09-APR-2001;
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10-APR-2001;
01-MAR-2002;
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                 The invention relates to novel polypeptides NOVX (NOV1-NOV8) and polypucleotides encoding them. The NOVX polypeptides can be expressed by standard recombinant methodology. The polypeptides, polynucleotides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), immune disorders (osteoarthritis), neurodegenerative disorders, Alzheimer's disease, pellepsy, hematopoletic disorders, inflammatory skin disease, epilepsy, hematopoletic disorders, inflammatory skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kekuda R,
Shimkets F
                                                                                                                                                                                                                                                                                                                 New isolated NOVX polypeptides and preventing, diagnosing or treating idiabetes, obesity, atherosclerosis, asthma, or infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVX; NOV6b; human; antidiabetic; anorectic; cardiant; hypotensive; antiatteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; noutropic; neuroprotective; antiparkinsonian; osteopathic; anticonvulsant; antiarthritic; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-713441/77.
)B; ABQ79947.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURAGEN CORP.
COR THERAPEUTICS.
                                                                                                                                                                                                                                                                 Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conley PB,
A, Leach MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2001US-273049P.

2001US-277791P.

2001US-279883P.

2001US-281248P.

2001US-282537P.

2001US-28264P.

2001US-282867P.

2001US-282867P.

2002US-0087887.
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                                                                                                                                                                                                                                                               47; 160pp;
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99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
  epilepsy,
nd various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bin-Yang
                                                                                                                                                                                                                                                                 English.
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Zerhusen BD,
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hematopoietic dyslipidemias.
                                                                                                                                                                                                                                                                                                                                       polymucleotides, useful for NOVX-associated disorders e.g., cancer, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hart M, Tomlinson JE, Topper D, Komuves L, Padigaru M;
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  disorders, inflammatory . The nucleic acids and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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99US-0146388 99US-0147004 99US-0147704 99US-0147706 99US-0147716 99US-0147716 99US-0147716 99US-0147716 99US-014811 99US-014972 99US-014972 99US-014972 99US-014972 99US-0151066 99US-015921 99US-015921 99US-0160768 99US-0160981 99US-01610081 99US-01610081 99US-01610081 99US-0161106 99US-0161106 99US-01611160 99US-01611161

18-NUG-1999
20-AUG-1999
21-AUG-1999
23-AUG-1999
25-AUG-1999
25-AUG-1999
27-AUG-1999
27-AUG

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CC polypeptides may also be used as targets for the identification of small CC molecules that modulate or inhibit neurogenesis, cell differentiation, CC cell proliferation, haematopoiesis, wound healing and angiogenesis, in CC gene therapy, in generation of antibodies that bind immunospecifically to CC acids are further used as hybridization probes, in chromosome mapping, CC tissue typing, preventive medicine, and pharmacogenomics. The nucleic sequence represents a human NOV6b polypeptide.

XX SQ Sequence 559 AA;

Query Match 17.5%; Score 7; DB 23; Length 559;

Best Local Similarity 100.0%; Pred: No. 37;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 11 KTISKLM 16

DB 11 KTISKLM 17

Search completed: July 24, 2003, 12:21:18
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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on:
                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                          Score
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365.801 Million cell updates/sec
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40
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                           US-07-899-535A-4
US-07-899-535A-1
US-09-107-532A-4959
US-09-328-352-6982
US-09-107-532A-4041
US-07-783-726-2
US-08-445-342A-2
US-08-445-342A-2
US-09-328-352-4855
US-09-328-352-4855
US-09-337-357-55
US-09-537-357-55
US-09-537-357-53
US-09-537-357-53
US-09-537-357-53
US-09-537-357-53
US-09-537-357-53
US-09-537-357-53
US-09-107-532A-5317
US-08-445-342A-11
US-08-445-342A-11
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US-08-974-833-11
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a 27, Appli
a 4, Appli
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a 1982, Appli
a 2, Appli
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4855, Ap
5654, Ap
55, Appl
52, Appl
52, Appl
531, Appl
531, Appl
11, Appl
16, Appl
9,7,7
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US-09-065-383-30
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                              TELEX:
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40 amino acids
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Sequence 6, 1	Sequence 11,	Sequence 6, 1	Sequence 17,	Sequence 17,		Sequence 15,	æ	U	O	Sequence 86,			Sequence 83,	Sequence 82,	Sequence 81,	Sequence 80,	Sequence 79,
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ALIGNMENTS

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Sequence 30, Application US/09065383
Patent No. 6391543
GENERAL INFORMATION:
                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/842,385
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.P1
TELEPHONE: 847/935-1729
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT
                                                                                                                                                                                                                                                                                                                                               ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                 TELEPHONE:
TELEFAX: 8
                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Abboti
CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
ROBERTS-RAPP, LISA
ROUSELL, JOHN C.
STROUPE, STEPHEN D.
INVENTION: REAGENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 Abbott
                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                  847/938-2623
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amino acid

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Query Match 100.0%;
Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KRATOCHVIL APPLICANT: ROBERTS-RA APPLICANT: RUSSELL, JAPPLICANT: STROUPE, STITLE OF INVENTION: RTITLE OF INVENTION: FUNDBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
FILING DATE:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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APPLICANT:
APPLICANT:
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                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                             NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/8
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                              TOPOLOGY:
                                                                                                                                                                                               TELEFAX: 847/938-2623
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T: 100 Abbott Park Road
Abbott Park
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                                                                                                                            518 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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RUSSELL, JOHN C.
STROUPE, STEPHEN D.
METHODS USEFUL
MENTION: REAGENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                linear
                                                               No. 6391543e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR DETECTING DISEASES OF THE PROSTATE 33
                                                                                                                                                                                                                                                                                                                               08/842,385
                                                                                                                                                                27:
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Score 40;
Pred. No.
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DB 4;
3.7e-35;
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US-09-394-272-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Sheth, Anil R.
APPLICANT: Sarde, Seema
APPLICANT: Panchal, Chand
TITLE OF INVENTION: Pharm
TITLE OF INVENTION: Adeno
TITLE OF INVENTION: Adeno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver.
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
                             ATTORNEY/AGENT INFORMATION:
NAME: Loud, George A.
REGISTRATION NUMBER: 25,814
REFERENCE/DOCKET NUMBER: S&B-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-0960
TELEFAX: 703-415-0962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Craterostigma plantagineum
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JENGTH: 1081
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                 APPLICATION NUMBER: US/07/899,535A FILING DATE: 16-JUN-1992 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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Y: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Panchal, Chandra J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheth, Anil R.
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100.0%; Pred. No.
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o. 17;
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                                                                                                                                   US-07-899-535A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application Patent No. 5428011 GENERAL INFORMATION:
                                                                  Matches
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Loud, George A.
REGISTRATION UNMER: 25,814
REFERENCE/DOCKET NUMBER: S&B-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-0960
TELEPAX: 703-415-0962
                                                                                                                                                                                                                                                                   TELEX: 24 8614
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sheth, Anil R.
APPLICANT: Garde, Seema
APPLICANT: Panchal, Chandra J.
APPLICANT: Panchal, Chandra J.
TITLE OF INVENTION: Pharmaceutical Preparations For
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Ca
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,535A
FILING DATE: 16-JUN-1992
CLASSIFICATION: 514
CLASSIFICATION: 514
                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2001 Jef
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                              LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 22202
                                                                                  Local Similarity
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
 78
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                                                                6,
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amino acid
GY: linear
VEKKOP 83
                                 VEKKOP 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001 Jefferson Davis Highway, Suite 306
                                                                  Conservative
                                                                                                                                                                                    linear
                                                                                                                                               . protein
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                                                           15. v.,
100.0%; F1
                                                             15.0%; Score 6; DB 1
100.0%; Pred. No. 22;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adenocarcinoma, Stomach Cancer and Breast Cancer.
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                                                                                  DB 1;
5. 22;
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                                                                                                Length 94;
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                                                                Indels
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RESULT 6

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US-09-328-352-6982
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LOCATION: (B) LOCATION 1...157;
SEQUENCE DESCRIPTION: SEQ ID NO: 4959:
US-09-107-532A-4959
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Sequence 4959, Application US/09107532A
Patent No. 6583775
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
UTILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                   GENERAL INFORMATION:
APPLICANT: GARY L. BETCON et al.
APPLICANT: GARY L. BETCON et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6982
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                               Sequence 6982,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                        Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4959:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII

CURRENT APPLICATION IDATA:
APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRICK APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/ACENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
PREFERENCE/COLOR NUMBER: 40,489
PREFERENCE/COLOR NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                               Application US/09328352
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RESULT 9

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; TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-6982
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Best Local Similarity
Matches 6; Conserve
                                                                                                                                                          NAME/KEY: misc_feature;
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LOCATION: (B) LOCATION 1...333;
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SEQUENCE DESCRIPTION: SEQ ID NO: 404
US-09-107-532A-4041
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GENERAL INFORMATION:
                                                                                        Matches
                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4041: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                    HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
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                  85 PKVEKK 90
                                                   2 PKVEKK 7
                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (781) 893-8277
TOTREAX: (781) 893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                      LENGTH: 333 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Waltham
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                                                                                        Conservative
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                                                                                    15.0%; Score 6; DB 4;
100.0%; Pred. No. 70;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                             4041:
                                                                                                                       Length 333;
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RESULT 10
US-08-445-342A-2
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                                                                                                                                                                    Sequence 2, Application US/08445342A Patent No. 5830726
                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PABSE, PATTER 1.
REGISTRATION UNMBER: MITS
REFERENCE/DOCKET NUMBER: MITS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6598
TELEPAX: 404-572-655
                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                            APPLICANT: Zimmerman, Joseph, J. APPLICANT: Langer, Robert, S. TITLE OF INVENTION: The Heparinase TITLE OF INVENTION: Heparinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Langer, Robert S.
TITLE OF INVENTION: The Heparinase
TITLE OF INVENTION: Heparinum
                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: 8118
STRANDEDNESS: 8118
STRANDEDNESS: 8118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: UPFILING DATE: 19911023
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                    205 KVEKKD 210
                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                3 KVEKKD 8
                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georgia
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                                                                                                        Moreman, Kelley
Cooney, Charles, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasisekharan, Ramnath
Moreman, Kelley
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                        Sasisekharan, Ramnath
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                             k; Pred. No. 80;
0; Mismatches
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                                                          gene
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                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                            from Flavobacterium
                                                                                                                                                                                                                                                                                                                                                            Length 384;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09066481B
Patent No. 6217863
                                                                                                                                                                      -09-066-481-2
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: RATIONALLY DESIGNED POLYSACCHARIDE TITLE OF INVENTION: LYASES DERIVED FROM HEPARINASE I FILE REFERENCE: M0656/7038/HCL CURRENT APPLICATION NUMBER: US/09/066,481B CURRENT FILING DATE: 1999-01-19 EARLIER APPLICATION NUMBER: US 60/008,069 EARLIER APPLICATION NUMBER: US 60/008,069 EARLIER FILING DATE: 1995-10-30 NUMBER: OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ERNST, STEFFAN
APPLICANT: GANESH VENKATARAMAN
APPLICANT: COONEY, CHARLES L
APPLICANT: LANGER, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GODAVARTI, RANGANATHA
APPLICANT: SASISEKHARAN, RAMNATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (404) 873-87. INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                           TYPE: P
                                                                                                                                                                                         TYPE: PRT ORGANISM: Flavobacterium Heparinum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y Match 15.0%; So Local Similarity 100.0%; 1 local Similarity 100.0%; 1 local Similarity 0; 100.00%; Solution 100.00%; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (404) 873-8795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MI
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CLASSIFICATION:
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                                                                              Score 6; 1; Pred. No:
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                                                                                                             Length 384;
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                                                                                                                                                                                                                                                                                                                                                       US-09-537-357-54
TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE TITLE OF INVENTION: LYASE AND USES THEREOF FILE REFERENCE: 06027.0002 CURRENT APPLICATION NUMBER: US/09/537,357 CURRENT FILING DATE: 2000-03-29 NUMBER OF SEQ ID NOS: 56 SOFTMARE: FastSEQ for Windows Version 4.0 SEQ ID NO 54
                                                                                                                                                                                                                                                                   Sequence 54, Application Patent No. 6271018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application PC/TUS9209124
GENERAL INFORMATION:
APPLICANT: Massachusetts Institut
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Best Local
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: AMINO ACID
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PLOOS/MS-DOS

SOFTWARE: PATENTIAN

APPLICATION NUMBER: PCT/US92/09124

APPLICATION NUMBER: PCT/US92/09124
                                                                                                                                                                                                                     APPLICANT:
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MITS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404.815-6508
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HYPOTHETICAL:
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Nathalie Tijet
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1100 Peachtree Street, Suite 2800
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Pred. No.
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Gaps

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APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5654
LENGTH: 425
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5654
Search completed: July 24, 2003, 12:28:38
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US-09-134-001C-5654
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LENGTH: 408
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4855
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US-09-328-352-4855
; Sequence 4855, Application US/09328352
; Patent No. 6562958
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; ORGANISM: Guayule
US-09-537-357-54
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Warches 6; Conservative
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Best Local Similarity luu.
"---hes 6; Conservative
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APPLICANT: Gary L. Bercon et al.
APPLICANT: Gary L. Bercon et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                     237 KTISKL 242
                                                                                              30 KTISKL 35
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                                                                                                                                               15.0%; Score 6; DB 4;
100.0%; Pred. No. 88;
tive 0; Mismatches
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Job time : 4.62665 secs

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Result
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                      Score
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     ຑຑຑຑຑຑຑຑຑຑຑຑຑ
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*
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Match Length
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Gapop 60.0 , Gapext 60.0
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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            1.4 US-10-012-896-1003
1.5 US-10-205-823-271
1.5 US-09-925-300-1027
1.0 US-09-980-285-2
1.5 US-10-291-337-2
1.5 US-09-884-260A-54
1.5 US-09-884-260A-52
1.5 US-09-884-260A-52
1.5 US-09-884-260A-53
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1.5 US-09-884-260A-53
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US-10-291-360-6
US-10-291-360-1
US-10-291-360-2
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            Sequence 4, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 271, App
Sequence 271, App
Sequence 272, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 54, Appl
Sequence 55, Appl
Sequence 53, Appl
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US-10-217-700-4

ALIGNMENTS

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RESULT 2
US-10-291-360-6
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Sequence 6, Application US/10291360
Publication No. US20030119744A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT FILING DATE: 2012-08-12
CURRENT FILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10217700 Publication No. US20030070191A1 GENERAL INFORMATION:
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Best Local (
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TYPE: PRT
ORGANISM: Craterostigma plantagineum
                                                                                                                                                                                                                                                                Local Similarity hes 7; Conservat
                                                                                                                                                                                           903 KTISKLM
                                                                                                                                                                                                                    30 KTISKLM 36
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Sequence

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GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of
FILE REFERENCE: 06508-051-US-02
CURRENT APPLICATION NUMBER: US/10/291,360
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
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GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
                                                             Sequence 2, Application US/10291360 Publication No. US20030119744A1
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Publication No.
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/291,360
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: Polypeptide 76-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                      DATABASE ACCESSION NUMBER: GI 131436
DATABASE ENTRY DATE: 1988-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE: Molecular cloning of a small prostate protein, known as beta-TITLE: microsemenoprotein, PSP94 or beta-inhibin, and demonstration of transcripts TITLE: non-genital tissues.
                                                                                                                                                                                                                                                                                                                                                                                              DATE: 1989
                                                                                                                                                                                                                                                                                                                                                                                                              ISSUE: 3
PAGES: 1310-1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: Ulvsback, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OURNAL: Biochem. Biophys. Res Commun
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                                                                                                                                                                                                         4 VEKKDP 9
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100.0%; Fi
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RESULT 5
US-10-012-896-1003
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                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FAST.SEQ for Windows Version 3.0
SEQ ID NO 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1003, Application US/10012896 Publication No. US20020183251A1
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                                  Matches
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                                                Best Local Similarity
                                                                  Query Match
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The Trant Trantife
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CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                        APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 102
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                  PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: recombinant human PSP94 (rHuPSP94) produced from yeast
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                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT
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4 VEKKOP 9
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Fanger, Gary R.
Wantanabe, Yoshi
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Hepler, William T.
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Vinals de Bassols, Carlota
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robert A
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                                                  15.0%; Score 6; DB 14; 100.0%; Pred. No. 59;
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100.0%; Pred. No.
                                    Mismatches
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98 VEKKDP 103

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PRIOR APPLICATION UNMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1027
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-300-1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 271
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-271
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APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALO1
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
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Matches 6; Conservative 0;
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Patent No. US20020151681A1
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CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
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APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson C
APPLICANT: Gannavarapu, Mai
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
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Endege, Wilson O.
Gannavarapu, Manjula
Gorbatcheva, Bella
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100.0%; Pred. No.
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 384
TYPE: PRT
ORGANISM: Pedobacter heparinus
US-10-291-337-2
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; TYPE: PRT
; ORGANISM: Pedobacter heparinus
US-09-802-285-2
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SEQ ID NO 2
SEQ ID NO 2
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APPLICANT: Pojasek, Kevii
APPLICANT: Shriver, Zachd
APPLICANT: Holley, Krist:
APPLICANT: El-Shabrawi, 1
APPLICANT: Venkataraman,
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Best Local Similarity
Matches 6; Conserv
                                         Matches
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Best Local (
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GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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APPLICANT: Sasisekharan, Ram
TITLE OF INVENTION: Heparinase III and Uses
FILE REFERENCE: M0656/7063HCL
CURRENT APPLICATION NUMBER: US/10/291,337
CURRENT FILING DATE: 2002-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Venkataraman, Ganesh
APPLICANT: Sasisekharan, Ram
TITLE OF INVENTION: Heparinase
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                                       Local Similarity tes 6; Conserv
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mes 6; Conserv
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5. US20020122793A1
3 KVEKKD 8
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Shriver, Zachary
Holley, Kristine
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Shriver, Zachary
Holley, Kristine
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100.0%; Pred. No. 67
Live 0; Mismatches
                                     15.0%; Score 6; DB:
100.0%; Pred. No. 1.0
tive 0; Mismatches
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NO. 1.6e+02;
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Best Local Similarity
Matches 6; Conserve
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; TYPE: PRT
; ORGANISM: Guayule
US-09-884-260A-54
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SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 448
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Best Local Similarity
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TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO)
TITLE OF INVENTION: LYASE AND USES THEREOF
FILE REFERENCE: 06027.0002U2
CURRENT APPLICATION NUMBER: US/09/884,260A
CURRENT FILING DATE: 2001-06-19
APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/884,260A
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 09/,537,357
PRIOR FILING DATE: 2000-03-29
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PRIOR APPLICATION NUMBER: 09/,537,357
PRIOR FILING DATE: 2000-03-29
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APPLICANT: Nathalie Tijet
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ORGANISM: Arabidopsis
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US20020098570A1
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100.0%; Pr
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100.0%; Pred. No. 1.7e+02;
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US-09-884-260A-53
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SEQ ID NO 52
SERVITA 465
TYPE: PRT
ORGANISM: Cucumis melo
                                                                                                                                                                                                                                                           Sequence 13297, Publication No.
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Best Local Similarity
Matches 6; Conserv
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PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 56
SOPTWARE: PRIOR SOPTWARE: PRIOR DATE: 2000-03-29
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PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 56
                                           FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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APPLICANT: IKEDA, HARUO
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CURRENT FILING DATE: 2001-06-19
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TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE
TITLE OF INVENTION: LYASE AND USES THEREOF
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APPLICANT: Nathalie '
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CURRENT FILING DATE: 2001-06-19
     PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
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ORGANISM: Flax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 468
TYPE: PRT
                                                                                                                                     PPLICANT:
                                                                                           PPLICANT: SAKAKI, YOSHIYUKI
PPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLECTIDES
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                         Application US/10156761 US20030119018A1
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JP 2001-272697
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f; Pred. No. 1.9
0; Mismatches
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Mismatches
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No. 1.9e+02;
0;
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Sequence 2, Application US/09950788
Patent No. US2002012323A1
GREERAL INFORMATION:
APPLICANT: MORCKEL, Bettina
APPLICANT: MORCKEL, Bettina
APPLICANT: SCHISCHKA, Natalie
APPLICANT: SCHISCHKA, Natalie
APPLICANT: PREFFERLE, Walter
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE PTSI PROTEIN
CURRENT APPLICATION NUMBER: US/09/950,788
CURRENT APPLICATION NUMBER: US/09/950,788
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: DE10045496.8
PRIOR FILING DATE: 2000-09-13
VOMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 568
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-950-788-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 13297
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-950-788-2
Search completed: July 24, 2003, 12:48:29 Job time: 7.79356 secs
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Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                             Matches
                                                                                                                                                                              Query Match
Best Local S
                                                                              24 YTMAAD 29
||||||
454 YTMAAD 459
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                                                                                                                                                           h 15.0%; Score 6; DB 10; Le Similarity 100.0%; Pred. No. 2.3e+02; 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                Length 568;
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Result
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Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                       Score
      400
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Match Length DB
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/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
/cgn2_6/ptodata/1/paa/US082_COMB.pep:*
/cgn2_6/ptodata/1/paa/US083_COMB.pep:*
/cgn2_6/ptodata/1/paa/US085_COMB.pep:*
/cgn2_6/ptodata/1/paa/US085_COMB.pep:*
/cgn2_6/ptodata/1/paa/US085_COMB.pep:*
/cgn2_6/ptodata/1/paa/US087_COMB.pep:*
/cgn2_6/ptodata/1/paa/US089_COMB.pep:*
/cgn2_6/ptodata/1/paa/US090_COMB.pep:*
/cgn2_6/ptodata/1/paa/US000_COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/paa/US06
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  US-08-842-385-9
US-09-991-681-30
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                                                                   Description
Sequence 9, Appli
Sequence 30, Appl
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ALIGNMENTS

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US-08-842-385-9
; Sequence 9, Application US/08842385
; GENERAL INFORMATION:
APPLICANT: CLIDITE, Tracey
ITILE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: POR DETECTING DISEASE OF THE PROSTATE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDORTES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDORTES: 100 ADDORT PARK Road
CITY: ADDORT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/842,385
FILING DATE:
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

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US-09-991-681-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
TELEFAX: 847/938-2623
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                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSKO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,681
FILLING DATE: 26-NOV-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
OFFICE TO THE TOTAL O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                            NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                 APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRANADOS, EDWARD N.
HODGES, STEVEN C.
HODGES, MICHAEL R.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
ROBERTS-RAPP, LISA
ROBERTS-RAPP, LISA
FOR DETECTING DISEASES OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Abbott Park
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TELEPHONE: 847/935-1729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             None
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                                                                              6084.US.P1
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US-10-221-279-7783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Custom
SEQ ID NO 7783
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7783, Application US/10221279 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-046
CURRENT APPLICATION NUMBER: US/10/221,279
CURRENT FILING DATE: 2002-09-06
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
NUMBER: CEC IN NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER: CEC IN NUMBER: 09/519,705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(141)
OTHER INFORMATION: Xaa = any amino acid or nothing
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                                      ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                      APPLICANT: Russell, John
APPLICANT: Colpitts, Tracey
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASE OF THE PROSTATE
                                                                                                                                                             NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
OPERATING SYSTEM:
                                                                                                    COUNTRY:
                                                                                                                             STATE:
                                                                                                                                            CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: None SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                     Application US/08842385
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ilarity 100.0%;
Conservative 0
    IBM Compatible SYSTEM: DOS
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Pred. No. 7.2e-34;
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GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: POTEMBEKI, PRISCILLA E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELECHONE: 847/937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/842,385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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                                 APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                         APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-Nov-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                   SOPTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                         KRATOCHVIL, JON D.

ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        un 100.0%; Score 40; DB 12; Length 467; Similarity 100.0%; Pred. No. 2.3e-33; 40; Conservative 0; Mismatches o. 17-2-1-
NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                    ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                         CITY: Abbott Park
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KLASS, MICHAEL R.
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RESULT 7
US-10-144-198-44
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FILE REFERENCE: 30 90 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 10/054,935
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/356,130
PRIOR PILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR PILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/117,229
PRIOR APPLICATION NUMBER: US 10/117,229
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                                                                                                                                        Sequence 44, Application US/10144198 GENERAL INFORMATION:
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Matches 40; Conserv
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APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR FILING DATE: 2002-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 10/197,824
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1770
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
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                                                                                                                                                                                                                                                                                                                                           40;
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                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 8.2e-33;
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PCT-US01-42950-495
Sequence 495, Application PC/TUS0142950
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: PCT/US01/42950
CURRENT FILING DATE: 2001-11-16
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PCT-US01-08631-40087
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PCT-US01-42950-495
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LENGTH: 1770
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SEQ ID NO 40087
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                                                       SOFTWARE: PatentIn version 3.0 SEQ ID NO 495 LENGTH: 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
                                                                                                              CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
SOPTUMBER: 07.5000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
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ORGANISM: Homo sapiens
                 ORGANISM: Homo sapiens
                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (941)..(950)
OTHER INFORMATION: Helper component proteinase domain identified by PFam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam score of 7.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (48)..(62)
OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX,
OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw score of 11.39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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PCT-US03-04508-32
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                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application PC/TUS0304508
GENERAL INFORMATION:
APPLICANT: IDEC PHARMACEUTICALS
APPLICANT: GATELY, DENNIS
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: US/10/416,993
CURRENT FILING DATE: 2003-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 037003/0301985
CURRENT APPLICATION NUMBER: ECT/US03/04508
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/57,140
PRIOR FILING DATE: 2002-02-19
PRIOR FILING DATE: 2002-02-19
                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2002-06-10 NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/386,759 PRIOR FILING DATE: 2002-06-10
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/396,082 PRIOR FILING DATE: 2002-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PROSTATE SPECIFIC GENES TITLE OF INVENTION: OR THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1839
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                LENGTH: 1872
                                                                            Local Similarity es 40; Conserv
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1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
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ilarity 100.0%;
Conservative 0
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llarity 100.0%;
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Conservative (
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                                                                                            Score 40; DB 1; 1
Pred. No. 8.7e-33;
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Pred. No. 8.5e-33;
; Mismatches 0;
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Pred. No. 8.5e-33;
; Mismatches 0;
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RESULT 12 PCT-US01-08631-40090

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GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION UNMEER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                   SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/356,130
PRIOR FILING DATE: 2002-02-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 10/054,935
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                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: DOMAIN
LOCATION: (1065)..(1074)
OTHER INFORMATION: Helper component proteinase domain identified by PFam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
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2035
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 10/144,198 FILING DATE: 2002-05-14
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 10/117,229
FILING DATE: 2002-04-08
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 10/197,824
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SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 2074
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                                                                                           Score 40; DB 1;
Pred. No. 1e-32;
                                                                           Mismatches
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                                                                                                             DB 1; Length 2221;
                                                                           0; Indels
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APPLICANT: Liu, Jingdong
APPLICANT: Lutfiyya, Linda L.
APPLICANT: Lutfiyya, Linda L.
APPLICANT: McIninch, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 37595
SEQ ID NO 7370
LENGTH: C.
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Job time : 61.2635 secs
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US-10-155-881-7370
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US-10-144-198-30
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Best Local
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TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
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                                                               494 KDPSRKKE 501
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                          and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB seq length: 0
DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                  Match Length
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/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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        US-10-367-978-32

US-09-439-410A-74

US-09-439-410A-47

US-10-273-573-10764

US-10-273-573-10764

US-10-273-573-108-36

US-10-373-573-8362

PCT-US03-20480-29

US-10-373-573-8362

PCT-US02-15910B-3

PCT-US02-15910B-5

PCT-US02-15910B-5

PCT-US02-15910B-52

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e 16, Appl
e 74, Appl
e 9406, Ap
e 10764, A
                              99, Appl
27, Appl
28, Appl
39, Appl
49, Appl
49, Appl
35, Appl
35, Appl
31, Appl
32, Appl
33, Appl
3407, Ap
365718, Ap
5718, Ap
5718, Ap
5718, Appl
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US-10-273-573-10246	US-10-463-190-109	US-10-463-190-108	US-10-463-190-104	US-10-463-190-103	US-10-463-260-5	PCT-US03-19070-5	US-10-461-148-9	PCT-US02-26584-16	US-10-461-148-1	PCT-US02-26584-3	US-10-411-910A-80	US-10-273-573-10760	US-10-032-037B-26	US-10-029-988B-26	US-10-273-573-10096	PCT-US03-20751-1	PCT-US02-15910B-50	US-10-098-221-7	
Sequence 10246, A	Sequence 109, App	Sequence 108, App	Sequence 104, App	Sequence 103, App	Sequence 5, Appli	Sequence 5, Appli	Sequence 9, Appli	16,	Sequence 1, Appli	3, A	Sequence 80, Appl	1076	26,	Sequence 26, Appl	Sequence 10096, A	Sequence 1, Appli	Sequence 50, Appl	Sequence 7, Appli	

ALIGNMENTS

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APPLICANT: GATELY, DENNIS
TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND
TITLE OF INVENTION: OR THERAPEUTICS
FILE REFERENCE: 037003-0301988
CURRENT APPLICATION NUMBER: US/10/367,978
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR PILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 89
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; Sequence 32, Application US/10367978
; GENERAL INFORMATION:
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-450-055-16
                                                                                                                                                                                                                                                                                                                                                                   US-10-450-055-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-10-367-978-32
                                                                                              CURRENT APPLICATION NUMBER: US/10/450,055
CURRENT FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN Vers. 2.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/10450055 GENERAL INFORMATION:
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                                                                                                                                                                                                                               APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENTION: Novel genes of Corynebacterium
FILE REFERENCE: 936 2000
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US-09-439-410A-74
                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-10-273-573-9406
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US-09-439-410A-74
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LENGTH: 123
TYPE: PRT
                                    Sequence 10764, Application US/10273573 GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 74
LENCTH: 39
TYPE: PRT
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GENERAL INFORMATION:
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APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
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CURRENT FILING DATE: 1999-11-11
NUMBER: OF SEQ ID NOS: 118
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CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
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APPLICANT: Duzic, Emir
TITLE OF INVENTION: AGS PROTEIN AND NUCLETIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: 1919/60388-B
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 10994
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-01-26
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100.0%; Pred. No. 20;
tive 0; Mismatches
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"""hes 5; Conserve
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US-09-439-410A-47
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Best Local Similarity
Matches 5; Conserva
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-979-99
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US-10-374-979-99
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US-10-273-573-10764
                                                                                                                        Sequence 47, Application US/09439410A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF S
SEQ ID NO 99
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SEQ ID NO 10764
APPLICANT: CISMOWSKI, MATY
APPLICANT: Duzic, Emir
TITLE OF INVENTION: AGS PROTEIN AND NUCLETIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: 1919/60388-B
CURRENT APPLICATION NUMBER: US/09/439,410A
CURRENT FILLING DATE: 199-11-11
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-10-23
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PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 1999-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 032796-021
CURRENT APPLICATION NUMBER: US/10/374,979
CURRENT FILING DATE: 2003-03-04
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TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 10994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/071,449
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PRIOR FILING DATE: 2000-04-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                 174 VEKKD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 KTISK 53
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100.0%;
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84;
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SOFTWARE: PatentIn version 3.1 SEQ ID NO 47 LENGTH: 189

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; LENGTH: 191
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-2
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                                                                                                                                                                            NUMBER OF SEQ ID NOS: 10994
SOPTWARE: Custom
SEQ ID NO 8362
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8362, Appli
GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,908
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ZHOU, YONGMING
APPLICANT: FOWKE, LARRY C.
APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER
APPLICANT: AGRICULTURE AND AGRIFOOD CANADA
TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 4810-62237
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/770,160 PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (64)..(87)
OTHER INFORMATION: TRANSFORMING PROTEIN P21 RAS SIGNATURE domain identified by
OTHER INFORMATION: eMATRIX, accession number PR00449C, p-value=3.250e-20, raw:
OTHER INFORMATION: 17.27
                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                              ENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match
12.5%; Score 5; i
Local Similarity 100.0%; Pred. No.
hes 5; Conservative 0; Mismatci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 191;
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US-10-450-186-49 RESULT 11

Sequence 49, Application US/10450186
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; GRIF

INCYTE CORPORATION; GRIFFIN, Jennifer A.;

YAO, Monique G.; DUGGAN, Brendan M.;

APPLICANT:

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                                                                                                                                                                                                                                                              APPLICANT: TRAN, Uyen K.
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: ENZYMES
FILE REFERENCE: PF-1452 PCT
CURRENT APPLICATION NUMBER: PCT/US03/20480;
CURRENT FILING DATE: 2003-06-26
PRIOR APPLICATION NUMBER: US 60/39,067
PRIOR FILING DATE: 2002-06-28
                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 104
SOFTWARE: PERL Program
SEQ ID NO 29
LENGTH: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application PC/TUS0320480 GENERAL INFORMATION:
                                                     Matches
                                                                            Query Match
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Best Local :
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APPLICANT:
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                                                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7511840CD1
                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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OTHER INFORMATION: Ras family domain identified by PFam, accession name
OTHER INFORMATION: value=1.6e-82, PFam score of 287.6
                                                                                                                                                                        TYPE: PRT
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                                                                Local
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les 5; Conserv
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                                                  l Similarity
5; Conserv
WWENA
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                                                                                                                                                                                                                                                                                                                                                                   BULLOCH, Sean A.
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                                                                                                                                                                                                                                                                                                                                                                                  CHANG, Hsin-Ru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELLIOTT,
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                                                                                                                                                                                                                                                                                                                                                                                                             David
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reena
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                                                                100.0%;
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                                                              Score 5; I
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Pred. No.
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                                                                 DB 1;
o. 97;
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. 91;
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                                                                            Length 226;
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                                                     Indels
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*Query Match
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PCT-US02-15910B-35
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                                                    PCT-US02-15910B-35
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7486536CD1
US-10-450-186-49
                                                                                                                 NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application PC/TUS0215910B GENERAL INFORMATION:
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Best Local Similarity
Matches 5; Conserv
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LENGTH: 242
                                                                                                                                                                                                                                                                                                APPLICANT: Rixon, Mark W.
APPLICANT: Gross, Jane A.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REFERENCE: 01-20PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-06-09
PRIOR APPLICATION NUMBER: PCT/US01/48517
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255,639
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/293,343 PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US02/15910B CURRENT FILING DATE: 2002-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/257,852
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/260,105
PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S. APPLICANT: CHAWLA, Narinder K.; LU, Yan; APPLICANT: ELLIOTT, Vicki S.; LU, Dyung Aina M.; APPLICANT: HAFALIA, April J.A.; AZIMZAI, Yalda; APPLICANT: KHAN, Farrah A.; TRAN, Uyen K. TITLE OF INVENTION: SECRETED PROTEINS FILE REFERENCE: PI-0345 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PERL Program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/262,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/450,186
                                                                                                 TYPE: PRT
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ORGANISM: Homo sapiens
                                                                         ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-18
APPLICATION NUMBER: US 60/263,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/263,090 FILING DATE: 2001-01-19
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LAL, Preeti G.; LEE, Ernestine A.;
RAMKUMAR, Jayalaxmi; THANGAVELU, Kavitha;
VII Viming; LEE, Sally;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TANG, Y. Tom; NGUYEN, Danniel B.;
WARREN, Bridget A.; HONCHELL, Cynthia D.;
GIETZEN, Kimberly J.; BAUGHN, Mariah R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.5%; Score 5; DB |
100.0%; Pred. No. 1e
:ive 0; Mismatches
       12.5%;
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       Score 5;
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Sequence 29 Application PC/TUS0215910B
GENERAL INFORMATION:
APPLICANT: Rixon, Mark W.
APPLICANT: Rixon, Mark W.
APPLICANT: Gross, Jane A.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins;
FILE REFERENCE: 01-20PC
CURRENT APPLICATION NUMBER: PCT/US02/15910B
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH. 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ ID NO 6
; LENGTH; 251
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-15910B-6
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                                                                                           RESULT 15
PCT-US02-15910B-31
                                                                                                                                                                                                                         Query Match
Best Local Similarity
""" hes 5; Conserve
                                                                                                                                                                                                                                                                                                               ; TYPE: PRT ; ORGANISM: Homo sapiens PCT-US02-15910B-29
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PCT-US02-15910B-29
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PCT-US02-15910B-6
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                                                       Sequence 31, Application PC/TUS0215910B GENERAL INFORMATION:
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Matches 5; Conservative C
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APPLICANT: Rixon, Mark W.
APPLICANT: Gross, Jane A.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rixon, Mark W.
APPLICANT: Gross, Jane A.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REFERENCE: 01-20PC
CURRENT APPLICATION NUMBER: PCT/US02/15910B
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/293,343
PRIOR PLICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.0%;
nes 5; Conservative
                                                                                                                                                                      138 KTISK 142
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                                                                                                                                                                                                                                            12.5%; Score 5; DB
100.0%; Pred. No. 1.
tive 0; Mismatches
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s; Pred. No. 1.1
0; Mismatches
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CURRENT APPLICATION NUMBER: PCT/US02/15910B
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/293,343
PRIOR APPLICATION NUMBER: 60/293,343
PRIOR APPLICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-15910B-31

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps O;

ORGANISK: 142

Search completed: July 24, 2003, 12:46:19
Job time: 1.3713 secs
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Title:
Perfect score:
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Maximum DB seq length: 200000000
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: pir3:*
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Query Match 17.5%; Score 7; DB 2; Ler Best Local Similarity 100.0%; Pred. No. 10; Matches 7; Conservative 0; Mismatches 0;	RESULT 2 T24492 T24492 hypothetical protein T05A10.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to C; Accession: T24492 R; Sulston, J. submitted to the EMBL Data Library, November 1995 A; Reference number: Z19898 A; Accession: T24492 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-406 <wil> A; Cross-references: EMBL: Z68108; PIDN: CAA92135.1; GSPI A; Experimental source: clone T05A10 C; Genetics: A; Gene: CESP:T05A10.3 A; Map position: X A; Introns: 50/1; 76/3; 98/3; 131/1; 167/3; 242/1; 294/</wil>	Query Match Best Local Similarity 100.0%; Pred. No. 10; Matches 7; Conservative 0; Mismatches 0; Qy 29 DKTISKL 35 Db 97 DKTISKL 103	RESULT 1 T04817 T04817 T04817 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #t. C;Accession: T04817 R;Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M. submitted to the Protein Sequence Database, February: A;Reference number: Z15385 A;Accession: T04817 A;Residues: 1-406 -BEV a A;Cross-references: EMBL:AL035440 A;Experimental source: cultivar Columbia; BAC clone F. C;Genetics: A;Map possition: 4 A;Introns: 41/2; 73/3; 94/2; 165/1; 186/2; 210/3; 251. A;Note: F10M23.280	ALIGNMENTS	30 6 15.0 252 2 B32053 31 6 15.0 254 2 T42936 32 6 15.0 274 2 T25783 33 6 15.0 281 2 D72397 34 6 15.0 311 2 S23395 35 6 15.0 313 2 E91006 37 6 15.0 313 2 E9500 38 6 15.0 313 2 E64981 39 6 15.0 317 2 S75694 40 6 15.0 317 2 S75694 41 6 15.0 324 2 F69504 42 6 15.0 324 2 F769504 43 6 15.0 331 2 A86278 44 6 15.0 331 2 A86278 45 6 15.0 335 2 T48161
	gans #text_change 18-Feb-2000	Length 406; 0; Indels 0; Gaps 0;			hypothetical prote hypothetical prote hypothetical prote hypothetical prote conserved hypothet hypothetical prote hypothetical prote penicillin-binding penicillin-binding penicillin-binding hypothetical prote proliferating-cell hypothetical prote hypothetical

Mewes, H

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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Cha Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-dependent helicase [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
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D90183
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submitted to the EMBL Data Library, April 1997
submitted to the sequence of C. elegans cosmid B0261
                                R;Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hoheisel, J.; Mewes, Augmitted to the Protein Sequence Database, March 1999
                                                                       protein kinase homolog M3E9.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 20-Sep-1999
C;Accession: T05050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A99139
A; Accession: D90183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
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rences: GB:AE006641;
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se: strain Bristol N2; clone B0261
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o. 17;
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A;Pathway: sucrose biosynthesis
A;Pathway: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase
C;Superfamily: sucrose-phosphate synthase; sucrose biosynthesis
                                                                           A; Description: catalyzes the formation of
                                                                                            C; Function:
                                                                                                                A;Gene: sps2
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sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: T09837
R;Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D. Plant Physiol. 115, 113-121, 1997
A;Title: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation A;Reference number: Z16874; MUID:97451773; PMID:9306694
A;Accession: T09837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein At2g31660 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T05050
A;Molecule type: DNA
A;Residues: 1-1029 <BEV>
A;Cross-references: EMBL:AL022223
A;Experimental source: cultivar Columbia;
A; Experimental source: ABA-treated
                                         A; Molecule type: mRNA
A; Residues: 1-1081 < ING>
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A; Residues: 1-1037 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: E84723
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C;Superfamily: protein kinase xa21; leucine-rich alpha-2-glycoprotein repeat homology;
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A; Introns: 428/2; 862/2
                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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Matches
                  Cross-references: EMBL:Y11795; NID:g2190349; PIDN:CAA72491.1; PID:g2190350
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E.: Umayam, L.; Tallon,
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sucrose-6-phosphate

from

UDPglucose and D-fruc

homology

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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Meok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-73 <GLA>
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AE1595
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A;Note: submitted to the EMBL Data Library, January 1995
A;Note: the authors translated the codon AAT for residue 39
                                                                                                                                                                                                                                                                                                          Biochem. J. 311, 567-573, 1995
A;Title: Differential modulation of expression of the two acylphosphatase isoenzymes by
A;Reference number: S59137; MUID:96033055; PMID:7487897
A;Accession: S59138
                                                                                                                                                                                                                                                                                                                                                       R;Chiarugi, P.; Raugei, G.; Mai
Biochem. J. 311, 567-573, 1995
                                                                                                                                                                                                                                                                                                                                                                                    acylphosphatase (EC 3.6.1.7), muscle - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 08-May-1995 #sequence revision 23-Aug-1997 #text_change 07-May-1999
C;Accession: S59138; S52327
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A;Experimental source: strain Clip11262
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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AE1595
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A; Residues: 1-78 < CH2>
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llarity 100.0%;
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69
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                                                       15.0%; but
100.0%; Pr
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0; Mismatches
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k; Pred. No. 23;
0; Mismatches
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29;
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Dussurget, O.;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <KUR>
A;Cross-references: GB:BA000018; PID:g13700197; PIDN:BAB41495.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                       R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aur A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acylphosphatase (EC 3.6.1.7), skeletal muscle - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Feb-1997
C;Accession: A61427
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997
C;Accession: S41663
                                                                                                                                                                                                                                                                                        conserved hypothetical protein SA0271 [imported] - Staphylococcus aureus (strain C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: D89792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-96 <BER>
C;Superfamily: acylphosph
C;Keywords: hydrolase; sk
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A61427
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A;Molecule type: protein
A;Residues: 1-91 <FER>
C;Superfamily: seminal plasma protein
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A;Title: Amino acid sequence of beta-microseminoprotein A;Reference number: S41663; MUID:94161559; PMID:8117114
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S41663
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Pred. No.
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J. Biol. Chem. 255, 6868-6874, 1980

A;Title: The complete amino acid sequence of horse muscle acylphosphatase A;Receesion: A01015; MUID:80227852; PMID:6248536
A;Molecule *****
                                                                                                                                                            C;Superfamily: acylphosphatase C;Keywords: acetylated amino end; hydrolase F;1/Modified site: acetylated amino end (Ser) #status experimental F;21/Disulfide bonds: interchain #status predicted F;21/Binding site: glutathione (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                      R;Mizuno, Y.; Yamazaki, M.; Takasawa, T.; Kizaki, T.; Shiokawa, H.
J. Biochem. 97, 1135-1142, 1985
A;Title: Amino acid sequence of acylphosphatase from porcine skeletal muscle.
A;Reference number: A01016; MUID:85289095; PMID:2993259
A;Accession: A01016
                                                                                                                                                                                                                                                                                                                                                                                                                                               acylphosphatase (EC 3.6.1.7), skeletal muscle - pig
N;Alternate names: acylphosphate phosphohydrolase
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 10-May-1996
C;Accession: A01016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: acylphosphate phosphohydrolase
C;Species: Equus caballus (domestic horse)
C;Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 #text_change 17-May-1996
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                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 1-98 <MIZ-
C;Comment: 1,3-Diphosphoglycerate and carbamoylphosphate are possible substrates of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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A;Residues: 1-98 <CAP>
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Best Local :
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KTISKL 89
                                        KTISKL 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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NESULT 15

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R;Camici, G.; Manao, G.; Modesti, A.; Stefani, M.; Berti, A.; Cappugi, G.; Manao, G.; Modesti, A.; Stefani, M.; Berti, A.; Cappugi, G.; Manao, G.; Modesti, A.; Stefani, M.; Berti, A.; Cappugi, G.; Manao, G.; 1-15, 1986

A;Title: The complete amino acid sequence of bovine skeletal muscle acylphosphatase. A;Recession: A29578

A;Recession: A29578

A;Rolecule type: protein

A;Residues: 1-98 <CAM>
C;Superfamily: acylphosphatase
C;Keywords: acetylated amino end; hydrolase
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;21/Disulfide bonds: interchain #status predicted
F;21/Binding site: glutathione (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec:1993 #sequence_revision 31-Dec-1993 #text_change 10-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acylphosphatase (EC 3.6.1.7), skeletal muscle - bovine
                                                                                                    Query Match
Best Local S
Matches 6
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84 KTISKL
                                               30 KTISKL 35
                                                                                                    Conservative
                                                                                                    15.0%; Score 6; DB 100.0%; Pred. No. 35
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Search completed: July 24, 2003, 12:27:21 Job time: 7.80234 secs

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FMR1 ANTEL
EF12 DAUCA
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MSMB PIG

MSPA SAGOE

MSMB HUMAN

FILN BUCAP

PAPE ECOLI

YCR BACTK

PBP7 ECOLI

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TAD3 YEAST

SECF RHOCA

GJP SULSO

EXOB AZOME

TOSA LISIN

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EMBL; AFC HSSP; PO7 InterPro; InterPro; InterPro; InterPro; InterPro; Pfam; PFC PFAM;	This SWIS between the Europ use by modified entities or send a	SEQUEN STRAIN STRAIN STRAIN Crantz (In) P -i- FU AM BI -i- SU -i- SU	FIA FIA FIA FIA FIA FIA FIA DIS-DIS- FIA DIS-DIS- FIA DIS-DIS- FIA DIS-DIS- FIA DIS-DIS- FIA DIS-DIS- FIA DIS- D	UL 44411337
PRO 115 PO 7157 PO 7157 PO 115 PO	WISS-In the ropean y non ed and dan e	UENCE FROM N. AIN=(V. MBRA ANDON S., Hu elongation f. ntz.).";) Plant Gene FUNCTION: TH. AMINOACYL-TRA BIOSYNTHESIS SUBCELLULAR SIMILARITY: EF-TU/EF-1A.	MANES SC-1998 SC-1998 SC-1998 SC-1998 SC-1998 From for escuryota; V natophyta; V natophyta; V natophyta; V	თ თ თ თ თ თ თ თ თ თ თ
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EMBL; AF041463; AAC39447.1; HSSP; P07157; AALP InterPro; IPR004539; EF1 alpha. InterPro; IPR004539; EF GTBbind InterPro; IPR004161; EFTU Cterm. InterPro; IPR004161; EFTU CTERM; PF00009; GTP EFTU D2. Pfam; PF00009; GTP EFTU D3; 1. Pfam; PF03144; GTP EFTU D3; 1. Pfam; PF03144; GTP EFTU D3; 1. PFRINTS; PR00315; ELONGATNFCT. TIGRFAMS; TIGR00483; EF-1 alpha; PR051TE; PS00301; EFACTOR GTP; 1 Elongation factor; Protein boss NP BIND 91 95 NP_BIND 91 95 SEQUENCE 449 AA; 49371 MW; 7	iis SWISS-PROT entry is copyright. It tween the Swiss Institute of Bioinfo we European Bioinformatics Institute by non-profit institutions as loudified and this statement is not remotities requires a license agreement send an email to license@isb-sib.ch	ENCE FROM N.A. IN=CV: MBRA 534; ndono S., Hughes J., Brown K., elongation factor 1-alpha gene Ltz.); plant Gene Register PGR98-052. FUNCTION: THIS PROTEIN PROMOTES AMINOACYL-TRNA TO THE A-SITE OF BIOSYNTHESIS. SUBCELLULAR LOCATION: Cytoplasm SUBCELLULAR LOCATION: THE GTP- EF-TU/EF-1A SUBFAMILY.	ARD; , Crea , Last , Last , Last alpha alpha antae; ntae; liophy ales;	4447 1 4447 1 4447 1 4447 1 4447 1 1 4751 1 1 5 1 8 1 8 1 1 1 1 1 1 1 1 1 1 1 1
1; alpha. Tebind. Cterm. D2. 1. 2; 1. 2; 1. 2; 1. GTP; 1. GTP (BY	ppyright. e of Bio. Institut utions as is not agreemen agreemen	Brown K., 1 alpha gene pGR98-052. IN PROMOTES A-SITE OF CYtoplasm. TO THE GTP-1	PRT; 4. sequence up encotation ((EP-1-alpha) (Manioc). Streptophyta /ta; eudicoty; Euphorbiacea	EFIA MAIZE EFIA ORYSA EFIA PEA EFIA SOYBN EFIA VICFA EFIA WICFA EFIA WICFA EFIA WICFA EFIA DAUCA MYBH DICDI C74 PARART GUAA YEAST ALIGNMEN
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	hrough a c the EMBL restrict intent is by and fo w.isb-sib	C DIN Ce	; Tracheophyta eudicots; Rosi	Q41803 O64937 Q41011 P25698 Q034534 Q0395313 P29521 P34127 Q40077 Q10097 Q96242 P38625
	collaboration outstation outstation it in no war commercia. ch/announce	s M.A.; ssculenta DING OF BIN	phyta; Rosidae;	zea mays (moryza sativ pisum sativ glycine max vicia faba triticum ae daucus caro dictyosteli parthenium schizosaccha rabidopsis saccharomyc

Query Match Best Local Similarity

17.5%; Score 7; DB 1; 100.0%; Pred. No. 3.2;

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RESULT 3
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SEQUENCE
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update).
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDD-glucose-fructose-
                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97451773; PubMed=9306694;
Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.;
"Analysis of cDNA clones encoding sucrose-phosphate synthase in
relation to sugar interconversions associated with dehydration in the
resurrection plant Craterostigma plantagineum Hochst.";
Plant physiol. 115:113-121(1997).
-i- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREFORE PLAY A MAJOR ROLLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Lamiales; Lamiales incertae sedis; Torenieae;
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Pfam; PF00534; Glycos_transf_1; T.

Transferase; Glycosyltransferase; Phosphorylation; Multigene DOMAIN 245 248 POLY-SER.
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ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
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SUBUNIT: Homodimer or homotetramer
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PHOSPHORYLATION IS NOT ESSENTIAL
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RESULT 4
ACYM MOUSE
ID ACYM MOUSE STANDARD; PRT; 97 AA.
AC p56375; Q8BQX2;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Acylphosphatase, muscle type isozyme (EC 3.6.1.7) (Ac phosphohydrolase).
GN ACYP2 OR ACYP.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E C Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; OK Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; OK Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N RA Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morra RA Schellenberg K., Steptoe M., Tan F., Underwood K., Mo Theising B., Wylie T., Lennon G., Soares B., Wilson R SEQUENCE FROM N.A.
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J. Protein Chem. 10:91-102(1991).
-!- FUNCTION: ITS PHYSIOLOGICAL ROLE IS NOT YET CLEAR.
-!- CATALYTIC ACTIVITY: An acyl phosphate + H(2)0 = a fatt:
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01-JUN-1994 (Rel. 29, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
Acylphosphatase, muscle type isozyme (EC 3.
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PROSITE; PS00150; ACYLPHOSPHATASE 1; 1.
PROSITE; PS00151; ACYLPHOSPHATASE 2; 1.
Hydrolase; Acetylation; Multigene_family.
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ACYP2 OR ACYP.
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HSSP; P00818; 1APS.
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    -!- SIMILARITY: BELONGS TO THE ACYLPHOSPHATASE FAMILY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
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39
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Pred. No.
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,
RA Baldarelli R., Hill D.P., Bult C., Corbini C., Corbani L.E., Cousins S.,
RA Baldarelli R., Hill D.P., Bult C., Forrest A., Frazer K.S.,
RA Gasterland T., Brustc V., Chochia C., Corbani L.E., Cousins S.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vasunishaw Boris A., Yanagisawa M., Shimada K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hara A., Hashizume W., Imotani K., Inshit Y., Itoh M., Kagawa I.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RC STRAIN-CS-BL-J-GJ; TISSUE-Mammary gland;
RX MEDLINE-22388557; PubMed=12477932;
RX MEDLINE-23388557; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schaler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaler G.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Listenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holterield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA ROdriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RGeneration and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
EMBL; AA285985; -; NOT_ANNOTATED_CDS.
EMBL; AA120674; -; NOT_ANNOTATED_CDS.
EMBL; AK046238; BAC32679.1; ALT_INIT.
EMBL; AK099134; BAB26095.2; ALT_INIT.
EMBL; BC027642; AAH27642.1; -.
HSSP; P00818; 1APS.
                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
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Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
CATALYTIC ACTIVITY: An acy
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ween the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               + phosphate.
SIMILARITY: BELONGS TO THE ACYLPHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produ-
een the Swiss Institute of Bioinformatics
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An acyl phosphate + H(2)O = a
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Best Local
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Best Local
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ACT_SITE 22 22

ACT_SITE 40 40

CONFLICT 13 13

CONFLICT 54 54

SEQUENCE 97 AA; 10895 MW;
                                                                                                                                                                      Hydrolase;
MOD_RES
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                        ProDom; PD001884; Acylphosphatase; 1.

PROSITE; PS00150; ACYLPHOSPHATASE 1; 1.

PROSITE; PS00151; ACYLPHOSPHATASE 2; 1.

PROSITE; PS00151; ACYLPHOSPHATASE 2; 1.

Hydrolase; Acetylation; Multigene—family.

MOD RES

ACT_SITE

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A1

APOTENTIAL.
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P07033;
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01-APR-1988 (Rel. 07, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0112; ACYLPHPHTASE.
ProDom; PD001884; Acylphosphatase; 1.
PROSITE; PS00150; ACYLPHOSPHATASE 1;
PROSITE; PS00151; ACYLPHOSPHATASE 2;
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001792; Acylphosphatase, Pfam; PF00708; Acylphosphatase; 1. PRINTS; PR00112; ACYLPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acylphosphatase.";
Ital. J. Biochem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Muscle;
MEDLINE=86223180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphohydrolase).
ACYP2 OR ACYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A29578; QPBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ramponi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
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Pfam; PF00708; Acylphosphatase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P00818; 1APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     + phosphate.
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: ITS PHYSIOLOGICAL ROLE IS NOT -!- CATALYTIC ACTIVITY: An acyl phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOVIN
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                                                                                   6,
                                                                                                       Similarity
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                                          KTISKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. 35:1-15(1986).
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                                                                                                                                                                      98
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                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35:1-15(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=3011706;
                                                                                                                                                                      11046 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modesti A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%;
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Pred. No.
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F -> L (IN REF.

E -> K (IN REF.
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E -> K (IN REF. 2; BAC32649)
0F3510AFC2AAA15B CRC64;
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                                                                                   Mismatches
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                                                                                <u>,</u>
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                                                                                                                                                                                                                                                                                 "Three-dimensional structure of structure analysis.";
J. Mol. Biol. 224:427-440(1992).
-!- FUNCTION: ITS PHYSIOLOGICAL
-!- CATALYTIC ACTIVITY: An acyl
                                                                                                                                                                                         ProDom; F
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89329032; PubMed=2547076; Saudek V., Wormald M.R., Williams R.J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saudek V., Atkinson R.A., Williams R.J.P., Ramponi G.; "Identification and description of alpha-helical regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=80227652; PubMed=6248536;
Cappugi G., Manao G., Camici G., Ramponi G.;
"The complete amino acid sequence of horse m
J. Biol. Chem. 255:6868-6874(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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ACYP2 OR ACYP.
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28-FEB-2003 (Rel. 41, Last annotation
Acylphosphatase, muscle type isozyme
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                                                                    HELIX
                                                                                                                                                                                                            PDB; 1APS; 15-7UL-92.
InterPro; IPR001792; Acylphosphatase; 1.
Pfam; PF00708; Acylphosphatase; 1.
PRINTS; PR00112; ACYLPHPHTASE.
                                                                                                                                                                                                                                                      PIR; A01015; QPHO.
                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NUMBER PUBMEDLINE=92219262; PubMed=1313885;
                                                                                                                                                                                                                                                                                                                                                                                      acylphosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF ALPHA HELICES. MEDLINE=89178637; PubMed=2538623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P00818;
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28-FEB-2003
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                                                                                                                                                                      Hydrolase; Acetylation;
                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                     "Identification and description of beta-structure scylphosphatase by nuclear magnetic resonance spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                              D-structure.
                                                                                                                                                                                                                                                               + phosphate.
SIMILARITY: BELONGS
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                                                                                                                                                                                PD001884; Acylphosphatase; 1.; PS00150; ACYLPHOSPHATASE 1; 1.; PS00151; ACYLPHOSPHATASE 2; 1.
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(Rel. 01,
(Rel. 41,
         78633453
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        Created)
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ACETYLATION.
GLUTATHIONYLATION
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                                                                                                                                                                                                                                                               ACYLPHOSPHATASE
                                                                                                                                                                                                                                                                                ROLE IS NOT phosphate +
                                                                                                                                                                                                                                                                                                                        G., Williams R.J.P.;
acylphosphatase. Refinement
                                                                                                                                                                                                                                                                                                                                                                                    resonance spectroscopy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  horse muscle acylphosphatase.";
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(EC 3.6.1.7) (Acylphosphate
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                                                                                                                                                                      Multigene family;
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H(2)O = a fatty
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                                                                                                                                                                                                                                                               FAMILY
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RESULT
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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01-APR-1990
15-SEP-2003
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier L., Allen M., Bowles
Kucaba T., Lacy M., Le M., Le
Schellenberg K., Steptoe M.,
Waterston R., Wilson R.,
Submitted (MAY-1997) to the I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manao G., Camici G., Modesti A., Liguri G., Cappugi G., Ramponi G.; Cappugi G., Ramponi G.; "Human skeletal muscle acylphosphatase: the Mol. Biol. Med. 2:369-378(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                              Chiarugi P., Raugei
                                             MEDLINE=96033055;
                                                                  TISSUE=Heart;
                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Testis;
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MEDLINE=86174259;
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                                                 PubMed=7487897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=6100723;
3., Modesti A.,
                                                                                 FROM N.A.
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                           G.,
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Primates;
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Last annotation updat
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                                Marzocchini R.,
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expression
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04B4CFE1B03C3E00 CRC64;
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 of the two acylphosphatase
                                Fiaschi T., Ciccarelli C.,
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RESULT
ACYM_PI
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MOD RES
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MEDLINE-85289095; PubMed-2993259;
Mizuno Y., Yamazaki M., Takasawa
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                      "Amino acid sequence muscle.";
                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                         ACYP2 OR ACYP
                                                                                                                                                                                                                                                                                                                                                                           phosphohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Acylphosphatase, muscle type isozyme (EC 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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PRODUM; PD00184; ACYLPHOSPHATASE 1; 1.
PROSITE; PS00150; ACYLPHOSPHATASE 2; 1.
PROSITE; PS00151; ACYLPHOSPHATASE 2; 1.
HYDTO1886; ACECYlation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0003998; F:acylphosphatase activity; GO; GO:0006796; P:phosphate metabolism; TAS. InterPro; IPR001792; Acylphosphatase. Pfam; PF00708; Acylphosphatase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:180; ACYP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X84195; CAA58988.1; -. PIR; S59138; S52327. HSSP; P00818; 1APS.
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EMBL; BC012290; AAH12290.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S
or send an émail to license@isb-sib.ch).
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European Bioinformatics Institute.
                 + phosphate.
SIMILARITY: BELONGS
                                                        FUNCTION: ITS PHYSIC CATALYTIC ACTIVITY:
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                                                                            97:1135-1142(1985).
N: ITS PHYSIOLOGICAL
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Cetartiodactyla; Suina; Suidae;
                                                                                                                                       of acylphosphatase
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Pred. No
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POTENTIAL.
3B77201DCBFB0E30 CRC64;
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                 ACYLPHOSPHATASE FAMILY
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                                                    ROLE IS NOT phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                   Kizaki T., Shiokawa
ase from porcine skel
                                                                                                                                                                                                                                                                                                                                                                                            n update)
(EC 3.6.1.7)
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lo. 11;
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                                                      YET CLEAR. H(2)O = a
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skeletal
                                                      fatty
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RESULT 9
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Best Local S
Matches 6
                                            PRINTS; PR00112; ACYLPHETIAL...

PRODOM; PD001884; Acylphosphatase; 1.

PROSITE; PS00151; ACYLPHOSPHATASE_1; 1.

PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.

PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.

PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.

PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.

Hydrolase; Acetylation; Glutathionylation; Mult
MOD_RES_1 1 1 ACETYLATION.

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P00820;
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MOD_RES
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PRINTS; PR00112; ACYLPHPHTASE
ProDom; PD001884; Acylphosphatase; 1.
PROSITE; PS00150; ACYLPHOSPHATASE 1; 1.
PROSITE; PS00151; ACYLPHOSPHATASE 2; 1.
                                                                                                                                                                                                        InterPro; IPR001792; Acylphosphatase. Pfam; PF00708; Acylphosphatase; 1. PRINTS; PR00112; ACYLPHPHTASE.
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Kizaki T., Takasawa T., Mizuno Y., Shiok
Kizaki T., Takasawa T., Mizuno Y.,
Panino acid sequence of acylphosphatase
J. Biochem. 97:1155-1161(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphohydrolase).
ACYP2 OR ACYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acylphosphatase, muscle type isozyme (EC 3.6.1.7)
                                                                                                                                                                                                                                                                             PIR; A91988; QPRB
HSSP; P00818; 1AP
                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Monomer (RI
                                                                                                                                                                                                                                                                                                                                                                                    Arch. Biochem. Biophys. 241:418-
-!- FUNCTION: ITS PHYSIOLOGICAL
-!- CATALYTIC ACTIVITY: An acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                     form Ral.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Ramponi G.;
"Rabbit skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Manao G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Skeletal muscle;
MEDLINE=85305733; PubMed=2994566;
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1 ACETYLATION.
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NGS TO
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100.0%;
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POTENTIAL.
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  8B10CA8568683FB0 CRC64;
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ACYLPHOSPHATASE I
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                                                                                                                            Multigene family.
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H(2)O = a fatty acid
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                                                                (PARTIAL)
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28-FEB-2003 (Rel. 41, Last annotation update)
Beta-microseminoprotein precursor (Prostate secreted protein) (Prostate secretory protein PSP94) (PSP-94)
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                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE=94161559; PubMed=8117114;
Fernlund P., Granberg L.B., Roepstorff P.;
"Amino acid sequence of beta-microseminoprotein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 21
TISSUE-Seminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96117078; PubMed=8562060;
Tanaka T., Itahana K., Andoh N., Takeya T., Sato E.;
"Expression of prostatic secretory protein (PSP)-like
porcine corpus luteum: isolation and characterization
encoding PSP94-like protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SURROUNDING BLOOD VESSELS. SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity) TISSUE SPECIFICITY: CORPORA LUTEA, MOSTLY IN THE LUTEAL CELLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
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ilarity 100.0%; Pred. No. 11
Conservative 0; Mismatches
                                                               Conservative
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Inhibits the
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                                                                                                                             A.
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42:149-156(1995)
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100.0%; F1
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                                                                                                                                        BETA-MICROSEMINOPROTEIN.
BY SIMILARITY.
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OR 67 (BY SIMILARITY).
OR 66 (BY SIMILARITY).
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BY ROLLDONE CARBOXYLIC ACID.
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                                                                                           Length 111;
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MSMB_HUMAN
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097936;
28-FEB-2003
                                                                      MSMB HUMAN STANDARD; PRT; 114 AA.

P08118; P11999; Q13125; Q9UC59;

01-AUG-1988 (Rel. 08, Created)

01-AUG-1988 (Rel. 08, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Beta-microseminoprotein precursor (Prostate secreted seminal protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=99421644; PubMed=10491085; Maekinen M., Valtonen-Andre C., Lundwall A.; "New world, but not old world, monkeys carry beta-microseminoprotein."; Eur. J. Biochem. 264:407-414(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saguinus oedipus (Cotton-top tamarin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
Beta-microseminoprotein A1 pre
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                        MSMB OR PRSP.
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    -!- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similari-
    -!- SIMILARITY: BELONGS TO THE BETA-MICROSEMINOPROTEIN FAMILY.

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annotation updat
precursor (msp-A
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BETA-MICROSEMINOPROTEIN A1.

BY SIMILARITY.

BY SIMILARITY.

OR 69 (BY SIMILARITY).

OR 68 (BY SIMILARITY).

BY SIMILARITY.
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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(msp-A1)
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NCBI_TaxID=9606; [1]

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hallon E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fahey J., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Fah
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE:
TISSUE=Prostate;
MEDLINE=96032566; PubM
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Biochim.
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                                                                                                                                                                                                                      TISSUE=Prostate;
MEDLINE=22388257;
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                            Baijal-Gupta
                                                                                                                                                                                                                                                                                                                                                                                                               "Alternative splicing of PSP94 amino acids) mRNA in prostate t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu A.Y., Bradner R.C., Vessella R.L.; "Decreased expression of prostatic sec prostate cancer.";
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MEDLINE=94115955;
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Nolet S., Mbikay M.,
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                                                                                                                                                                                                                                                                                          specific pres (KLE).";
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Liu W.Y., Kwok S.C.M.
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Ketteman M., Young A.C.,
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secreted by
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[12]
SEQUENCE OF 21-50 AND 113-114.
MEDLINE=92028964; PubMed=1930232;
Liang Z.G., Kamada M., Koide S.S.;
"Structural identity of immunoglobulin binding fasecretory protein of human seminal plasma.";
secretory protein Res. Commun. 180:356-359(1991)
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                                                                                                                                                                                                                                                                                                                              Ghafouri B., Stahlbom B., Tagesson C., Lindahl M. "Newly identified proteins in human nasal lavage non-smokers and smokers using two-dimensional gel peptide mass fingerprinting.";

Proteomics 2:112-120(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seidah N.G., Arbatti N.J., Rochemont J. "Complete amino acid sequence of human Prediction of post Gln-Arg cleavage as FEBS Lett. 175:349-355(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99421644; PubMed=10491085;
Maekinen M., Valtonen-Andre C., Lundwal
"New world, but not old world, monkeys
                                           between
                                                              This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human seminal plasma beta-microseminoprotein: its purifi characterization, and immunohistochemical localization."; Int. J. Biochem. Cell Biol. 27:603-611(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95401076;
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Seidah N.G., Arbat
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MEDLINE=85199974; P
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                                                                                     I- TISSUE SPECIFICITY: Strongly expressed i breast and penis. Also expressed in pany deodenum, colon, trachea, lung, salivay tube. PSP94 is expressed in lung and bre found in kidney and bladder.
I- MISCELLANEOUS: SPECIFIC RECEPTORS FOR TH SPERWATOZOA AND IN THE BROSTATE.
I- SIMILARITY: BELONGS TO THE BETA-MICROSEW
                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way field and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                            Name=PSP57
                                                                                                                                                                                                                                                          Name=PSP94;
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bka Y., Schmid K.,
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Sequence=VSP_003275, VSP_vv...
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Also expressed in pancreas, esophagus, stomatrachea, lung, salivary glands and fallopian trachea, lung and breast, whereas PSP57 is
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EMBL; M34375; AAA59871.1.
EMBL; M59928; CAA41002.1.
EMBL; X57928; CAA41002.1.
EMBL; X57930; CAA41002.1.
EMBL; X57930; CAA41002.1.
EMBL; X57931; CAA41002.1.
EMBL; S67815; AAB29732.1.
EMBL; S67815; AAB29732.1.
EMBL; W22178; AAB23755.1.
EMBL; U22178; AAB33556.1.
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MEDLINE-22084549; PubMed=12089438; Tamas I., Klasson L., Canbaeck B., Naesl Wernegreen J.J., Sandstroem J.P., Moran "50 million years of genomic stasis in e Science 296:2376-2379(2002).
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                                                                                                         Buchnera aphidicola (subsp. Schizaphis graminum)
Bacteria; Proteobacteria; Gammaproteobacteria; E
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57; AAH05257.1;
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Marklund B.-I., Tennent J.M., Garcia E., Hamers A., Baga M.,
Lindberg F., Gaastra W., Normark S.;
"Horizontal gene transfer of the Escherichia coli pap and prs
                                                                                                                                                                                                                                                                                                    "Lindberg F., Lund B., Normark S.;
"Gene products specifying adhesion of uropathoge are minor components of pill.",
proc. Natl. Acad. Sci. U.S.A. 83:1891-1895(1986)
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01-AUG-1988 (Rel.
15-SEP-2003 (Rel.
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use by non-profit institutions as long as its content
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entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
               operons as a mechanism adhesive properties.";
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Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                                                                                                                                 "Structure and antigenic properties of proteins of uropathogenic Escherichia of . Bacteriol. 170:1887-1894(1988).
                                                                                                                                                                                                                                                      STRAIN=J96
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InterPro; IPR001543; SpoA.
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                                                                                                                                                                                                                    und B., Lindberg
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F., Normark S.;
: 2225-2242 (1992)
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P21733;
01-MAY-1991
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-!- SUBCELLULAR LOCATION: Secreted; tip of the pilus.
-!- MISCELLANEOUS; Strains of E. coli that cause infection of the human urinary tract produce pap-pil which are hair-like appendages consisting of about 1000 helically arranged subunits of the protein papA. These pili mediate binding to digalactoside-
                                                                                                                  01-MAY 1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 29.1 kDa protein in CRYB1 5'region (ORF2).
Bacillus thuringiensis (subsp. kurstaki).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X61238; CAA43556.1; -.
EMBL; M13239; AAA24280.1; -.
EMBL; M20146; AAA24288.1; -.
EMBL; X61239; CAA43568.1; -.
EMBL; X61239; CAA43568.1; -.
PIR; A25134; YQECPE.
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between
MEDLINE-8913178; PubMed=2914879;
Widner W.R., Whiteley H.R.;
"Two highly related insecticidal crystal proteins of
thuringiensis subsp. kurstaki possess different host
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REVIEW
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InterPro; IPR004086; FimbrialPapE.
Pfam; PF00419; Fimbrial; 1.
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J. Struct. Biol. 124:201-220(1998)
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                                                                STRAIN=HD-1;
                                                                             SEQUENCE FROM N.A.
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PIR; B32053; B32053.
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                                                                                                                                 DB 1
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                                                                                                                                                          Length 252;
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                                                                                                                                                                                                                  CRC64;
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Perfect score:
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
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40
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sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_virus:*
sp_vertebrate:*
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Q91FG9
Q8DT68
Q22192
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Q951P2
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                                       O96ch9 homo sapien
Q9ulh6 homo sapien
Q9ulh6 homo sapien
Q94544 castanaa sa
P93272 malus domes
Q91f99 chilo iride
Q8dtf8 streptococc
Q22192 caenorhabdi
Q98233 arabidopsis
Q81787 plasmodium
Q01441 caenorhabdi
Q01441 caenorhabdi
Q980c0 sulfolobus
065580 arabidopsis
Q9sip2 arabidopsis
Q8w556 arabidopsis
                                                                                                                                                           Q8n4y4 homo sapien
                                                                                                                                                                                 Description
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Q8I0M6	Q81995	Q819A6	Q9BJE8	Q9U1Q1	Q8RD54	Q8K261	Q8IAU2	Q9S394	Q9XET1	8MXV8Q	Q97WG5	Q8S1K0	Q964U2	Q8SDA0	Q9SB99	Q9L0T5	Q92B33	Q8LGF9	Q9SBR6	Q92FF9	Q8BQX2	Q8S2A4	Q99WU4	Q9T124	QBKNUB	Q9VXR1	Q92C89	Q8MVT2
Q8i0m6 plasmodium		Q8i9a6 plasmodium		a	Q8rd54 thermoanaer	\mathbf{r}		lactobac		Q8vxw8 arabidopsis		Q8s1k0 oryza sativ		Q8sda0 pseudomonas		Q910t5 streptomyce	_		7	Q92ff9 listeria in			4.	Q9t124 bacteriopha	Q8knu8 bacillus th	Q9vxr1 drosophila	9 lister:	Q8mvt2 myxine glut

ALIGNMENTS

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RESULT 2
Q96CH9
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Q8N4Y4
  SEPPPE
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                                                                                                                                                                                                                                Matches
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Best Local Similarity
                      Q96CH9;
Q96CH9;
Q1-DEC-2001
01-DEC-2001
01-OCT-2002
                                                                                                                                                                                                                             EMBL; BCO
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    OBN4Y4,
O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to KIAA1244 protein (Fragment).
                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033191; AAH33191.1; -...
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8N4Y4
Hypothetical
Homo sapiens
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ب
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                                                                                                                                  403
                                                                                                                                                1 SPKVEKKDPSRKKEWWENAGNKIYTWAADKTISKLMTEYK 40
                                                                                                                                                                                40;
                                                                                                                                  SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 442
                                                                                                                                                                                                                               589 AA;
(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
1 protein (Fragment)
s (Human)
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Pred. No. 2.2e-3;
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RESULT 4
Q945D4
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Best Local S
Matches 40
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Best Local S
Matches 40
"Wound-responsive genes
Submitted (SEP-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9ULH6; Q96P46;
01-MAY-2000 (TrE
01-OCT-2002 (TrE
01-OCT-2002 (TrE
                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Translation elongation factor 1 alpha-like protein
Castanea sativa (Sweet chestnut).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta,
Eukaryota; Viridiplantae; Streptophyta; Embryophyta,
Spermatophyta; Magnoliophyta; endicotyledons; core e
eurosids I; Fagales; Fagaceae; Castanea.
MCBI TaxID=21020;
                                                                                                                                                                          Q945D4
Q945D4;
                                                                                                                                                                                                                                                                                                                                                                                      "KIAA1244 as a novel distantly related member (BIG3) of the subfamily of ARF GEFs."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF413080; AAL04174.1; -
                              SEQUENCE FROM N.A. Schafleitner R., W
                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000904; Sec7. SMART; SM00222; Sec7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Colon;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
[1]
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                                                                                                                                                                                                                                                                                                                                                 al protein.
1770 AA;
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(TrEMBLrel.
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ilarity 100.0%;
Conservative 0
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                              Wilhelm
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Primates;
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                                                                                                                                                                                                                                                                                                                                                 195845 MW;
      m E.;
of chestnut.";
the EMBL/GenBank/DDBJ databases.
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22,
22,
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Pred. No. 5.
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Pred. No. 2.2e-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                       Embryophyta; Tracheophyta;
edons; core eudicots; Rosidae;
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RESULT 6
Q91FG9
ID Q91F
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Best Local S
Matches 7
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Best Local S
Matches
                                                                                                                                                                      Q91FG9
Q91FG9;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                      apple fruit development.";
J. Am. Soc. Hortic. Sci. 122:752-757(1997).
EMBL; U80268; AACO6383.1; -.
InterPro; IPR004150; EFTU Cterm.
Pfam; PF03143; GTP_EFTU_D3; 1.
NON_TER 1
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01-MAY-1997 (TrEMBLrel. 03,
01-MAR-2002 (TrEMBLrel. 20,
                                                     Delius H., Darai G., Fluegel R.M.;
"DNA analysis of insect iridescent virus
permutation and terminal redundancy.";
J. Virol. 49:609-614(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Granny Smith;
Dong Y.-H., Janssen B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Rosales; Rosaceae; Maloideae; Malus.
 MEDLINE=86174607; |
Lorbacher de Ruiz |
"Insect iridescent
                                                                                             SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID=10488;
[1]
                                                                                                                              Viruses; dsDNA viruses,
                                                                                                                                       Chilo iridescent virus
                                                                                                                                                            01-MAR-2003
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              Dong Y.-H., J
Gardner R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malus domestica (Apple) (Malus sylvestris)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elongation factor 1 alpha (Fragment).
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                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3750;
                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolating and characterizing genes differentially
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                                                                                                                                                                                                      PRELIMINARY;
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z H., Gelderblom F
nt virus type 6 ir
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                                                                                                                           (CIV)
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 n H., Hofmann W., Darai G.; induced toxic degenerative
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MEDLINE-942....
Schnitzler P., Sonntag K.C., Muller ....
Konin E.V., Darai G.;
"Insect iridescent virus type 6 encodes a polypeptide related "Insect iridescent virus type 6 encodes a polypeptide related largest subunit of eukaryotic RNA polymerase II.";
""" Virol. 75:1557-1567(1994).
                                                                                                                                                                                                                 distinct family within the 'DEAD/H' superfamily: implications evolution of large DNA viruses.";
Virus Genes 8:151-158(1994).
                                                                                                                                                                                                                                                             MEDLINE=94353641; PubMed=8073636;
Sonntag K.C., Schnitzler P., Kooni
"Chilo iridescent virus encodes a
                                                                                                                                                                                                                                                                                                             chromosomal HMG protein homologue, and a putative GTP plin the genome of Chilo iridescent virus.";
Nucleic Acids Res. 22:158-166(1994).
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SEQUENCE FROM N.A.
MEDLINE=92196996; PubMed=1549908;
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                                                                                                                                   Sonntag K.C., Schnitzler P., Janssen W., Dara "Identification of the primary structure and the genome of insect iridescent virus type 6 coordinates 0.310 and 0.347 (7990 bp).";
                                                                                                                                                                                    MEDLINE=95213160;
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                                                                                                                                                                                                                                                                                                                                                                         Delius H., Darai
                                                                                                                                                                                                                                                                                                                                                                           Schnitzler P., Hug M., Delius H., Darai C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of the gene encoding the majo
insect iridescent virus type 6 by polymerase
J. Gen. Virol. 74:873-879(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of the third origin of insect iridescent virus type 6."; Virus Genes 6:333-342(1992).
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Sonntag K.C., Darai G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequences of the genom Virus Genes 6:19-32(1992).
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Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the rep
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iridescent virus type 6:
the viral genome.";
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Delius H., Darai G.;
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ltau J.B., Fischer M.,
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6: further evidence for circular permutation
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and the coding capacity of
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Best Local
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SEQUENCE FROM N.A.

STRAIN=UA159 / ATCC 700610 / Serotype c;

STRAIN=E22295663; PubMede112397186;

MEDLINE=22295663; PubMede112397186;

Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Ajdic D., McShan W.M., McShan W.M., McShan W.M., McShan W.M., McShan W.M., Tian R., Kenton S., Jia H., Lin S.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,

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Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,

Carson M.B., Primeaux C., Tian R., Kenton S., Lin S., Lin S.,

Carson M.B., Lin S., Lin S.,
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MEDLINE=98141693; PubMed=9482589;

Bahr U., Tidona C.A., Darai G.;

"The DNA sequence of Chilo iridescent virus between coordinates 0.101 and 0.391; similarities in coding insect and vertebrate iridoviruses.";

Virus Genes 15:235-245(1997).
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Jakob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the First Complete DNA Sequence
Iridovirus: Coding Strategy of the Genome of
Virology 286:182-196(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
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                                            pathogen."
Proc. Natl
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InterPro; IPR004274; NIF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=21342589;
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Virus Genes 18:243-264(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99125223;
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Genes 17:243-258(1998)
        AE014983; AAN59160.1;
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C.A., Bahr U.,
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Pred. No.
                                                99:14434-14439(2002)
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synthase g
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J.J.;
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e SEQUENCE FROM N.A.
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 2, 01-OCT-2002 (TrEMBLrel. 22, AVR9 elicitor response like F10M23.280 OR AT4G26940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z68108; CAA92135.1; -.
WormPep; T05A10.3; CE03635.
InterPro; IPR001534; Worm_family_2.
Pfam; PF01060; DUF290; 1.
SEQUENCE 406 AA; 48925 MW; 8922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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                                                                         Bevan M., Lecharny A., Chefdor F., Krivitzky M., Kreis M., Hoheisel J., Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                         SEQUENCE FROM N.A.
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RESULT 11
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Q81787; Q81787; 01-MAR-2003 01-MAR-2003 01-MAR-2003

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Created)

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Submitted (MAR-2002) to the EMBL/Gen
EMBL; AY085383; AAM62612.1; -
InterPro; IPR002659; Glyco trans 31.
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01-OCT-2002 (TrEMBLrel. 22, Last sequency
01-MAR-2003 (TrEMBLrel. 23, Last annotaty
01-MAR-2003 (TrEMBLrel. 23, Last annotaty
Avry elicitor response-like protein.
Arabidopsis thaliana (Mouse-ear cress).
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EMBL; AL161566; CAB79549.1; -.
EMBL; AL161566; CAB79549.1; -.
InterPro; IPR002659; Glyco_trans_31.
Pfam; PF01762; Galactosyl_T; 1.
SEQUENCE 406 AA; 45892 MW; 11411
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Lecharny A., Chefdor F.,
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haas B.J., Volfovsky N., Feldmann K.A., Flavell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                      "Full-Length cDNA from Arabidopsis thaliana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                         PF01762;
NCE 407
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
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                                               29
                                                                                         l Similarity
7; Conserv
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  DKTISKL 104
                                               DKTISKL 35
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                                                                                                                                                                                                                                                                                                                                                        Troukhan M., Alexandrov N.,
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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AA; 46020 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Town C.D., Tr.B., White O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences greatly improve
                                                                                              <u>,</u>
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                                                                                                                    Score 7;
Pred. No.
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                                                                                                                                                                                            756C0F8866E1C952 CRC64;
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red. No. 25;
Mismatches
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RESULT 12
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                                        Query Match
Best Local S
Matches 7
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          001441;
                                                                                                                                                                           "Direct Submission.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
EMBL; U97016; AAB52350.2; -
WormPep; B0261.1; CE29531.
InterPro; IPR001005; Myb DNA_binding.
Pfam; PF00249; myb DNA_binding; 1.
SMART; SM00717; SANT; 1.
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Bristol N2;
Scheet P., Gattung S.;
"The sequence of C. ele
Submitted (APR-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
B0261.1.
                                                                                                                                  Hypothetical SEQUENCE 7
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ438840; CAD27565.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=NIG203;
                                                                                                                                                                                                                                                                                                                                                                                          Waterston
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32
                                        Similarity 7; Conserv
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ISKLMTE 38
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                                                                                                                               11 protein; DNA-binding; Nuclear protein. 779 AA; 87113 MW; 64B5E808EA5A9674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 04, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
1 87.1 kDa protein.
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                                        Conservative '0;
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7) to the
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                                                                 17.5%; Score 7;
100.0%; Pred. N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 5; Pred. No. 36; 0; Mismatches
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                         NO.
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                                                              DB 5;
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                                                                                    Length 779;
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                                           Indels
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                                      Gaps
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OG5580
AC O6558
AC O6558
AC O6558
DT 01-AU
DT 01-M2
DT 01-M2
DT 01-M3
DE Recep
DE Protec
GN M3E9.
OS Arabi
OC Eukar
OC Sperm
OC Sperm
OC NCBI
RN (11)
RP SEQUE
RA Mewes
RL Submit
RN (2)
RN SEQUE
RA Mayer
RA Mayer
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                             065580;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-7005 (Tremblance)
01-MAR-2003 (Tremblance)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

De Moors A., Erauso G., Fletcher C., Kozera C.J., Medina N., P.

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., P.

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.; "The complete genome of the cremarchaeon Sulfolobus solfataricus P2."; Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
EMBL, AE006673; AAK40723.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18,
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                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidersides (I); Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        065580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001650; Helicase, Pfam; PF00270; DEAD; I. Pfam; PF00271; helicase C; 1. SMART; SM00487; DEXDC; I. SMART; SM00490; HELICC; 1.
SEQUENCE FROM N.A. Vandenbol M., Jallet Mayer K.F.X.;
                                                                                                     Bevan M., Vandenbol M., Jallet on Mewes H.W., Mayer K., Schueller Submitted (MAR-1998) to the EMBI
                                                                                                                                                                                                                                                                                                                                                                               M3E9.30 OR AT4G26540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus solfataricus
                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                   NCBI_TaxID=3702;
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                              Portetelle
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Last annotation update)
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5. 51;
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Zimmermann I Smith A., M Submitted (I

Mewes H.W., Lemcke (MAR-2000) to the

W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P., Mewes H.W., Lemcke K., Mayer K.F.X.; (MAR-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases [3]

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Q9SIP2
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Matches 7
                                                                                                                 SEQUENCE FROM N.A.

STRAIN=CV. COlumbia;

MEDLINE=20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Pujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome 2 of the plant Arabidopsis

thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9SIP2;
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PRINTS; PRO0019; PROT kinase; 1.

PROSITE; PS50502; LRR FS; 6.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 1029 AA; 112970 MW; OBE6FCF91D21386B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE FROM N.A. STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel 13, Created)
01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-CCT-2002 (TrEMBLrel 22, Last annotation update)
Putative importin (Nuclear transport factor) protei
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN
EMBL; AL022223; CAA18216.1; -.
EMBL; AL161565; CAB79509.1; -.
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VOLCKAERT G., Grymonprez B., Voet M., Robben J., Mewes H
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
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                                                                                        Nature 402:761-768(1999).
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o. 57;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007071; AAD24943.1; -.
InterPro; IRR001494; Importinb_N.
                                                                                    Pfam; PF03810; IBN NT; I.

PROSITE; PS50166; IMPORTIN B NT;
SEQUENCE 1037 AA; 118966 NW;
721 TISKLMT 727
                   31 TISKLMT 37
                                        Similarity
7; Conserv
                                         Conservative
                                                     17.5%; Score 7;
100.0%; Pred. No.
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4DE90DCCF7B3C6DA CRC64;
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Search completed: July 24, Job time: 15.2987 secs

2003, 12:25:52

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Title:
Perfect score:
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6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

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12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

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                                             AAO19168
AAM50812
AAW85472
AAO19165
AAO19169
ABG09728
ABG09731
               AAU36030
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Human prostate-spe
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(BILL, (COHE, (COLP, (FRIE, (GORD, (GRAN, (HODG, (KLAS,	23-APR 23-APR	26-NOV	04-JUL	US2002	Homo	Human EST;	Human	27-NOV	AA019	SULT 1 019168 AAO19		. <u>4</u> .	44	Δ :	41	4 (ω u 9 0	37	36	ω ω 4 π	3 3 3 2	ωu	29	28	26	2 2 5 4	23	21	19	17 18	16	14	13	111	10
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						scific sequence; prostate c cytostatic; gene therapy.	protein fragment #4.			IO AA.	ALIGNMENTS	4.	7	$\tilde{\omega}$	วร	ភេដ	5 F	259	594	158)88 765	287	382	787 3 7 4	36	38	555	5	ະພ	AAG50368 AAG50367	ü	ລິພ	8 2	3262	္မ
						cancer; PS118;						isopentyl di	brasiliensi	secreted	Human protein NOV1	protei	protei	Human kinase PKIN-	Human protein sequ	Mycobacterium tube	Herbicidally activ	Human transducin p	Arabidopsis thalia	Novel human diagno	Tobacco quinolate		dopsi dopsi	idopsi	bidopsi	Arabidopsis thalia Arabidopsis thalia	abidopsi	rabidopsi	Helicobacter pylor	ade bebro	Mouse oocyte prote

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Billing-Medel
Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS118 prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-665429/71.
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Russell JC,
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(ROBE/)
(RUSS/)
(STRO/)
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                                                                                                                                 (FRIE/)
(GORD/)
(GRAN/)
(HODG/)
                                                                                                                                                                                                                    (COPL/)
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                                                                                                        FRIEDMAN P N.
GORDON J.
GRANADOS E N.
HODGES S C.
KLASS M R.
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RUSSELL J C.
STROUPE S D.
                                                                KRATOCHVIL J D. ROBERTS-RAPP L.
                                                                                                                                                                                                                    COPLPITTS T L.
                                                                                                                                                                                                                                                                   BILLING-MEDEL P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 AA;
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Hodges
PA, Cohen
Hodges SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           marker immunogenic
                                                                                                                                                                                                                                                                                                               97US-0842385
                                                                                                                                                                                                                                                                                                                                                        98US-0065383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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M, Coplpitts TL, Friedman Klass MR, Kratochvil JD,
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Klass MR,
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Pred. No. 2.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TL, Friedman
R, Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QD,
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                    PN,
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Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                    Gordon J;
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RESULT 3
AAW85472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in non-prostate tissue. PS118 polypeptides, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostate; intraspithelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of FS118 polynucleotides in transfected host cells, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 40; Conserv
                                           Billing-medel PA,
Granados EN, Hod
Russell JC, Stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of an immunogenic polypeptide comprising amino acids 332-371 of human prostate-specific PS118 polypeptide (see AAM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting presence of target PS118 polynuclectide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
WPI; 1998-610000/51.
N-PSDB; AAV82812.
                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                      AAW85472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-187683/24.
                                                                                                                                      23-APR-1997;
                                                                                                                                                                    23-APR-1998;
                                                                                                                                                                                                   29-OCT-1998
                                                                                                                                                                                                                                 WO9848054-A1
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                            EST clone; PS118;
                                                                                                                                                                                                                                                                                                                         PS118 protein
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                                                                                                         (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK
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                                              Stroupe
                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                        Hodges
                                                                                                                                                                                                                                                                                                                           encoded by consensus sequence
                                                                                                                                      97US-0842385
                                                                                                                                                                    98WO-US08239
                                                                                                                                                                                                                                                                                              prostate tumour tissue; prostatic disease; cancer.
                                            Cohen M, Colpitts TL, es SC, Klass MR, Krat pe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No. 2.8e-21;
); Mismatches 0;
                                                           B TL, Friedman
Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
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                                                         PN, Gordon J
Robertsrapp
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Best Local :
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                               Billingel
Granados E
WPI; 2002-665429/71
                                                                                                                 (GORD/)
(GRAN/)
(HODG/)
                                                                                                                                                            (COLP/)
                                                                                                                                                                                                        23-APR-1998;
23-APR-1997;
                                                                                                                                                                                                                                        26-NOV-2001; 2001US-0991681.
                                                                                                                                                                                                                                                             04-JUL-2002
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                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                    Human; prostate;
                                                                                                                                                                                                                                                                                                                                                         Human prostate-specific PS118 protein fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                      AAO19165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17;
                                                                                                                                                  (FRIE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Updated on 25-MAR-2003 to correct PI field.)
                                                                                             (KRAT/)
                                                                                                         (KILAS/)
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                                                                                                                                                                                                                                                                                                                          expressed
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                                                                                                                                            COHEN M.
COLPITTS T L.
FRIEDMAN P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
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              . JC,
                                                            KLASS M R.
KRATOCHVIL J 1
ROBERTS-RAPP 1
RUSSELL J C.
STROUPE S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                 GRANADOS E N.
HODGES S C.
                                                                                                                                        GORDAN J.
                                                                                                                                                                                 BILLINGEL P A.
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                                    PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518
                   Hodges
Stroupe
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llarity 100.0%;
Conservative (
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X
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                                                                                                                                                                                                       98US-0065383
97US-0842385
                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                          prostate-specific sequence; prostate cancer;
equence tag; cytostatic; gene therapy.
                    SC,
                                                                                    F 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and proteins - used for diagnosis and disease, especially cancer, and also
                             Colpitts TL,
Klass MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 215; DB 19;
Pred. No. 4.9e-20;
; Mismatches 0;
                              Kratochvil
                              Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371
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                              Roberts-Rapp
                                         Gordan J;
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DT 01-M
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DT 02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                     Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate disease -
                                                                                                                                                                                                    Billing-Medel PA, Co
Granados EN, Hodges
Russell JC, Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neopl prostatitis; human; diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (BILL/)
(COHE/)
(COPL/)
(FRIE/)
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                                                                                                                                                                                                                                                                                                                          (KLAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                 (GRAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                         (GORD/)
                                                                                                                                     2002-187683/24.
DB; ABA91651.
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                                                                                                                                                                                                                                                                                                                                           GORDON J.
GRANADOS E N.
HODGES S C.
KLASS M R.
                                                                                                                                                                                                                                                                                                  KRATOCHVIL J
ROBERTS-RAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                     FRIEDMAN P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BILLING-MEDEL
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                                                                                                                                                                                                         Cohen M, Cop
ges SC, Klass |
upe SD;
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Pred.
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No. '
                                                                                                                                                                                                                              cs TL, Friedman
Kratochvil JD,
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hes 0;
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Roberts-Rapp
                                                                 prognosticating,
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rts-Rapp L;
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RESULT 6
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Matches
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome ,
                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                   Claim 20;
                                                                                                                                                                                                        N-PSDB; AAS73915.
                                                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                               SEQ ID No 40087; 103pp; English.
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                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                      Tang YT
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Pred. No. 4.9e-20;
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RRESULT 7
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CC Note: The sequence data for this partent did not appear in the printed confict of the invention, but was obtained in electronic format directly from WIPO at figure in the printed confict of the invention of the printed confict of the printed 
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; antiallergic; antinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide; cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                                                                                          New isolated polynucleotide, useful in research, diagnostic therapeutic methods, e.g. preventing or treating disorders i aberrant protein expression or biological activity -
                                                                                                                                                                                                                                                                WPI; 2002-590824/63.
N-PSDB; ABQ99421.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                              , Goodrich RW,
Xue AJ, Yang
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Pred. No. 2e-19;
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Claim

20; SEQ ID 495; 394pp; English

hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The polynucleotides are useful in diagnostics as expressed

(ABQ99268-ABQ99608) and proteins (ABP64682-ABP65022). The sequenuseful in therapeutic, diagnostic and research methods. The polynucleotides may be used in the field of molecular biology as The present invention relates to novel human coding sequences (ABQ99268-ABQ99608) and proteins (ABP64682-ABP65022). The seq

sequences are

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC sequence tags (ESTS) for identifying expressed genes or for physical CC mapping of the human genome. The proteins may be used as molecular weight CC markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or CC pluripotential state useful for re-engineering damaged or diseased CC tissues, transplantation, manufacture of bio-pharmaceuticals or the CC development of bio-sensors. The polynucleotides and proteins are useful for preventing, treating or ameliorating disorders involving aberrant CC protein expression or biological activity, e.g. haematopoietic disorders, CC central/peripheral nervous system diseases, mechanical and traumatic disorders, non-healing wounds, immune deficiencies and disorders, CC disorders, or cancer. The polynucleotide sequences of the invention were assembled from ESTs isolated mainly by sequencing by hybridiation, and CC assembled from ESTs isolated mainly by sequencing by hybridiation, and CC note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO Cat firm wino informly-published not segmences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                   WPI; 2001-639362/73.
N-PSDB; AAS73918.
                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                      11-OCT-2001
                                                                                                                                                                                                                                                                                                                    WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forension supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #9722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG09731 standard; Protein; 1982 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                  RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPKVEKKOPSRKKEWWENAGNKIYTMAADKTISKLMTEYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1839 AA;
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                                                                                                                                  Liu C,
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Pred. No. 2.1e-19;
); Mismatches 0;
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RESULT 9
AAU36030
ID AAU3
XX AAU3
AC AAU3
XX AAU3
XX AAU3
XX AAU3
XX Heli
XX Anti
Ax A
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Best Local Similarity
                                                                                                                                                                                                                                                                                                            26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                         Haselbeck R, Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2000;
23-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori cellular proliferation protein #343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ
                                       N-PSDB; AAS53889
                                                                        WPI; 2001-611495/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic cellular proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                              ELITRA PHARM INC
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2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibacterial; drug design.
                                                                                                                                                                                                                                                                                                               2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                                                                                                                         Ohlsen
Xu HH;
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Pred. No. 2.2e-19;
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                                                                                                                                                                             Wall D,
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                                                                                                                                                                             Trawick JD,
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RESULT 10
AAE06034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                         New egg-specific surface proteins, useful as immunogens in a vaccine preparation for modulating fertility, particularly useful for producing antibodies for temporary, reversible contraception methods -
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse oocyte protein 5; MOP5; egg specific surface protein; immunogen; vaccine; fertility; contraceptive; active immunisation; sterilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse oocyte protein 5 (MOP5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE06034 standard;
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                             Claim 1; Page 32-35; 41pp; English.
                                                                                                                                 N-PSDB; AAD11617, AAD11618
                                                                                                                                                 WPI; 2001-465367/50
                                                                                                                                                                                                                                                                                  19-JAN-2001; 2001WO-US01718
                                                                                                                                                                                                                                                                                                                     26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                     WO200153339-A2
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                                                                                                                                                                                                                                                   20-JAN-2000; 2000US-0177123
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                                                                                                                                                                                                                  (UYVI-) UNIV VIRGINIA PATENT FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKLWWSNLQNSLFTLLPDKLANALRISDLPESYQ
                                                                                                                                                                                Coonrod SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.7%;
                                                                                                                                                                                Wright P;
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Pred. No. 19
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The present sequence is mouse oocyte protein 5 (MOP5). The τ

Query Match Best Local Similarity

26.5%;

Score Pred.

57; No. DB 61;

24;

Length 682

Sequence

682 AA;

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RESULT 11
AAE32624
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to egg specific surface proteins (antigens) and nucleic acids encoding them. The proteins of the invention are involved in egg-sperm binding and fusion. They are useful as immunogens in vaccine preparation for modulating fertil. In particular, the proteins are useful for producing antibodies which are useful for temporary, reversible contraception methods. The contraceptive vaccine is especially useful for controlling fertility in human beings or agriculturally important livestock,
                                        The invention relates to peptidylarginine deiminase 6 (PAD6) polypeptides and polymucleotides. Polymucleotides of the invention are useful as targets for male and female contraception. Polypeptides of the invention are useful for screening small molecular weight modulators useful for controlling fertility disorders. They are also useful for screening therapeutic agents for fertility control related to the activity of PAD6. The invention is useful in gene therapy. The present sequence is mouse
                                                                                                                                                                        Claim 3; Page 25-28;
                                                                                                                                                                                                      New polynuclootide comprising a nucleotide sequence that encodes peptidylarginine deiminase 6, useful as targets for male and female contraception and for screening small molecular weight modulators of the enzyme activity
                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                      Gossen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse peptidylarginine deiminase 6 (PAD6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE32624 standard; Protein; 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sterilisation of female animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. cattle or pig. The invention also relates to the use of antibodies against such antigens for active immunisation or
                                                                                                                                                                                                                                                                                                  WPI; 2003-103517/09.
                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2001; 2001EP-0201601
                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2002; 2002WO-EP04552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200290531-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptidylarginine deiminase 6; PAD6; contraception; fertility disorder;
                                                                                                                                                                                                                                                                                                                                                                    (ALKU ) AKZO NOBEL NV.
                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 EDPNRQSKWLQDEMAFCYTQAPHKTVSLIL 347
                                                                                                                                                                                                                                                                                                                                    JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 KDPSRKKEWWENAGNKIYTMAADKTISKLM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 33.
                                                                                                                                                                                                                                                                                       AAD50412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       664 AA;
                                                                                                                                                                                                                                                                                                                                      Van Den
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.5%;
33.3%;
                                                                                                                                                                                                                                                                                                                                      Boogaart
                                                                                                                                                                        35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme
                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57; DB:
Pred. No. 59;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                      70
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RESULT 13
AAU35865
ID AAU35
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AC AAU35
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                                                                                                                     Matches
                                                                                                                             Query Match
Best Local :
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01-APR-1997;
24-JUN-1997;
                                                                                                                                                                            invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                          New
           14-FEB-2002
                            AAU35865;
                                          AAU35865 standard; Protein;
                                                                                                                                                      Sequence
                                                                                                                                                                                                               This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating
                                                                                                                                                                                                                                       Claim 8; Page 571-573; 2054pp; English.
                                                                                                                                                                                                                                                                                                                   Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                WO9843478-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHPO protein; Helicobacter infection; peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori GHPO 1138 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW98375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW98375 standard; Protein;
                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                        isolated Helicobacter polynucleotides - used to develop products
the diagnosis, prevention and treatment of Helicobacter
sctions and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                   1998-542293/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336
                                                                                     217
                                                                                                    11 RKKEWWENAGNKIYTMAADK----TISKLMTEYK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDPNRQSKWLQDEMAFCYTQAPHKTVSLIL 365
                                                                                   RLKLWWSNLONSLFTLLPDRLANALRISDLPESYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDPSRKKEWWENAGNKIYTMAADKTISKLM 36
                                                                                                                                                                      and diagnosis.
                                                                                                                                                     388 AA;
                                                                                                                     Conservative
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         (first entry)
                                                                                                                                                                                                                                                                                                                   Kleanthous H,
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97US-0833457.
97US-0881227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                             26.3%;
34.3%;
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                                                                                                                    Score 56.5; Di
Pred. No. 38;
5; Mismatches
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                                                                                                                                     DB 19;
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RESULT 14
AAG44032
ID AAG44
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AC AAG44
XX
AC AAG44
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XX
XX
XX
XX
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18-OCT-2000

(first entry)

AAG44032;

AAG44032 standard;

Protein; 219

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Matches
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Best Local
                                                                                                                                                                                                                                                                                                       for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this pattent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus, Salmonella typhi, Klabsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used for antibiotic development.
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                        of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Seq ID No 11458; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-611495/70.
N-PSDB; AAS53724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto
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  217
                                                 11
                                                                                                l Similarity
12; Conserv
                                                 RKKEWWENAGNKIYTMAADK----TISKLMTEYK 40
RIKLWWSNLQNSLFTLLPDRLANALRISDLPESYQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RT,
                                                                                                                                                                                                388 AA;
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2000US-257931P.
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2000US-207727P.
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Xu HH;
                                                                                                                    26.3%;
34.3%;
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                                                                                             Score 56.5; D
Pred. No. 38;
5; Mismatches
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was obtained in electronic
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                                                                                                  Indels
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99US-0139461 99US-0139461 99US-0139462 99US-0139463 99US-0139763 99US-0139763	-013945 -013945 -013945 -013945	99US-013949 99US-013945 99US-013945	99US-0139119. 99US-0139452. 99US-0139453.	99US-013809 99US-013854 99US-013884	99US-013752 99US-013750 99US-013772	99US-013639 99US-013678 99US-013722	99US-013562 99US-013602	99US-013494 99US-013512 99US-013535	99US-013437 99US-013476	99US-013421 99US-013422	99US-013425 99US-013421	99US-013248	99US-013248 99US-013248	99US-0132048. 99US-0132407.		99US-0130449. 99US-0130510.	99US-0129845 99US-0130077	99US-0128234. 99US-0128714	99US-0126785	თ დ	9908-012354	9908-0121825	2000EP-0301439			thaliana.	identification; signal ation assay; genetic made identification; sequence.	thaliana protein
11. 0. 2. 2. 3. 3. 3. 4. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5.		U sa O	3 2 9	7.					в.	9.	ш	7.	1 VI 145	B. 7	9.	. ·	5. 7.		S			5 G.	9.				<pre>gnal transduction pathway; metabolic pathway; ic mapping; gene expression control; promoter;</pre>	agment SEQ ID NO: 55105.
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99US-0149 99US-0149 99US-0150 99US-0150 99US-0151 99US-0151	- Sn6 - Sn6 - Sn6	9US-014 9US-014 9US-014	9US-014 9US-014 9US-014	9US-	9US- -SN6	-Sn6 -Sn6	9US-	- SD6 - SD6	-Sn6	9US-	-Sn6 -Sn6	-Sn6	-Sn6	-Sn6	9US-	-Sn6	-sn6	Sue-	-Sn6 -Sn6	-Sn6 -Sn6	9US-	- Sn6	-Sn6	-S06	-Sn6	-Sn6	- Sn6 - Sn6 - Sn6	9US-

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RESULT 15
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Best Local S
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04-OCT-1999
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  Arabidopsis thaliana
                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                Arabidopsis thaliana
                                                                                                            18-OCT-2000
                                                                                                                                      AAG50369;
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10; Conser
                                                                                                                                                               standard;
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nilarity 33.3%;
Conservative
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99US-0151930

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99US-0153758

99US-0154779

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99US-0155659

99US-0157753

99US-0157753

99US-0158232

99US-0158232

99US-0159294

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99US-0159294

99US-0159330

99US-0160980

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99US-0161406

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99US-0161359

99US-0161361

99US-0161361
                                                                                                                                                               Protein;
                                                                                                          entry)
                                                                               protein fragment
                                                                                                                                                               219
                                                                                                                                                                                                                                                                                        8;
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                                                                                SEQ ID NO: 63822.
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Search completed: July 24, Job time : 14.0015 secs
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Result
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Listing first 45 summaries
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Perfect score:
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US-08-568-459A-2
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Sequence 54, Appli
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ALIGNMENTS

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RESULT 1
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             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/842,38
PILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,41
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/235-1729
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APPLICANT: BILLIN
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APPLICANT: KLASS, MIC
APPLICANT: KLASS, MIC
APPLICANT: KRATOCHVIL
APPLICANT: ROBERTS RA
APPLICANT: RUSSELL, J
APPLICANT: STROUPE, S
TITLE OF INVENTION: F
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
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APPLICANT:
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APPLICANT:
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                     TELEX:
                                                                      TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                    CLASSIFICATION:
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GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
40 amino acids
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ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
VENTION: REAGENTS AND METHODS USEFUL
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STRANDEDNESS:

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KRATOCHVI
APPLICANT: ROBERTS-R
APPLICANT: RUSSELL,
APPLICANT: STROUPE,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                            TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                             LENGTH:
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                                                                                          STRANDEDNESS:
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                                                                                                                                                                                   TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                          amino acid
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RUSSELL, JOHN C.
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KLASS, MICHAEL R.
KRATOCHVIL, JON D.
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                                                              No. 6391543e
                                                                                         single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE PROSTATE
 100.0%;
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Pred. No. 5.6e-23;
 Score 215; DB 4;
Pred. No. 1.3e-21;
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               Length 518;
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; TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-5591
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US-09-328-352-5591
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APPLICANT: GATY L. Breton et al.

APPLICANT: GIVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
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LENGTH: 275
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INFORMATION FOR SEQ ID NO: 3889:
                                                                                                                                       FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332
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5. 6583275
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10; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 371
                                                                            NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
                   TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/107,532A
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45.5%; Pred. No.
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AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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TYPE: amino acid TOPOLOGY: linear

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LOCATION: (B) LOCATION 1...244
SEQUENCE DESCRIPTION: SEQ ID NO: 3889:
US-09-107-532A-3889
                                                                                                                                                                                                                                                                                           US-09-021-286-2
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; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-431-976-2
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Best Local (
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SEQ ID
                                         APPLICANT: Conkling, Mark
APPLICANT: Mendu, Nandini
APPLICANT: Mendu, Nandini
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Regulation of Quinolate Phosphoribosyl Transferase
TITLE OF INVENTION: Expression
FILE REFERENCE: 5051-338
CURRENT APPLICATION NUMBER: US/09/021,286B
CURRENT FILING DATE: 1998-02-10
EARLIER APPLICATION NUMBER: 60/049,471
EARLIER FILING DATE: 1997-06-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Regulation of Quinolate Phosphoribosyl Transferase TITLE OF INVENTION: Expression FILE REFERENCE; 5051-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Conkling, Mark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/431,976
CURRENT FILING DATE: 1999-10-29
SOFTWARE: PatentIn Ver. 2.0 EQ ID NO 2
                                  NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
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PRIOR FILING DATE: 1998-02-10
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No. 642352
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9; Conserve
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Song, Wen
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52.9%;
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31.8%;
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Pred. No.
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; ORGANISM: Nicotiana tabacum US-09-021-286-2
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                                                                                                                      ; TYPE: PRT; ORGANISM: Rhodococcus opacus US-09-986-536-2
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-09-986-536-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : ORGANISM: IPIHb (IPP isomerase from Hevea brasiliensis) US-09-296-754-2
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                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GEUEKE, BIRGIT
APPLICANT: HUMMEL, WERNER
APPLICANT: HUMMEL, WERNER
APPLICANT: BOMMARIUS, ANDREAS
TITLE OF INVENTION: L-Amino Acid Oxidase from
FILE REFERENCE: 215209USOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/296,754A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: KOPATIN 1.0
SEQ ID NO 2
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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                                                             Matches
                                                                         Query Match
Best Local
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Patent No. 646184
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                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: DE 100 55 512.8
PRIOR FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Korea Kumho Petrochemical Co. Ltd.
TITLE OF INVENTION: Isopentenyl diphosphate isomerase
FILE REFERENCE: PX99102/US
                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/986,536
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TYPE: PRT
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                                                                                                                                                                   ENGTH: 489
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es 12; Conserv
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313
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                           3 KVEKKDPSRK-----KEWWENAGNKIYTMAA--DKTISKLMTEY 39
                                                           l Similarity
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KAAKPSSSGKLGIEYSRRWWETE-DRIYGGASNTDKDISQIMFPY 356
                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09986536
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52.2%;
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52.9%;
                                                                         24.0%;
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                                                         Score 51.5; D
Pred. No. 47;
6; Mismatches
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Pred. No. 1
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Pred. No.
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Best Local 9
                                                                                                                                                                                                                                                                                      Sequence 35, Appli
Patent No. 6033823
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                       APPLICANT: RIEMENS, Adriana Marina APPLICANT: QUAX, Wilhelmus Johannes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MOUNTAIN OF SEQUENCES: CORRESPONDENCE ADDRESS.
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                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                        TLE OF INVENTION: Mutated Penicillin G Acylase Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                         CITY: Chicago
                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312)913-0002
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                                                                                                                                                          ADDRESSEE:
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13; Conserv
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                                                                                                                                                                                                                                                                                                        Application US/09285957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 amino acids
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                                                                                                                                           300 South Wacker Drive
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QUAX, Wilhelmus Johannes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                           Floppy disk
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23-APR-1997
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27.7%;
Release #1.0,
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Pred. No. 61;
3; Mismatches
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Version #1.30
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RESULT 12
US-08-469-486-52
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                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                    Patent No.
                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/553,690
CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hannon, Mike
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Pruit Development in Plants
FILE REFERENCE: 023070-099900US
                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1:
TYPE: PRT
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                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: ATROPOS (ATR) amino acid sequence
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Arabidopsis sp.
                                        APPLICANT:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 97
BLECOMMUNICATION INFORMATION:
TELEPHONE: (312) 913-0001
                             PPLICANT:
                                                                                                                                                                                                                                        Local Similarity
les 10; Conserv
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                                                                                        52, Application US/08469486
o. 5739281
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                 INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi, Yeonhee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fischer, Robert L.
                                        Thoegersen, Hans Christian
Holtet, Thor Las
                          Etzerodt,
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32.3%;
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27.7%;
Improved proteins
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Pred. No.
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              method for the refolding of
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                                                                                                                                                                                                                                                       No. 2.6e+02;
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ADDRESS

Boston

225 Franklin Street

Richardson

Massachusetts

NUMBER OF SEQUENCES:

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RESULT 13
US-08-469-658-52
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                                                                                                                                                                                                                                                                 Patent No. 571,...
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
HOLtet, Thor Las
APPLICANT:
Etzerodt, Michael
TITLE OF INVENTION:
IMPROVED METHOD FOR THE REFOLDING
TO INVENTION:
PROTEINS
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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FILING DATE: February 4, 1994
ATTORNEY,AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 06363/0
REFERENCE/DOCKET NUMBER: 06363/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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LENGTH: 4544 amino acids
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MEDIUM TYPE: Floppy disk
                   CURRENT APPLICATION DATA:
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                                   SOFTWARE: PatentIn Release #1.0, Version SOFTWARE: #1.25
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                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                       CITY: Boston
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                                                                                                                                                                      USA
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US/08/469,658
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Pred. No. 8.3e+02;
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US-09-107-532A-6640
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US-09-545-814-29
                                               Sequence 6640, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6416977 GENERAL INFORMATION:
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Best Local
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT FILLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,833
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 489
TYPE: PRT
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REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: Februar
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nes 12; Conserv
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TOPOLOGY: 1i
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                                                                                                                                                                                                                                                                                      Local Similarity
es 14; Conserv
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NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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                                                                                                                                                                                                                     29 DDKDPVKLQIAVGGWAEGGKKYSTMVAEKRKRSAFIRSVVDFMNEYK 75
                                                                                                                                                                                                                                                      5 EKKDPSRKK---EWWENAGNKIYTMAADK-----TISKLMTEYK 40
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N: 530
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Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                       Score 50.5;
Pred. No. 65;
                                                                                                                                                                                                                                                                                    Mismatches
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                                                  AND AMINO ACID SEQUENCES RELATING TO FAECIUM FOR DIAGNOSTICS AND THERAPEUT
                                                                                   and David Bush
                                                                                                                                                                                                                                                                                                                       DB 4;
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STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachisetts
COUNTRY: UGA
ZIF: 02354
COMPUTER READSACHISETS
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PRIOR APPLICATION NUMBER: US/09/107,532A
FILING DATE: 14 MR3; US/09/107,
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Result
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Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/US10E PUBCOMB.pep:*
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US-10-063-547-150
US-10-036-041-67
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US-10-063-547-1
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             Sequence 350, App
Sequence 2, Appli
Sequence 9082, App
Sequence 209, App
Sequence 106, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 67, Appl
Sequence 67, Appl
Sequence 150, App
Sequence 150, Appl
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Sequence 11458, A
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Sequence 90, Appl	8,8	e 90	e 150,	e 150,	90,	e 90,	e 150,	e 67,	e 67,	e 90,	67,	90,		90,	e 67,		90,		æ	90,	e 90,		e 90,	e 90,	æ	e 150,	e 67,	Sequence 90, Appl

ALIGNMENTS

US-09-815-242-11623

Sequence 11623, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:

RESULT 1

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-10-2-16
NUMBER OF SEQ ID NOS: 14110
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11623
LENGTH: 388
TYPE: PRT
ORGANISM: Helicobacter pylori

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                                                                  Sequence 350, Application US/09881752A Patent No. US20020115078A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11458
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APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
                                                                                                                                                                                                                                                                                                                                           09-815-242-11458
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PRIOR APPLICATION NUMBER: 60/207,727
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(388)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
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o. US20020061569A1
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Zyskind, Judith W.
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Pred. No. 7.7
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Pred. No. 1
                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                      DB 9;
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                                                                                                                                                                                                                                                                                                      Length 388;
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                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                  Gaps
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; SEQ ID NO 350
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-350
                                                                                                                                                                                                                                                                                          RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Nicotiana tabacum US-09-963-340-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-09-963-340-2
                                                                                                                                                                                                                                                                   US-10-156-761-9082
                                                                                                                                                                                                                          Sequence 9082, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 351
                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Conkling, Mark
APPLICANT: Mendu, Nandini
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Regulation of Quinolate Phosphoribosyl Transferase
TITLE OF INVENTION: Expression
FILE REFERENCE: 5051-338
CURRENT APPLICATION NUMBER: US/09/963,340
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Oomen, Raymond PITITLE OF INVENTION: Identifi: TITLE OF INVENTION: Encoding TITLE OF INVENTION: Genome FILE REFERENCE: 06132/041002
                                                                                                                                                           APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/021,286
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-10
NUMBER OF SEQ ID NOS: 3
                                  APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                     106 DPSLKVEWYVNDGDKVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 RIKLWWSNLQNSLFTLLPDRLANALRISDLPESYQ 251
APPLICATION NUMBER: US/10/156,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 RKKEWWENAGNKIYTMAADK----TISKLMTEYK 40
                                                                                                                                                                                                                                                                                                                                                                                            8 DPSRKKEWWENAGNKIY 24
                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
9; Conserva
                                                                                                                    IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oomen, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     25.6%;
llarity 52.9%;
Conservative
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Encoding No. US20020115078A1el Helicobacter Polypeptides in the
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Pred. No. 27;
4; Mismatches
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Pred. No. 19;
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                                      US-10-050-704-106
                                                          RESULT 7
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                                                                                                                                                                                                                                                                    US-09-712-363-209
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Sequence 106, Application US/10050704
Publication No. US20030050442A1
                                                                                                                                                                              Best Local Similarity 31.6%;
Matches 12; Conservative
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9082
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Best Local
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Patent No. US20020164588A1
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PRIOR APPLICATION NUMBER: JF 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/165,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                                                    LENGTH: 462
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/179,531
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APPLICATION NUMBER: 60/118,206
FILING DATE: 1999-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 1999-05-14
APPLICATION NUMBER: 60/165,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/134,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/134,093 FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/126,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-02-01
APPLICATION NUMBER: 60/117,844
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-11-12
                                                                                                                179 APTVAGDDVFR--AWWDLAGNRAGPPSIARAVSKVIAE 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILING DATE: 1999-03-26
                                                                                                                                                1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTE 38
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8; Conserv
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42.1%;
                                                                                                                                                                                                          Score 53; DB
Pred. No. 64;
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                                                                                                                                                                                          8; Mismatches
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Pred. No.
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59;
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BY COMPARATIVE ANALYSIS
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US-10-160-293-4
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                                                                                                                                                                                                                                                                                                                                                             us-10-160-293-2
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Human
US-10-160-293-4
                                                                                                                                                                                                                                                             Sequence 2, Application US/10160293
Publication No. US20030022208A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10160293
Publication No. US20030022208A1
GENERAL INFORMATION:
APPLICANT: LINDQUIST, Erika et al.
TITLE OF INVENTION: USCLATED HUMAN SECRETED
TITLE OF INVENTION: UUSES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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APPLICANT: LINDQUIST, Erika et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED
TITLE OF INVENTION: NUCLEST ACID MOLECULES
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001241-PROV
CURRENT APPLICATION NUMBER: US/10/160,293
CURRENT FILING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 5
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CURRENT FILING DATE: 2002-06-04
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TITLE OF INVENTION: 62 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CL001241-PROV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.2%;
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Pred. No. 62;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52.5;
Pred. No. 36;
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ENCODING
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Publication No.
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APPLICATION NUMBER: 60/113605
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FILING DATE: 1999-04-27
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APPLICATION NUMBER: 09/311832
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APPLICATION NUMBER: 60/132379
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CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
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**APPLICATION NUMBER: 60/112514
**TYPE DATE: 1998-12-15
**CONTROL OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/113300
PILING DATE: 1998-12-22
APPLICATION NUMBER: 60/113430
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APPLICATION NUMBER: 60/125774
FILING DATE: 1999-03-23
APPLICATION NUMBER: 60/125778
                                                                 FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/131291
FILING DATE: 1999-04-27
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APPLICATION NUMBER: 60/131270
FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/131272
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APPLICATION NUMBER: 60/127706
FILING DATE: 1999-04-05
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APPLICATION NUMBER: 60/127035
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FILING DATE: 2000-05-22
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APPLICATION NUMBER: 09/816744
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APPLICATION NUMBER: 60/
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PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/064215
PRIOR TILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/082797
PRIOR APPLICATION NUMBER: 60/082797
PRIOR PILING DATE: 1998-04-22
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CURRENT APPLICATION NUMBER: US/10/006,867
CURRENT FILING DATE: 2001-12-06
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/088824
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FILING DATE: 1998-06-24
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                                6 KKDPSRKKEWWEN-AG---NKIYTMAA-----DKTISKLMT 37
                                                                                                                                                                                                                                                                                                                                                                                               LING DATE:
                                                                                                                                                                                                                                                                                1998-08-25
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                                                                       Score 52; DB
Pred. No. 88;
8; Mismatches
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US-10-077-040-1
                                                                                        ; GENERAL INFORMATION:
; APPLICANT: Faton, Dan L.
; APPLICANT: Fitraroff, El
; APPLICANT: Gerritsen, Ma
; APPLICANT: Goddard, Audr
                                                                                                                                                                                                                           RESULT 14
US-10-063-547-150
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                                                                                                                                                                                      Sequence 150, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                        APPLICANT:
                     APPLICANT:
                                                                            APPLICANT:
   PPLICANT:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,601
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0510 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/077,040
FILING DATE: 14-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lal, Preeti
Corley, Neil C.
Patterson, Chandra
TITLE OF INVENTION: HUMAN NEUROSECRETORY PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: 2379427
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            209 EEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLT 254
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                                                                                                                                                                                                                                                                                                                                       6 KKDPSRKKEWWEN-AG---NKIYTMAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CTTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
                                                      Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                          Filvaroff, Ellen
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: ISLTNOT01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
Gurney, Austin L. Watanabe, Colin K. Wood, William I.
                                                                                                                                                                                        Application US/10063547 o. US20020182638A1
                                                                                                                                                                                                                                                                                                                                                                              Conservative
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32.6%;
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Pred. No. 88;
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RESULT 15
US-10-036-041-67
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PRIOR FILING DATE: 1998-05-15
PRIOR PPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR APPLICATION NUMBER: 60/113430
PRIOR APPLICATION NUMBER: 60/113430
PRIOR APPLICATION NUMBER: 60/113405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 67, Appublication No
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ORGANISM: Homo Sapien
-10-063-547-150
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CURRENT APPLICATION NUMBER: US/10/036,041
CURRENT FILING DATE: 2001-12-26
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                                                                    FILING DATE: 1999-03-31
APPLICATION NUMBER: 60/127706
                                                                                                                                                                                                  APPLICATION NUMBER: 60/125774
FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/114140
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FILING DATE: 1998-12-23
                                                         FILING DATE:
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FILING DATE: 1999-03-24
                                                                                                                                                                APPLICATION NUMBER: 60/125778 FILING DATE: 1999-03-23
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                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/116843
                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/115552
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                                    APPLICATION NUMBER: 60/129122
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Similarity 32.6%;
15; Conservative
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Godowski, Paul
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No. US20020192751A1
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                                                       1999-04-05
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 60/130359
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Pred. No.
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PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
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PRIOR APPLICATION NUMBER: 60/162506
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APPLICATION NUMBER: PCT/US00/14042
FILING DATE: 2000-05-22
APPLICATION NUMBER: PCT/US00/15264
FILING DATE: 2001-06-20
APPLICATION NUMBER: PCT
FILING DATE: 2001-06-29
                                               APPLICATION NUMBER:
                                                                                                                          FILING DATE: 2000-12-20
APPLICATION NUMBER: PCT/US01/06520
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                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US00/23522 FILING DATE: 2000-08-23
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FILING DATE: 2001-06-05
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APPLICATION NUMBER: 09/644848
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APPLICATION NUMBER: 09/380142
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APPLICATION NUMBER: 60/132379
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                                                                                       FILING DATE: 2001-02-28
APPLICATION NUMBER: PCT/US01/17800
                                                                                                                                                            APPLICATION NUMBER: PCT/US00/34956
                                                                                                                                                                                                                   FILING DATE: 2000-08-24
                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US00/23328
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APPLICATION NUMBER: 60/131272
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 NUMBER: PCT/US01/21066
: 2001-06-29
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                                                                        2001-06-03
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                       Score
       215
215
                                                                                                                   Query
Match
       100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            July 24, 2003, 11:49:53; Search time 60.2635 Seconds (without alignments) 577.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5580241 seqs, 870357830 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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215
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: /cgn2 6/ptodata/1/paa/US06 (

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                                                                                                                   Length
       440
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   US-08-842-385-9
US-09-991-681-30
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Sequence 9, Appli
Sequence 30, Appl
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-09-513-996A-6382	מיני ביני ביני	-09-513-996A-551	-10-282-122A-5903	072-851-	-09-881-752A-350	-09-815-242-	-833-457-350	-US98-06371-	-US02-03987-1145	-10-053-853A	-10-181-612-2	-10-431-652-	-60-324-109-2402	-10-425-114-	10-219-999-3753	-09-803-110-	-09-739-449-	-60-360-039-1497	-60-360-039-1459	-60-360-039-1433	-60-360-039-	-10-072-851-1162	-09-815-242-1162	-08-993-002A-579	-US02-03987-1162	-08-993-002A-579	-08-625-811-1380	-08-993-002A-579	-60-360-039-	-09-791-537-9185	-10-437-963-1534	US-10-144-198-	-US03-01943-30	08631-	-US03-04508-	-10-416-993-	CT-US01-42950-	-US01-08631-	-10-144-198-44	T-US03-01943-	-09-991-681-	-08-842-385-6	-10-221-279-
equence 6382	03:0::0: 0::0::0:	emience 55105	equence 59031,	equence 11458,	equence	equence 1145	equence 350,	350,	quence 11458	equence 1179	equence 2, A	equence 5591	equence 2402	equence 4436	equence 3753	equence 9886	equence 9886	equence 1497	equence 1459	equence 1433	Sequence 11489, A	equence 1162	equence 1162	equence 5797	quence :	equence 5795,	equence 1380,	equence 5796,	equence 227	equence 91859,	(D	Sequence 30	equence 30.		equence 32, Appl	Sequence 499	equence 495,	quence 40087, A	ce 44,	quence 44, Appl	equence 27, I	9	equence 7783,

ALIGNMENTS

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US-08-082-385-9

US-08-082-385-9

Sequence 9, Application US/08842385

Sequence 9, Application US/08842385

Sequence 9, Application US/08842385

SEQUENCE 9, Tracey

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

TOURTS: USA

STREET: 10 Abbott Park Road

CITY: Abbott Park

STREET: 10 Abbott Park Road

COMPUTER READABLE FORM:

MEDIUM TYPE: Diakette

COMPUTER IS DOOM:

MEDIUM TYPE: DIAKETON

COMPUTER: IS COMPUTER: OF WINDOWS VERSION 2.0

COMPUTER: IS COMPUTER: OF WINDOWS VERSION 2.0

CURRENT APPLICATION DATA:

APPLICATION UMBER: US/08/842,385

FILING DATE:

CLASSIFICATION: 435
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PRIOR APPLICATION DATA:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
TELEPEAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                              COMPUTER: IBM COMPATIBLE

COPERATING SYSTEM: DOS

SOFTWARE: FASELSEQ for Windows Version

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/991,681

FILING DATE: 26-NOV-2001

CLASSIFICATION: <UNKnown>

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                APPLICATION NUMBER: 09/065,383
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
                 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                             STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                               CITY: Abbott Park
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLPITTS, TRACEY L. FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRANADOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 215; DB 12; 100.0%; Pred. No. 1.5e-20;
847/935-1729
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                                     6084.US.P1
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US-10-221-279-7783
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                                                                                                                                                                                                                                                                                                    Sequence 6, Applicat
GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 12360
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides FILE REFERENCE: 21272-046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/221,279
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(141)
OTHER INFORMATION: Xaa = any amino acid or nothing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hyseq,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 30:
                             COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                   APPLICANT: Colpitts, Tracey
TITLE OF INVENTION: REAGENTS AND
TITLE OF INVENTION: FOR DETECTIN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 141
                                                                                                                                                                                                                                                                 APPLICANT: Russell, John APPLICANT: Colpitts, Trav
                                                                                                         LABET: 100 Abbott Park Road CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
                                                                                                                                                                                                                                                                                                                        Application US/08842385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
                                                                                                                                                                                                                                                                                                                                                                                                                     SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 40 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10221279
   IBM Compatible YSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-03-07
                                                                                                                                                                                                                              REAGENTS AND METHODS USEFUL FOR DETECTING DISEASE OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 215; DB 25; 100.0%; Pred. No. 1.5e-20; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 215; DB 28;
Pred. No. 6.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 141;
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RESULT 5
US-09-991-681-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/09991681 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 847/938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTESEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-NOV-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
OFFICATION DATA:
OFFICATION DATA:
OFFICATION DATA:
OFFICATION DATA:
OFFICATION DATA:
OFFICATION DATA:
                                  APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRATOCHVIL, JON D.

ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
                                                                                                                                                                                                                                                                                                                                                     CITY: Abbott Park
STATE: IL
NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRANADOS, EDWARD N.
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                                                                                                                                                                                                                                                                                                                                                                                            100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                    USA
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RESULT 7
US-10-144-198-44
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TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 10/054,935
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-26
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR APPLICATION NUMBER: US 10/107,929
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/117,229
PRIOR FILING DATE: 2002-04-08
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Sequence 44, Application US/10144198
GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 44, Application PC/TUS0301943
GENERAL INFORMATION:
APPLICANT: ORIGENE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/197,824
PRIOR FILING DATE: 2002-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1770
                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
es 40; Conservative 0
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: None
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TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 27:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 518 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 215; DB 25; 100.0%; Pred. No. 3.3e-19;
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Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                    Sequence 495, Application PC/TUS0142950
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: PCT/US01/42950
CURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 44
                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 495
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SEQ ID NO 40087
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                                                                                             PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
SOFTWARE: Parcaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HYSSEG, INC
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/540,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Helper component proteinase domain identified by PFam, OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam score of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: DOMAIN
LOCATION: (941).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (48)..(62)
OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX,
OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw score of 11.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                      ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 215; DB 1; 100.0%; Pred. No. 1.5e-18; tive 0; Mismatches 0;
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                                                                                                                                          PCT-US03-04508-32
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; LENGTH: 1839
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 32, Application PC/TUS0304508
GENERAL INFORMATION:
APPLICANT: IDEC PHARMACEUTICALS
APPLICANT: GATELY, DENNIS
                                                                    Matches
                                                                                                     Query Match
                                                                                                                                                                                                               SEQ ID NO 32
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GENERAL INFORMATION
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: US/10/416,993
CURRENT FILING DATE: 2003-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
                                                                                                                                                                                                                                                PRIOR FILING DATE: 2002-06-10 NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/US03/04508
CURRENT FILING DATE: 2003-02-19
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PROSTATE SPECIFIC GENES TITLE OF INVENTION: OR THERAPEUTICS FILE REFERENCE: 037003/0301985
                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0
                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                           LENGTH: 1872
TYPE: PRT
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les 40; Conserv
                                                                                      Local Similarity
1686 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 1725
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                                   1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
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Pred. No. 1.5e-18;
); Mismatches 0;
                                                                                     Score 215; DB 1;
Pred. No. 1.5e-18;
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                                                                                                   Length 1872;
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RESULT 12 PCT-US01-08631-40090

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/356,130 PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 10/054,935 PRIOR FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
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PRIOR FILING DATE: 2000-08-23
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 3U 9U 901 PCT
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                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Helper component proteinase domain identified by PFam, OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
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OTHER INFORMATION: F
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LOCATION: (1065)..(1074)
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LOCATION: (11)..
                                                                                                                                                                                                               ENGTH: 2221
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IER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw score of 11.39
                                                                                               Local Similarity
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TH: 1982
                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2002-03-22
APPLICATION NUMBER: US 10/117,229
FILING DATE: 2002-04-08
                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 10/197,824
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 10/144,198
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 10/102,946
  2035
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                      SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 2074
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                                                                             Conservative
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Pred. No. 1.9e-18;
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Search completed: July 24,

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US-10-144-198-30
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SEQ ID NO 153423
LENGTH: 1065
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LENGTH: 2221
TYPE: PRT
                                                                  Matches
                                                                                                   Query Match
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CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221) B CURRENT APPLICATION NUMBER: US/10/437,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE:
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                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: (1)..(1065)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT4530_53380C.1.pep
                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa
                                                                                                                                                                      FEATURE
                                                                                  Local
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Wu, Wei
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Kovalic, David K.
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                                                              Score 65; DB
Pred. No. 55;
B; Mismatches
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Pred. No. 1.9e-18;
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Maximum Match 100%
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length: 2000000000
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1: /cgm2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgm2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgm2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgm2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

5: /cgm2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgm2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

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6 US-10-294-433-250
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US-10-367-978-32
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9399, Ap	8424, Ap	4, Appli	9406, Ap	2, Appli	10263, A	52, Appl	74, Appl	105, App	23, Appl	21, Appl	13, Appl	31, Appl	20, Appl	381, App	381, App	•	•	10847, A

ALIGNMENTS

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SEQUENCE 250, Application US/10294433
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
ITILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
FILE REFERENCE: 792C1P4
CURRENT APPLICATION NUMBER: US/10/294,433
CURRENT ETLING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/US01/14826
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/989,600
PRIOR APPLICATION NUMBER: 09/977,408
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR APPLICATION NUMBER: 10/115,831
                                                                                                                                                                                                                                                                                                                                                           US-10-294-433-250
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US-10-367-978-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR APPLILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 215; DB 6
Best Local Similarity 100.0%; Pred. No. 3.3e-1
Matches 40; Conservative 0; Mismatches
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TITLE OF INVENTION: PROSTATE SPECIFIC GENI
TITLE OF INVENTION: OR THERAPBUTICS
FILE REFERENCE: 037003-0301988
CURRENT APPLICATION NUMBER: US/10/367,978
CURRENT FILING DATE: 2003-02-19
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SEQ ID NO 7140
FENGRAPE: Custom
SEQ ID NO 7140
                                                                                                                                                                                                                                 ; NAME/KEY: DOMAIN
; LOCATION: (33)...(218)
; COTHER INFORMATION: short chain dehydrogenase domain identified by PFam,
; OTHER INFORMATION: accession name adh_short, E-value=1.5e-60, PFam score of 214.6
US-10-273-573-7140
RESULT 4
US-10-464-368-68
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US-10-294-433-250
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GENERAL INFORMATION:
APPLICANT: Hyseq, I
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Best Local S
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Best Local Similarity
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SEQ ID NO 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 21272-066
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                                                                                                                                                                                                                                                                                                                                    LOCATION: (34)..(52)
OTHER INFORMATION: GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE domain
OTHER INFORMATION: identified by eMATRIX, accession number PR00081A, p-value=6.226e-
OTHER INFORMATION: 13, raw score of 10.53
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10; Conservative
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Pred. No. 9.3;
5; Mismatches
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RESULT 6
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SOFTWARE: Patentin version 3.2
SEQ ID NO 67
LENGTH: 4545
                                      SOFTWARE: PatentIn version 3.2 SEQ ID NO 71
                                                                                                                                                                                                                                                                   Sequence 71, Application US/10464368 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                            APPLICANT: Ellies, Debra TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION FILE REFERENCE: 40716-IP-017 CURRENT APPLICATION NUMBER: US/10/464,368 CURRENT FILING DATE: 2003-06-16
                                                                                PRIOR APPLICATION NUMBER: 60/388,970 PRIOR FILING DATE: 2002-06-14 NUMBER OF SEQ ID NOS: 140
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
FILE REFERENCE: 40716-IP-017
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CURRENT FILING DATE: 2003-06-16
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APPLICANT: Eliles, Debra
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
FILE REFERENCE: 40716-IP-017
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CURRENT FILING DATE: 2003-06-16
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ORGANISM: MOUSE
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ORGANISM: HOMO SAPIENS
LENGTH: 4545
TYPE: PRT
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Pred. No. 1.6e+02;
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Pred. No. 1.6e+02;
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RESULT 9
US-10-032-037B-42
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US-60-479-073-335
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Best Local Similarity 44...
"---hes 8; Conservative
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Best Local :
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SEQ ID NO 335
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TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REFERENCE: 10793/46
CURRENT APPLICATION NUMBER: US/10/029,988B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
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APPLICANT: Saunders, Michael John Scott
APPLICANT: Logghe, Marc Georges
TITLE OF INVENTION: Amino acid sequences useful for developing compounds for the
TITLE OF INVENTION: prevention and/or treatment of metabolic diseases and nucleotide
TITLE OF INVENTION: sequences encoding such amino acid sequences.

FILE REFERENCE: D00590.70042.US
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CURRENT FILING DATE: 2003-06-17
                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 36.4%;
hes 12; Conservative
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                                                                  RQAPGQRLEWMGWSNAGN 55
                                                                                                  KKDPSRKKEW--WENAGN 21
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Pred. No.
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Pred. No.
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Query Match
Best Local Similarity
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US-10-287-971-18
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US-09-290-586A-19
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LENGTH: 329
TYPE: PRT
Sequence 18, Application US/10287971
GENERAL INFORMATION:
APPLICANT: Alsobrook, et al
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
FILE REFERENCE: 21402-480A
CURRENT APPLICATION UNMEBER: US/10/287,971
CURRENT FILING DATE: 2002-11-05
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GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/44
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US/10/032,037B
CURRENT FILING DATE: 2000-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
NUMBER OF SEQ ID NOS: 204
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CURRENT APPLICATION NUMBER: US/09/290,586A
CURRENT FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: JP 10-172147
PRIOR FILING DATE: 1998-06-05
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APPLICANT: VELASCO, G
APPLICANT: CAZORLA, M
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SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: IWATA, KAZUSHI
TITLE OF INVENTION: NOVEL HUMAN CATHEPSIN L2 PROTEIN, GENE ENCODING SAID
TITLE OF INVENTION: PROTEIN AND USE THEREOF
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TYPE: PRT
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CAMPO, Elias
LOPEZ-OTIN, Carlos
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CAZORLA, Maite
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Pred. No.
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Pred. No. 9.
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PRIOR APPLICATION NUMBER: 09/997,425

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US-10-287-971-18
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Best Local Similarity
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LENGTH: 1101
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 9476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9476, Application US/10273573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 10994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                          NAME/KEY: misc_feature
LOCATION: (1)...(1839)
OTHER INFORMATION: Xaa = X or * as defined in Table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                 OTHER INFORMATION: Ephrin receptor ligand binding domain identified by PFam, OTHER INFORMATION: accession name EPH_lbd, E-value=1.4e-84, PFam score of 294.4
                                                                                                                                                                                                                                                                                                                      LOCATION: (1331)...
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Receptor tyrosine kinase class V proteins domain identified OTHER INFORMATION: by eMATRIX, accession number BL00790B; p-value=1.000e-40, raw scontine information: of 21.59
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                  VAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 1839
                                 Local Similarity
nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/348,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/333,072 FILING DATE: 2001-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/393,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/338,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
10 SRKKEWWENAGN-KIYTMAADKTIS-----KLMTEY 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 DPSRKKEWWEN 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATION NUMBER: 10/035,568
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                                                     Score 45.5;
Pred. No. 3.
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Pred. No.
                                   Mismatches
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US-10-331-496A-60
                                                                                                                                                                                                                                                                                                                              US-10-029-988B-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-331-496A-60
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 41
LENGTH: 98
TYPE: PRT
                                                                                                                                                                                         Sequence 41, Application US/10029988B
GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                  PRIOR APPLICATION NUMBER: 60/258,948 PRIOR FILING DATE: 2000-12-29 NUMBER OF SEQ ID NOS: 204
                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/029,988B CURRENT FILING DATE: 2001-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/366,869
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PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/360,066
PRIOR FILING DATE: 2002-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/345,444
PRIOR FILING DATE: 2002-01-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: P5014R1-PCT
CURRENT APPLICATION NUMBER: US/10/331,496A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND RITLE OF INVENTION: TREATMENT OF TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2002-03-28
APPLICATION NUMBER: US 60/404,809
FILING DATE: 2002-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/405,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/368,679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/366,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2002-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1406 TKKSAFWSEAPYLKVDTIAADESFSQVDFGGRLMKDY 1442
                                                                                                                                                                                                                                                                                                                                                                                                                      462
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                                                                                                                                                                                                                                                                                                                                                                                                                      KVQKKDP---KEW---AAQYREAMEADLKAAAEAAAEAK 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WU, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILLIAMS, P. MICKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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 Mismatches

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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 606;
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Sequence 47, Application US/10032037B

Sequence 47, Application US/10032037B

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILLE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOPTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 41

LENGTH: 98

TYPE: PRT

ORGANISW: Hômo sapiens
Search completed: July 24, 2003, 12:16:54 Job time : 2.3713 secs
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US-10-032-037B-41
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US-10-029-988B-41
                                                                                                                                                                          Query Match 20.5%; Score 44; DB 6; Length 98; Best Local Similarity 44.4%; Pred. No. 23; Matches 8; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.5%; Score 44; DB 6; Length 98; Best Local Similarity 44.4%; Pred. No. 23; Matches 8; Conservative 4; Mismatches 4; Indels
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                                                                                       38 RQAPGQRLEWMGWINAGN 55
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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Gapop 10.0 ,
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1172.914 Million cell updates/sec
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A70518
T16522
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H85806
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C84430
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T02232
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1345	1017	802	727	572	547	342	238	230	205	149	921	338	318	26926	1984
N	N	N	N	N	N	N	N	N	N	N	N	N	N	_	N
н90975	T48452	I39665	T24284	S73730	A56575	E70109	A86160	C64396	AE2442	B96965	AC1327	A82890	T13015	I38344	A44396
hypothetical prote	hypothetical prote	penicillin amidase	hypothetical prote .	MG307 homolog H08_	puff-specific nucl	hypothetical prote	hypothetical prote	precorrin-2 methyl	hypothetical prote	hypothetical prote	isoleucyl-tRNA syn	hypothetical prote	phosphoprotein pho	titin, cardiac mus	P-type cation tran

ALIGNMENTS

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A;ACCEBBLOH: TILL:
A;ACCEBBLOH: A;ACCEBBLOH
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-604 <SEE>
A;Cross-references: EMBL:AL031545; PIDN:CAA20842.1; GSPDB:GN00068; SPDB:SPCC285.03
A;Cross-referencal source: strain 972h-; cosmid c285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Cellvibrio mixtus
C;Date: 15-Feb-1996  #sequence_revision 11-Apr-1997  #text_change 18-Jun-1999
C;Accession: S59632; S52742
R;Millward-Sadler, S.J.; Davidson, K.; Hazlewood, G.P.; Black, G.W.; Gilbert, H.J.; Clar Biochem. J. 312, 39-48, 1995
A;Title: Novel cellulose-binding domains, NodB homologues and conserved modular architec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Pathway: xylan degradation

C;Superfamily: Pseudomonas endo-1,4-beta-xylanase F; Streptomyces endo-1,4-beta-xylanase C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-621/Product: endo-1,4-beta-xylanase B #status predicted <MAT>
F;302-615/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>
F;403,516/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                 C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Nov-2000
C;Accession: T41249
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                                                                                                                                                                                           R,Seeger, K.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, September 1998 A;Reference number: Z21981 A;Reference number: Z21981 A;Accession: T41249
                                                                                                                                                                                                                                                                                                                                                                                                                                    DEAD box ATP-dependent RNA helicase - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z48926; NID:g757808; PIDN:CAA88762.1; PID:g757809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: S59632
A;Molecule type: DNA
A;Residues: 1-621 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: S59631; MUID:96077124; PMID:7492333 A;Accession: S59632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Cellvibrio mixtus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 43.;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTE 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%;
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A; Experimental & C; Genetics:
A; Gene: rodA_2
C; Superfamily: 1
                                                                                                                                                                                                                                                                                    probable rod shape-determining protein - Helicobacter pylori (strain J99)
(;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: D71804
C;Accession: D7180, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
D71804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: SPDB:SPCC285.03
A;Map position: 3
C;Superfamily: fruit fl
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                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-277 < KUR >
                                                                                                                                                                                                                                                                                                                                                                                                                         oxidoreductase yafB [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE001568; A;Experimental source: strain J99
                                                                                                                                                                                                                                      A;Reference number: A;Accession: AB3084 ·
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Best Local S
Matches 13
                                                                                                                                                                                                                                                      ;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                    ;Experimental
                                                                                                                                                                                                                                                                                                                                                                                                      ;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                   Matches
                                 Query Match
Best Local (
                                                                                                     Map position: linear chromosome;
                                                                                                                     Gene: yafB
                                                                                                                                                                                                                     Status: preliminary
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Best Local
                                                                                  Superfamily:
                                                                                                                                                                    Cross-references: GB:AE008689; PIDN:AAL45088.1;
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                                 Local Similarity
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                                                                                  aldehyde reductase
                                                                                                                                                    source: strain
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                   Conservative
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                               27.4%;
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                                                                                                                                                    C58
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               7;
                                 Score 59;
Pred. No.
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Pred. No. 8
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r.; Levy, R.; Li, !
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.;
                           C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision
C;Accession: AE1698
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                                                                                                     AE1698
                                                                                                                   RESULT 7
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                                                                                isoleucyl-tRNA synthetase [imported] -
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Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S..
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo.
A;Reference number: A69250, MUID:98049343; PMID:9389475
A;Accession: A69407
                                                                                                                                                                           A;Cross-references: GB:AE001017; GB:AE000782; NID:g2689340; PIDN:AAB89988.1; C;Superfamily: conserved hypothetical protein MJ1034
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-104 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal recognition particle, subunit SRP19 (srp19) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: AGR L_1141
A;Map position: linear c
C;Superfamily: aldehyde
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A; Residues: 1-277 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Goodner, B.; Hinkle, G.; G
A.; Liu, F.; Wollam, C.; Al
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable oxidoreductase PA4167 [imported] - Agrobacterium tumefaciens (strain C58, Cereo
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: A69407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: G98202
                                                                                                           Query Match
Best Local
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52
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                                                                                                             Similarity
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EKKYP--
                                      EKKDPSRKKEWWENAGNKIYTMAADKTISKLMTE 38
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                                                                                     Conservative
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-KSWWEEGGRVVVEKRGTKT--KLMIE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.;
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                                                                                                         27.2%;
                                                                                     Score 58.5; DI
Pred. No. 2.8;
1; Mismatches
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Pred. No.
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6.7;
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Markelz, B.;
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27-Nov-2001 Listeria innocua

#text_change 14-Dec-2001

(strain

Clip11262)

Dussurget, O.;

F.; Berche, P.; ; Entian, K.D.;

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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1698
                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, F. Nature 409, 529-533, 2001
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A;Experimental source: strain O1:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A:Reference number: A99629; MUID:21156231; PMID:11258796
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C;Superfamily: isoleucine-tRNA ligase
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A;Experimental source: strain Clip11262
C;Genetics:
                                   A; Reference number: A85480; A; Accession: H85806
                                                   A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: H85806
                                                                                                                                                                                    hypothetical protein Z2984 [imported] - Escherichia coli (strain O157:H7, substrain C_i; Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-158 < HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A99629; A; Accession: F90958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: F90958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein ECs2638 [imported] - Escherichia coli (strain O157:H7,
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                 A;Status: preliminary
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type: DNA
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35.7%;
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26.2%;
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Pred. No. 7.7;
7; Mismatches
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Pred. No. 36;
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M.; Shinagawa,
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Voss, H.; Wehland,
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A;Gene: At2g01880
A;Map position: 2
C;Superfamily: tartrate-resistant acid phosphatase; phosphoesterase core homology C;Keywords: iron; metalloprotein; phosphoric monoester hydrolase F;1-21/Domain: signal sequence #status predicted <SIG>F;2-304/Product: acid phosphatase #status predicted <MAT>F;42-121/Domain: phosphoesterase core homology <PEC>F;48,81,84,226/Binding site: iron (Asp. Asp. Tyr. His) #status predicted F;81,119,189,224/Binding site: iron (Asp. Asp. Tyr. His) #status predicted
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z2984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable acid phosphatase (EC 3.1.3.2) At2g01880 precursor [similarity] - Arabidopsis
N;Alternate names: purple acid phosphatase
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Nov-2001
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Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C., A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, M.; Wallin, M.; Wallin, M.; Wallin, M.; Wallin, W.; Wallin, 
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A; Residues: 1-304 <STO>
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C; Superfamily: rod :
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A; Residues: 1-388 < TOM>
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    ;120,198/Active site: His
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shape-determining protein
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35.7%;
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Pred. No. 20;
S; Mismatches
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Pred. No. 9
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Score 56;

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Length 304;

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probable membrane protein YGL075c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G3219
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: S64082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Imanishi, S.; Hashizume, K.; Nakakita, M.; Kojima, H. Plant Mol. Biol. 38, 1101-1111, 1998 A;Title: Differential induction by methyl jasmonate of careference number: Z14631; MUID:99084761; PMID:9869416 A;Accession: T02232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-450 <HIM>
A;Cross-references: EMBL:AE000011; GB:U00089; NID:g1673740; PIDN:AAB95741.1; PID:g16737.
A;Cross-references: EMBL:AE000011; GB:U00089; NID:g1673740; Data Library, November 1996
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A; Variety: ATCC 29342
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
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; Pred. No. 2
9; Mismatch
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8; Mismatches
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Pred. No.
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cein G3219
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D09_orf450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:BAA21616.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.; Matsubayashi, Y.; Hashimoto,
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Job time : 6.2796
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July 24,

2003, 11:58:08

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RESULT 15
T04172
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Plant J. 11, 363-371, 1997
A;Title: Cloning of a Ca(2+)-ATPase gene and the role of A;Reference number: Z15255; MUID:97260952; PMID:9107028
A;Accession: T04172
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                                                                                                                                                                                                      F;106-130/Domain: calcium binding #status predicted <CA2>F;236-256/Domain: calcium binding #status predicted <CA3>F;317-336/Domain: calcium binding #status predicted <CA4>F;513-696/Domain: ATP binding #status predicted <ATP>
                                                                                                                                                                                                                                                                                         C; Keywords: hydrolase; phosphoprotein
F;39-56/Domain: calcium binding #status predicted <CAl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ca2+-transporting ATPase (EC 3.6.3.8) - C;Species: Oryza sativa (rice)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain S288C
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A;Residues: 1-387 <RIE>
A;Cross-references: EMBL:Z72597; NID:gl322588;
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A; Accession: S64082
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                                                                                                                                           F;358/Active site:
                                                                                                                                                                                    F;610-784/Domain:
                                                                                                                                                                                                                                                                                                                              C; Superfamily: Na+/K+-transporting ATPase alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1048 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
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REPIR; D71804; D71804.

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REPIR; D71098; PTSW RODA SPOVE; 1.

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PROSIT
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 This SWISS-PROT entry is copyright. It is produced through a obetween the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                      MEDLINE=21914566; PubMed=11916385;
Pakhomova O.N., Deep S., Huang Q., Zwieb C., Hinck A.!
"Solution structure of protein SRP19 of Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaeoglobaceae; Archaeoglobus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001
                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                      recognition particle.";
Biochemistry 39:12862-12874(2000).
                                                                                                                                                                                                                                                                                                                                                   Diener J.L., Wilson C.;
"Role of SRP19 in assembly of the Archaeoglobus fulgidus signal
                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
MEDLINE=20496765; PubMed=11041851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20150251; PubMed=10684931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=VC-16 / DSM 4304 / ATCC 49
MEDLINE=98049343; PubMed=9389475;
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                                                      SUBCELLULAR SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ng archaeon Archaeoglobus fulgidus.";
390:364-370(1997).
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
gnition particle 19 kDa protein (SRP19).
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                                                  Cytoplasmic.

THE SRP19 FAMILY.
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete
SEQUENCE
                                                             This SWISS-PROT entry is copyright. It is produced through a copyright the SWISS Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                    HELPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; AF1258; -. HAMAP; MF_00305; -; 1. InterPro; IPR002778; SRP19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01922; SRP19; 1. ProDom; PD006609; SRP19; 1.
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                                        or send an
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                                                                                                                                                                                                                          (By similarity).
SIMILARITY: BELONGS TO THE FTSW/RODA/SPOVE FAMILY.
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1KVV; 20-MAR-02.
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                                             email to license@isb-sib.ch).
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AAD08600.1;
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35, Last sequence update)
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44.1%;
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PROSITE; PSO0428; PTSW_RODA SPOVE; 1.
Peptidoglycan synthesis; CeIl wall; Cell division; Cell shape;
Transmembrane; Inner membrane; Complete proteome.
TRANSMEM 7 27
POTENTIAL.
TRANSMEM 39 59
POTENTIAL.
        EMBL; AE000011; AAB95741.1; -.
PIR; $73419; $73419.
HSSP; 007347; IFFH.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR000897; $RP54.
                                                                                                                                                                                                                                                                                                                                                                                                                     MYCPN
                                                                 entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                    use by non-profit institutions a modified and this statement is not
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                                                                                                                  between
                                                                                                                           This
                                                                                                                                                                                                                                           pneumoniae."
                                                                                                                                                                                                                                                                     MEDLINE=97105885; PubMed=894
Himmelreich R., Hilbert H.,
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
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01-NOV-1997 (Rel. 35, Last seg
16-OCT-2001 (Rel. 40, Last ann
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P75054;
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 InterPro;
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                                                                                                   veen the Swiss Institute of Bioinformatics Institute.
                                                                                                                                            SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS
                                                                                                              SWISS-PROT entry is copyright. It is produ
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ilbert H., Plagens H.,
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SRP54_SPB
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Last annotation update)

rticle protein (Fifty-four
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5; Mismatches
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Pred. No. 7.
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77195EA88052BBF1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                         homolog).
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RESULT 5
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                                                                                                                                                                                                                                                                    Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
-!- FUNCTION: Signal-recognition-particle assembly, binds directly to T.S. RNA and mediates binding of the 54 kDa subunit of the SRP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSTV49;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Signal recognition particle 19 kDa protein (SRP19).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METKA
SR19_N
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NP_BIND
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Pfam; PF02881; SRP54 N; 1.
Pfam; PF02978; SRP SPB; 1.
ProDom; PD000819; SRP54; 1.
         HAMAP; MF 00305; -; 1.
InterPro; IPR002778; SRP19.
Pfam; PF01922; SRP19; 1.
ProDom; PD006609; SRP19; 1.
                                                                                                the European Bioinformatics Institute. There are no use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR00959; ffh; 1.
PROSITE; PS00300; SRP54; 1.
                                                             EMBL; AE010445; AAM02764.1;
                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                           -!- SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21927647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanopyrus kandleri.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRP19 OR MK1551
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                                                                                                                                                                                                                                              similarity).
SUBUNIT: Arc
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molecule of 300 nucleotides
                                                                                                                                                                                                                    SRP19 (By similarity)
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recognition particle;
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O THE SRP19 FAMILY.
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Pred. No. 10;
9; Mismatches
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M-DOMAIN.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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Signal recognition particle;

RNA-binding; Ribonucleoprotein;

YGL075C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

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Matches 13
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01-OCT-1996
01-NOV-1997
01-NOV-1997
37 kDa cell
             P53159;
01-OCT-1996
01-OCT-1996
15-DEC-1998
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Cell v
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STRAIN-ATCC 26555;
MEDLINE-95387219; PubMed=7658300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and characterization of CSP37, putative membrane protein of Candida al J. Bacteriol. 179:4654-4663(1997).
                                                                                                                                                                                                                                               EMBL; U89676; AAB66368.1;
EMBL; S79004; AAB35168.1;
                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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SEQUENCE
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Fonzi W.A., Sentandreu R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97386400; PubMed=9244249;
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oning of cDNAs coding for Candida albicans cell surface prote
Med. Vet. Mycol. 33:105-111(1995).
SUBCELLULAR LOCATION: Cell wall.
                                                              YEAST
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(Rel. 34, Last sequence update)
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(44.6 kDa protein in RPL7A-HSF1 intergenic
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5; Mismatches
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albicans.";
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Matches 13
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                                                                                                                                                                                                                                                                                                                                                             PPCK_DEIRA
Q9RVP6;
16-OCT-2001
                                                                                                                                                                                                                                                                                                    QYKYFO, (QYKYFO, 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.7)
Phosphoenolpyruvate carboxylase)
                                    radiodurans R1.";
Science 286:1571-1577(1999).
-!- CATALYTIC ACTIVITY: ATP
                                                                                                    Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      DEIRA
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"Sequence analysis of 203 kilobases
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                                                                                           Fraser C.M.;
                                                                                                                                                                                                                                      Deinococcaceae;
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                    Bacteria; Deinococcus-Thermus;
                                                                                                                                                                                                                                                                                Deinococcus radiodurans
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TRANSMEM
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                                                                             Genome sequence of the radioresistant bacterium Deinococcus
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; S0003043; MPS2.
G0:0005635; C:nuclear membrane; IDA.
G0:0005816; C:spindle pole body; IDA.
G0:0005200; F:structural constituent of
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al protein; Transmembrane.
311 327 POTENTI
387 AA; 44585 MM
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nilarity 46.4%;
Conservative
            Rate-limiting gluconeogenic
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                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
LOCATION:
                                                                                                                                                                                                                                                       Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9290212;
mar M., Schaefer M., Mue
                                      +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB
Pred. No. 16;
4; Mismatches
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                                      oxaloacetate
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                    Deinococci; Deinococcales;
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(By
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            enzyme
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                                        ADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                        +
                                                                                                                                                                                                                                                                                                            (PEPCK)
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                                      phosphoenolpyruvate
                                                                                                                                                                           Peterson
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            EMBL; U38804; AAC08267.1; --
PIR; S73302; S73302;
InterPro; IPR000185; SecA.
Pfam; PF01043; SecA protein
PRINTS; PR00906; SECA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996
01-OCT-1996
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECA POI
P51381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001950; AAF10554.1; ALT_INIT.
HSSP; P22259; 1AYL.
TIGR; DR0977; -
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                                                                                                                                                                                                                                                            Plant Mol. Biol. Rep.
                                                                                                                                                                                                                                                                          genome.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2787
                                                                                                                                                                                                                                                                                                                                                                                                                    Preprotein translocase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGR00224; pckA; 1.

TIGREAMS; TIGR00224; pckA; 1.

PROSITE; PS00532; PEPCK ATP; 1.

PROSITE; PS00532; DepcK ATP; 1.

Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Complete ATP (BY SIMILARITY).

NP_BIND 237 244 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00453; atypical; 1.
InterPro; IPR001272; PEPCK_ATP.
Pfam; PF01293; PEPCK_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformat:
the European Bioinformatics Institute. The:
use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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                                                                                         or send
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                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                           Porphyra purpurea
  TIGRFAM8;
                                                                                                                                                                                                                                                                                     "Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                         FUNCTION: INVOLVED IN PROTEIN EXPORT AND IMPORT. CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF ATP TO PRE-SECRETORY PROTEINS ACROSS THE MEMBRANE. SUBCELLULAR LOCATION: Chloroplast. SIMILARITY: BELONGS TO THE SECA FAMILY.
                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
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an email to license@isb-sib.ch).
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TIGR00963; secA; 1.
                                                                                                                                                                                                                                                                                                                                                               Rhodophyta;
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(Rel. 34,
(Rel. 35,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50951 MW;
                        protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                     secA subunit.
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Pred. No. 22;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22FDC11A2321E942 CRC64;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                      collaboration -
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RESULT 10
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                                                                                                                                                                                                                                                                              Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D. Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D. Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Brodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; Submitted (PEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y130 ME
Q57594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01312; SECA; 1.

Protein transport; ATP-binding; Chloroplast; Translocation; Transport.

NP_BIND 98 105 ATP (BY SIMILARITY).

SEQUENCE 884 AA; 101325 MW; A415846D12B90B2B CRC64;
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=JAL-1 / DSM 2661 / ATCC 43067; MEDLINE=96337999; PubMed=8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical MJ0130.
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                                                                EMBL; U67470; AAB98112.1; TIGR; MJ0130; -.
                                                                                                                  or send
                                                                                                                                  entities requires a
                                                                                                                                                                                                                                                                -i- SIMILARITY: STRONG, TO M.JANNASCHII MJ1218 AND MJ1531
-i- SIMILARITY: TO TYPE I RESTRICTION ENZYME SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota;
Methanocaldococcaceae; |
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                                Pfam; PF01420; Methylase
                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome
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                                                                                                                s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273:1058-1073(1996).
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1420; Methylase_S; 2.
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(Rel.
(Rel.
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               protein;
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37, Last sequence 40, Last annotation
 39061 MW;
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28.1%;
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Last annotation update)
               Complete
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Methanocaldococcus.
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Pred. No. 43;
proteome.
5184D68686274603 CRC64;
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Query Match

24.7%;

Score 53;

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SR54_MYCGE
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Matches 13; Conserv
NP_BIND
NP_BIND
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                                                                                                                                                                                                                                                             #InterPro; Irav. RP54; 1.
Pfam; PF00448; SRP54, N; 1.
Pfam; PF02978; SRP SPB; 1.
Pfam; PF02978; SRP SPB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J. Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann Mguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
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                                                                                                                                                                                                ProDom; PD000819; SRP54; 1.
SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR00959; ffh; 1.
PROSITE; PS00300; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U39684; AAC712
PIR; C64205; C64205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                  Complete
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InterPro; IPR004125; SRP54 SPB.
InterPro; IPR004780; SRP_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR; MG048
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                                                                                                     DOMAIN
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                                                                                                                                                                            ignal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A SMALL CYTOPLASMIC RNA (SC-RNA) MOLECULE AND PROTEIN FFH (BY SIMILARITY) DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIBOSOMES (BY SIMILARITY)
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pean Bioinformatics Institute. There are no restrictions
non-profit institutions as long as its content is in
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M-DOMAIN.
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GTP (BY SI
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                                                                                                                                                                       GTP-binding;
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8; Mismatches
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                                                                                                                                                                         RNA-binding
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RESULT 12
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RX MEDLINE=2238857; PubMed=12477932;
RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Fasher G.J., Wallain G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullainy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RGeneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22093564; PubMed=12098761; Rong Y.P., Liu F., Zeng L.C. Ma "" "Cloning and all "
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QBWXD2; Q96CB3; Q96GB8; Q99GG7;

28-FEB-2003 (Rel. 41, Created);

28-FEB-2003 (Rel. 41, Last sequing);

15-SEP-2003 (Rel. 42, Last anno
                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human secretogranin III mRNA, complete cds." Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pituitary;
Song H., Peng Y., Huang
Luo M., Chen J., Hu R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                secretory granules.
TISSUE SPECIFICITY: Expressed
                                                                                                                                                  skeletal muscle.
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42, Last annotation updat
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Pred. No.
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for

commercial

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RESULT 13
SYL_BORBU
       DESCRIPTION OF THE PROPERTY OF
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Best Local
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051267;
30-MAY-2000
30-MAY-2000
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Leucyl-tRNA s
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CONFLICT
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huàng W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwin Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B. Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal;
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EMBL; AF453583; AAL67331.1; -.
EMBL; BC014539; AAH14539.1; -.
EMBL; BC009511; AAH109511.1; ALT_INIT.
Genew; HGNC:13707; SCG3.
HAMAP; MF_00049; -; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00133; tRNA-synt_l; 1.
                                                                                                                                              EMBL; AE001135; AAB91495 PIR; C70131; C70131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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                                                                                                                     TIGR; BB0251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:580-586(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A. TRAIN=ATCC 35210 /
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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6.1.1.4) (Leucine--trnA ligase) (LeuRS)
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K -> R (IN REF. 1).

A -> V (IN REF. 1 AND 2).

EEL -> ROF (IN REF. 1).

E33A87692A783808 CRC64;
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v Gwinn P
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TIGRFAMs; TIGR01494; ATPase P-type; PROSITE; PS00154; ATPASE E1 E2; 1.
Hydrolase: Transmamhtane - T
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ATX1_I
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J. Cell Biol. 120:385-398(1993).
-!- CATALYTIC ACTIVITY: ATP + H
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                              TRANSMEM
                                                                                                                                                                                               EMBL; X65738; CAA46646.1;
                                                                                                                                                                                                                                       modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                 Krishna S., Cowan
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93132070;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
Eukaryota; Alveolata;
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ATP (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL)
                  POTENTIAL.
CYTOPLASMIC
                                       EXTRACELLULAR (POTENTIAL)
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POTENTIAL.
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"KMSKS" REGIO
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A Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
A Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
A Weichselgartner M., de Simone V., Obermaler B., Mache R., Mueller M.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
A Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
A Kreis M., Delseny M., Puigdomenech P., Watson M., Bancroft I.,
Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
A Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
A Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
A Vos P., Hohelsel J., Zimmermann W., Wedler H., Roben J.,
Langham S.-A., McCullagh B., Bilham L., Robben J.,
A Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
A Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
A Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
A Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
A Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
A Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
A Mooilman P., Stein Lankhorst R., Rose M., Hauf J., Koetter P.,
A Mooilman P., Rlein S., Feldpausch M., Lamberth S., Van den Daele H.,
A De Keyser A., Buysshaert C., Gielen J., Vullarroel R., De Clercq R.,
Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
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Matches 12
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein phosphatase PP1 isozyme
TOPP6 OR PP1BG OR AT4G11240 OR F8L21.30.
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01-FEB-1996 (Re
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                                                                                                                                                                                                                                                                                 STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A novel Arabidopsis type 1 protein phosphatase is highly expressed in male and female tissues and functionally complements a conditional cell cycle mutant of Aspergillus."; plant J. 7:823-834(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                          Lin Q., Li J., Smith R.D., Walker J.C.;
"Molecular cloning and chromosomal mapping of type one
serine/threonine protein phosphatases in Arabidopsis thaliana.";
plant Mol. Biol. 37:471-481(1998).
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RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., Meves H.-W., Stocker S.,
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RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
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RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
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RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I. K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.,
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RODE STANDARD R., Martienssen R., McCombie W.R.,
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RODE STANDARD R., McCombie 
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EMBL; U80921; AAC39460.1; -.
EMBL; AL096882; CAB51408.1; -.
EMBL; AL161531; CAB51225.1; -.
PIR; T13015; T13015.
HSSP; P08129; 1FJM.
InterPro; IPR004843; M-ppestrase.
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-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein
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Q8N4Y4;
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Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update)
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EMBL; BC033191; AAH33191.1; -.
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SEQÜENCE 589 AA; 66086 MW; 8041EEA348DE65F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similar to KIAA1244 protein Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 100.0%; Score 215; DB 4; 1 Similarity 100.0%; Pred. No. 2.1e-19; 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
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RESULT
Q81995
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Q9ULH6
                                                                                                                                                                                                                                                                                                  SON BEACH
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   RRAPP RNN
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                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 40
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                 "KIAA1244 as a novel distantly
subfamily of ARF GEFs.",
Submitted (AUG-2001) to the EN
EWBL; AF413080; AAL04174.1;
InterPro; IPR000904; Sec7.
SWART; SM00222; Sec7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ULH6; Q96P46;
01-MAY-2000 (TrE
01-OCT-2002 (TrE
                                                                                                                                                Q81995;
Q81995;
Khattab A., Kremsner P.G., Klinkert M.Q.; "Plasmodium falciparum placental isolates express common surface antigen var genes o J. Infect. Dis. 0:0-0(2003).
                                                                                                                  01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC014227; AAH14227.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                          SEQUENCE FROM N.A.
STRAIN=Gb174;
                                                                         Eukaryota; Alveolata; NCBI_TaxID=5833;
                                                                                                      Erythrocyte membrane protein
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Hong W..;
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9HTIN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Mammalia; Eutheria;
                                                                                             Plasmodium
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                                                                                              falciparum.
                                                                                                                                                                                                                                                                                                 l protein.
1770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    592 AA; 66400 MW;
                                                                                                   (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
(TremBlrel. 23, Last annotation update)
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                            Primates;
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                                                                                                                                                                                                                                                                                                 195845 MW;
                                                                                                                                                                                                                                                                                                                                                                        distantly related member
                                                                                  Apicomplexa;
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22,
22,
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                      Score 215; DB 4
Pred. No. 7e-19;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 215; DB 4;
Pred. No. 2.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                           Catarrhini;
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F4A1E807B0DF47B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                 5E996E36A6F92AB4 CRC64;
                                                                                   Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1770
                                                                                                                                                            177
           e separated of limited
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                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae;
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                                                                                                                                                                                                                                                                           4; Length 1770;
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                                                                                                                                                                                                                                                                                                                                                                        (BIG3) of the
                                                                                   Plasmodium
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           by time and space diversity.";
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RESULT 6
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1D Q811
AC Q811
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AC Q811
D7 01-M
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Q819A5
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Matches
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Best Local
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                     Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., "Genome semmenca"
                                                                                                                                                                                                                                                                                                                                                                                                                             Q8IIU0;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF5
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Erythrocyte membrane protein 1 Gb172var4 (Fragment).
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                                                                                                                                                                                                                                                                                                                           Hypothetical protein. PF11_0074.
Plasmodium falciparum Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                               STRAIN=3D7
                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                    NCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Gb172;
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  "Genome sequence of falciparum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTTDKENETKRQEWWNGNGPKIWNAMLCALSYNTNEKTFKDKVHSQLTTTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKDDTKRKEWWENNRSHIWQAMVCGLSHHIDEETARKTLTE
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177 AA;
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193 AA;
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                                                                                                                                                                                                                                                                                                                           Apicomplexa; Haemosporida; Plasmodium
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placental isolates
antigen var genes (
                                                                                                                                                                                                                                                                                                                                                                                                          23,
                   human malaria
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.76
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                               307)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .75DB2DCAF9E34C42 CRC64;
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                   parasite
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Q819A6;
Q819A6;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                  "Plasmodium falciparum placental isolates se express common surface antigen var genes of J. Infect. Dis. 0:0-0(2003).

RMBL; AF547105; AAN86287.1; -.

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Q9BJE8;
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J. Infect. Dis. 183:1165-1169(2001).
EMBL; AF334805; AAKZ8128.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Erythrocyte membrane protein 1 (Fragment).
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EMBL; AE014837; AAN35663.1;

Hypothetical protein.

SEQUENCE 743 AA; 88542 MY
                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  STRAIN=Gb172;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=70
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-JUN-2001
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Local Similarity
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Pred. No. 3.3;
3; Mismatches
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                                                                                           4CB7755687DAF997
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Q8I0M6;
01-MAR-2003
                                                                            STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome O BAC OSJNBa0044H10 genomic sequence.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO84405; AAN64492.1;
SEQUENCE 1062 AA; 115365 MW; A9118DDDCF3B20A4 CRC64;
                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
177 AA;
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                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21166 MW; 40E8DD10B01EF18A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.2%;
                                             30.2%;
32.3%;
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placental isolates
antigen var genes o
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                                 Score 65; DB
Pred. No. 10;
8; Mismatches
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Last annotation update)
1 Gb35varPAM5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65;
Pred. No.
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                                                        Length 1062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 12
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Best Local S
Matches 16
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PRINTS; SM0633; Glyco_10; 1.

SMART; SM00633; Glyco_SYL HYDROL F10; 1.

PROSITE; PS00591; GLYCOSYL HYDROL F10; 1.

Glycosidase; Hydrolase; Signal; Xylan degradation.

POTENTIAL

POTENTIAL

POTENTIAL

POTENTIAL

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POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Putative ATP-dependent RNA helicase C285.03.
SPCC285.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  074491 PRELIMINARY;
074491; P78908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96077124; PubMed=7492333; Millward-Sadler S.J., Davidson K., Hazlewood G.P., Black G.W., Gilbert H.J., Clarke J.H.; Gilbert H.J., Clarke J.H.; "Novel cellulose-binding domains, NodB homologues and conserved modular architecture in xylanases from the aerobic soil bacteria Pseudomonas fluorescens subsp. cellulosa and Cellvibrio mixtus."; Biochem. J. 312:39-48 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U1-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Endo-beta-1,4-xylanase precursor (EC 3.2.1.8).
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01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005088; CBM 15.
InterPro; IPR001000; Glyco_hydro_10.
Pfam; PF03326; CBM 15; 1.
Pfam; PF00331; Glyco_hydro_10; 1.
PRINTS; PR00134; GLHYDRLASE10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z48926; CAA88762.1; -. HSSP; P14768; 1CLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Mixtus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Cellvibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cellvibrio mixtus.
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MEDLINE=98162722; PubMed=9501991;
Yoshioka S., Kato K., Nakai K., C
                                                                                                                                                                                                   Seeger K.,
Submitted
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=39650;
                                                                             STRAIN=PR745
                                                                                                                  SEQUENCE OF 115-604 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               VCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                               , Harris D., (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.8%;
43.2%;
                                                                                                                                                                                               , Lyne M., Rajandream M.A., Barrell to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
5; Mis
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             830E5B959D2C3AB8 CRC64;
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Ή.
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    Nojima H.;
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                                                                                                                                                                                                                                Barrell B.G.;
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RESULT 13
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                                        Query Match
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Matches 12
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Best Local S
Matches 14
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Q8I9B1;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                  NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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DNA RES: 4:363-369(1997).
NA RES: TO OTHER "DEAD"
-!- SIMILARITY: TO OTHER "DEAD"
EMBL; AL031545; CAA20842.1; -.
EMBL; D89259; BAA13920.1; -.
                                                                                                                EMBL;
                                                                                                                                    Khattab A., Kremsner P.G., Klinkert M.Q., "Plasmodium falciparum placental isolates separated express common surface antigen var genes of limited
                                                                                                                                                                                                              Erythrocyte membrane protein 1 Gb170var4 (Fragment).
Plasmodium falciparum.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
PROSITE; PS00039; DEAD_ATP_HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000629; DEAD_box.
InterPro; IPR001650; Helicase_
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenebB
                                                                                                                  J. Infect. Dis. 0:0-0(2003).
EMBL; AF547100; AAN86282.1;
                                                                                                                                                                       STRAIN=Gb170;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=5833;
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114
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                                         l Similarity
12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M00490; name
PS00039; DEAD ATE inding;
ATP-Binding;
ATP (
KDNEKHKEWWEKHGHEIWRGMLCALTKDVKEIQKKQK 150
                     KDPSRKKEWWENAGNKIY---TMAADKTISKLMTEYK 40
                                                                                                                                                                                                                                                                                                                                            PKIEKKS-KRNKRKWLNDENKTHVTASEAAIERL
                                                                                                                                                                                                                                                                                                                                                                PKVEKKDPSRKKEWWENAGNKIYTMAADKTISKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 protein;
180 187
292 295
120 120
123 123
401 40
482 48
502 50
516 51
527 55
578 55
                                                                                   181 AA;
                                          Conservative
                                                                                                                                                                                                                                               (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                         PRELIMINARY;
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21277 MW;
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482
504
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295
120
123
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                                                                                                                                                                                                                                                                                                                                                                                                                               68344 MW;
                                                   28.6%;
                                          8
                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
n 1 Gb170var4 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                     Score 63.5; DE Pred. No. 8.6; 5; Mismatches
                                         Score 61.5; D
Pred. No. 4.2;
8; Mismatches
                                                                                                                                                                                                                                                                     Created)
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L -> F (IN REF. 2).
R -> P (IN REF. 2).
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- v
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N - ^
                                                                                                                                                                                                                                                                                                                                                                                                                                        V -> L (IN REF. 2).
Y -> C (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RR -> KK (IN REF. 2).
VA -> FP (IN REF. 2).
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د-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F (IN REF. 2).
Y (IN REF. 2).
L (IN REF. 2).
W (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            вох
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                                                                                                                                                                                                                                                                                         181
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RESULT 15
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL392145; CAC08248.1; -.

Interpro; IPR001130; TatD Dass.

PROSITE; PS01090; TATD 2; 1.

PROSITE; PS01090; TATD 2; 1.

PROSITE; PS01090; TATD 2; 1.
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Q81973,
Q1-MAR-2003 (TrEMBLrel. 23,
Q1-MAR-2003 (TrEMBLrel. 23,
Q1-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9FT44 PRELIMINARY; PRT; 3306 AA.
09FT44; PRTHIMINARY; PRT; 3306 AA.
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-6D55;

Khattab A., Kremsner P.G., Klinkert M.Q.;

Khattab A., Kremsner P.G., Klinkert M.Q.;

Khattab A., Kremsner P.G., Klinkert M.Q.;

"Plasmodium falciparum placental isolates separated by time and space express common surface antigen var genes of limited diversity.";

J. Infect. Dis. 0:0-0(2003).

EMBL; AF547142; AAN6324.1; -.

NON TER 177 177

NON TER 177 177
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Erythrocyte membrane protein 1 Gb55var3 (Fragment).
Plasmodium falciparum.
Plasmodium falciparum.
Enkaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I.,
Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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nes 11; Conservative
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177 AA;
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llarity 31.8%; Pred. No. 8.7;
Conservative 9; Mismatches
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                           1107863 seqs, 158726573 residues
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35
                                                                                                                                                      | SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:
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SUMMARIES
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ALIGNMENTS

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Human protein SEQ	ABP64835	23	1839	100.0	35	7
	ABG09728	22	1807	100.0	35	6
PS118 prostate mar	AAM50809	23	518	100.0	35	ຫ
Human prostate-spe	AA019165	23	518	100.0	35	4.
PS118 protein enco	AAW85472	19	518	100.0	35	ω
PS118 prostate mar	AAM50811	23	35	100.0	35	N
Human prostate-spe	AA019167		35	100.0	35	ب
Description	ij	8	Query Match Length DB ID	Query Match	Score	Result No.

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RESULT 1
AAO19167
ID AAO19167
XX AAO19167
XX AAO20
XX AAO1
XX Huma
XX Huma
XX Huma
XX Homc
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(GRAN/)
(HODG/)
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                                                                                                                                                                                                                                                                                                                                                                      23-APR-1998;
23-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate; prostate-specific sequence; prostate cancer; PS118; EST; expressed sequence tag; cytostatic; gene therapy.
                                     COHEN M.
COLPITTS T L.
FRIEDMAN P N.
GORDAN J.
GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                                                      BILLINGEL P A.
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97US-0842385.
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RESULT 2
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    PITTON TO THE PROPERTY OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
Billing-Medel
Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                      27-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                              US2001055758-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS118 prostate marker immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPI;
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Russell JC,
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(ROBE/)
(RUSS/)
(STRO/)
                                                                                                                                                                                                               (COPL/)
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                                                                                                                           (GORD/)
(GRAN/)
(HODG/)
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                                                                                                                                                                                           FRIE/)
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                                                           KLASS M R.
KRATOCHVIL J D.
ROBERTS-RAPP L.
                                                                                                                         GORDON J.
GRANADOS E N.
HODGES S C.
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ROBERTS-RAPP
RUSSELL J C.
STROUPE S D.
                                                                                                                                                                                         COPLPITTS T L. FRIEDMAN P N.
                                                                                                                                                                                                                                                         BILLING-MEDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 AA;
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Hodges
PA, Cohen
Hodges SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                                                                97US-0842385
                                                                                                                                                                                                                                                                                                                                            98US-0065383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲.
M, Coplpitts TL, Friedman Klass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colpitts TL,
Klass MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Friedman
Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
PN, Gordon J
Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gordan J;
Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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RESULT 3
AAW85472
ID AAW8
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Best Local S
Matches 35
                                                                    Billing-medel
Granados EN,
Russell JC, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in non-prostate tissue. PS118 polypeptides, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostatic intraspithelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polymented in transfected host cells, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and resgents of the antibodies of diagnostic use. The methods and resgents of the contraction of the contract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
WPI; 1998-610000/51
N-PSDB; AAV82812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of an immunogenic polypeptide comprising amino acids 283-317 of human prostate-specific PS118 consensus sequence (see Polypeptide (see AAM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate than
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST clone; PS118; prostate tumour tissue; prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS118 protein encoded by consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW85472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 44; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Russell JC,
                                                                                                                                                                      (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                      23-APR-1997;
                                                                                                                                                                                                                                                                                                                   29-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity
35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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llarity 100.0%;
Conservative (
                                                                         Stroupe
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(first entry)
                                                                                               PA, Co
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                                                                                                                                                                                                                      97US-0842385
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                                                                      Cohen M, Colpitts TL, Friedman es SC, Klass MR, Kratochvil JD, pe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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Pred. No. 2.7
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
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Best Local S
Matches 35
                            Billingel
Granados E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a cDNA library made from prostate tumour tissue. Recombinant PS118 protein is used to detect PS118-specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of prostatic disease, particularly cancer, and to identify subjects at
                                                                                           (HODG/)
(KLAS/)
(KRAT/)
                                                                                                                         (COHE/)
(COLP/)
(FRIE/)
(GORD/)
(GRAN/)
WPI;
                   Russell
                                                                      (ROBE/)
                                                                                                                                                                                                  23-APR-1998;
23-APR-1997;
                                                                                                                                                                                                                                26-NOV-2001; 2001US-0991681.
                                                                                                                                                                                                                                                     04-JUL-2002
                                                                                                                                                                                                                                                                         US2002086316-A1
                                                                                                                                                                                                                                                                                                                            Human; prostate;
                                                                                                                                                                                                                                                                                                                                               Human prostate-specific PS118 protein fragment #1.
                                                                                                                                                                                                                                                                                                                                                                       27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                               AAO19165 standard; Protein; 518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New P118 nucleic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Updated on 25-MAR-2003 to correct PI field.)
2002-665429/71
                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                  expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283
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                                                           KRATOCHVIL J I
ROBERTS-RAPP I
RUSSELL J C.
STROUPE S D.
                                                                                                                          GORDAN J. GRANADOS
                                                                                                    HODGES S C.
                       EN,
                                                                                                                                           COLPITTS T L. FRIEDMAN P N.
                                                                                                                                                                             BILLINGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                   COHEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostatic
                  Stroupe
                           Cohen |
Hodges
                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                                                                 98US-0065383.
97US-0842385.
                                                                                                                                                                                                                                                                                                                e; prostate-specific sequence; prostate cancer; sequence tag; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93-94;
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Ω E
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                                                                                                                                                                                                                                                                                                                                                                      entry)
                  SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and proteins - used for diagnosis and disease, especially cancer, and also
                            Colpitts TL,
Klass MR, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 17;
Pred. No. 3.2e-28;
                            , Friedman
Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317
                            'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                           Gordan J;
Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٥,
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Best Local (
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                                                                                                  Billing-Medel I
Granados EN, I
Russell JC, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a number of prostate-specific sequent derived from the human PS118 gene. These can be used in the detection monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (BST) library.
            Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate disease -
                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                   PS118; prostate; man
benign prostatic hyp
prostatitis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring prognosticating, preventing, treating, or determining predisposition individual to diseases and conditions of prostate, e.g. prostrate
                                                                                                                                                                                                     (COPL/)
(FRIE/)
(GORD/)
                                                                                                                                                                                                                                                                                                                                          US2001055758-A1.
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM50809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 42-43; 58pp; English.
                                                                                                                                                                                                                                                                                              23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PS118 prostate marker partial sequence
                                                                                                                                                                      (KLAS/)
                                                                                                                                                                                                                                                                        23-APR-1997;
                                                                                                                                                                                                                                                                                                                    27-DEC-2001
                                                                                                                                                                                              (GRAN/)
                                                                                                                                                                                                                                       COHE/)
                                                                    2002-187683/24.
DB; ABA91651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
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                                                                                                                                                KLASS M R.
KRATOCHVIL J
ROBERTS-RAPP
                                                                                                                                                                              FRIEDMAN P N.
GORDON J.
GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                 BILLING-MEDEL P
                                                                                                                                                                                                                           COPLPITTS T L.
                                                                                                                                                                                                                                        COHEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 518 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFOSESSTPSTGGFSGKETPSEDDRSOSREHMGES
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nilarity 100.
Conservative
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                                                                                                   Stroupe
                                                                                                                          PA,
                                                                                                               Hodges
                                                                                                                                                                                                                                                                      97US-0842385
                                                                                                                                                                                                                                                                                              98US-0065383.
                                                                                                                                                                                                                                                                                                                                                                                   marker; prostate cancer; tumour; metastasis;
hyperplasia; prostatic intraepithelial neoplasia;
an; diagnosis; therapy; vaccine.
                                                                                                    Cohen
es SC,
pe SD;
                                                                                                                                                 M, Coplpitts TL, Friedman
Klass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                          PN,
                                                                                                              Roberts-Rapp
                                  prognosticating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518;
                                                                                                                          Gordon J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monitoring,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences
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\begin{array}{c} CCCC\times S\times S\times S & 
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CC consensus sequence is found at least 12 times more often in
CC prostate than in non-prostate tissue. PSI18 polypeptides,
including derivatives of the present sequence, polypucleotides,
CC antibodies, agonists and inhibitors are useful for detecting,
CC diagnosing, staging, monitoring, prognosticating, preventing and
CC treating (including by genetic immunisation), or determining the
CC predisposition of an individual to, diseases and conditions of the
CC prostate, such as benign prostatic hyperplasia, prostate cancer, tumours and
CC prostatic intraepithelial neoplasia, prostate cancer, tumours and
CC prostatic intraepithelial neoplasia, prostate cancer, tumours and
CC of PSI18 polymetides in transfected host cells. The methods
CC and reagents of the prostate and may also provide new markers
CC which can differentiate between the clinically important and
CC unimportant prostate cancers without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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The invention relates to isolated polynucleotide (I) and the invention probes, (I) is useful as hybridisation probes, and for chromomers.
                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT,
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-639362/73.
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                                                                                                                                                                           SEQ ID
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2000US-0649167
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                                                                                                                                                                   No 40087; 103pp; English.
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Pred. No. 3.2e-28;
Mismatches 0;
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Cc specification, but was obtained in electronic format directly from WIPO application, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coaquilation disorder; nootropic; antiallergic; antinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                                                                      New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity -
                                                                                                                                                                                                                WPI; 2002-590824/63.
N-PSDB; ABQ99421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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35; Conserv
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Pred. No. 1
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an T,
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                                                                                                                                                                                                                                                                                                             P, Asundi V, Drmanac RT;
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Claim 20; SEQ ID

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RESULT 8
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CC (AB099268-AB099608) and proteins (ABP6482-ABP65022). The sequences are
CC useful in therapeutic, diagnostic and research methods. The
CC polynuclectides may be used in the field of molecular biology as
CC for the recombinant production of protein, or in generation of anti-sense
CC DNA or RNA. The polynuclectides are useful in diagnostics as expressed
CC markers, or as nutritional sources or supplements. The proteins may be used as molecular weight
CC markers, or as nutritional sources or supplements. The proteins may be
CC used to maintain and expand cell population in a totipotential or
CC pluripotential state useful for re-engineering damaged or diseased
CC tissues, transplantation, manufacture of bio-pharmaceuticals or the
CC development of bio-sensors. The polynucleotides and proteins are useful
CC rorein expression or biological activity, e.g. haematopoietic disorders,
CC central/peripheral nervous system diseases, mechanical and traumatic
CC contral/peripheral nervous system diseases, mechanical and traumatic
CC disorders, non-healing wounds, immune deficiencies and disorders,
CC disorders, or cancer. The polynucleotide sequencies of the invention were
CC assembled from ESTs isolated mainly by sequencing by hybridisation, and
CC in some cases, sequences obtained from one or more public databases.
CC Stephing of the printed control of the printed
CC cat fire, wiso. intrub/published not sequences.
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Best Local S
Matches 35
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations testionsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                       WPI; 2001-639362/73.
N-PSDB; AAS73918.
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                                                                                                                                                                                                                                           RT,
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Pred. No. 1e-27;
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RESULT 9
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CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO as formation.
X D D X P I X P X P R R R R R R R R X P X P X X P X X P X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X 
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Best Local :
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-25931P.
16-FEB-2001; 2001US-269308P.
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                         N-PSDB; AAS53198
                                                      WPI; 2001-611495/70
                                                                                                                Haselbeck R,
Yamamoto RT,
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; antibacterial; drug design.
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                                                                                                                                                 Zyskind JW,
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999
16-APR-1999
119-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
28-APR-1999
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                                                                                                                                                                                                                                                Arabidopsis thaliana
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                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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nes 8; Conserv
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                                                                                                                                                                                                                                                                       sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprise sequences of antisense nucleic
                                                                                                                                                                                 2000EP-0301439
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 9908-0123180.
9908-0125788.
9908-0126788.
9908-01267462.
9908-01267462.
9908-01267362.
9908-0126734.
9908-0126714.
9908-0130077.
9908-0130449.
9908-0130891.
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                                                                                                                                                                                                                                                                                mapping; gene expression control; promoter;
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13-UUL-1999
14-UUL-1999
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01-JUN-1999;
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21-MAY-1999;
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99US-0144005.
99US-0144086.
99US-0144325.
99US-0144332.
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99US-014435.
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99US-0140695.

99US-0140823.

99US-0140991.

99US-0141847.

99US-0141847.

99US-0142154.

99US-0142390.

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99US-0142303.

99US-0142907.

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RESULT 11
AAY27570
ID AAY27570;
XX AAY27570;
AC AAY27570;
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Matches 7
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RESULT 12
AAG24568
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Best Local Similarity
Thes 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC CC portion (e.g. AAX84924) for increasing the stability of the fused CC protein as compared to the human protein only.

CC The invention relates to 125 novel genes and their fragments (nucleic CC acid sequences: AAX84933-X85057; amino acid sequences AAY27567-Y27933) CC which are useful for preventing, treating or ameliorating medical CC conditions e.g. by protein or gene therapy. Also, pathological CC conditions can be diagnosed by determining the amount of the new polypurcleotides. Specific uses are described for each of the 125 polynucleotides, based on which tissues they are most highly expressed in (see AAX8493) for described uses).
25-FEB-1999
05-MAR-1999
09-MAR-1999
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                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG24568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG24568 standard; Protein; 160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 350-351; 507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secreted proteins and coding sequences useful for treating disorders of the immune system and hyperproliferative disorders
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N-PSDB; AAX84936.
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Kyaw H, Lafleur DW,
Ruben SM, Shi Y, Sc
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W, Moore PA, Ni J, Olsen
Soppet DR, Wei Y;
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sen HS, Rosen CA;
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99US-0144325.
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RESULT 13
AAY26036
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The present sequence is a secreted protein if87 1, encoded by known if87_1 (deposited as ATCC 98600) isolated from human adult uterus clibrary. Recombinant secreted proteins can be produced by
                                                                                                                                                                 WPI; 1999-385352/32.
N-PSDB; AAX80671.
                                                                                                                                                                                                                           Agostino MJ, Clark HF, Collins-Racie LA, Fechtel K, Jacobs K, Lavallie ER, McCoy Steininger RJ, Treacy M, Wong GG;
                                                                                                                                                                                                                                                                                                                                                    30-NOV-1998;
04-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; cytokine; cell proliferation; immune stimulation; vaccine; immune suppression; haematopolesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostasis; thrombolytic; receptor; ligand; anti-inflammatory; cadherin; tumour; gene therapy.
                                                                                 Claim 25; Page 111; 124pp; English
                                                                                                                          New polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1998;
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Conservative 0;
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JM, Merberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiarthritic; antinicrobial; vulnerary; cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; vasotropic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease; Huntington's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen; food employers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transforming host cells and culturing them under suitable conditions. The polynucleotide and protein are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Some predicted biological activities include cytokine and cell proliferation/ differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic and thrombollytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and formation activity. The polynucleotide encoding secreted
                                                                                                                                                               Jacobs K,
Treacy M,
Disclosure; Page 476; 619pp; English
                                nervous system disorders
                                                   diseases such as
                                                                                                                    WPI; 2001-639363/73
                                                                                                                                                                                                                                                    30-MAR-2000;
04-DEC-2000;
                                                                                                                                                                                                                                                                                                      22-MAR-2001; 2001WO-US09369
                                                                                                                                                                                                                                                                                                                                                                        WO200175068-A2
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein if87_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU39003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU39003 standard; Protein; 186 AA.
                                                                                                                                                                                                                     (GEMY ) GENETICS INST INC.
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                                                                                                                                              H
                                                                                                                                                                                                                                                                                                                                                                                                                                        supplement;
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                                                                                                    AAS59221.
                             human proteins, useful as vaccine for treating various such as autoimmune disorders (e.g. multiple sclerosis), system disorders (e.g. stroke) -
                                                                                                                                              McCoy JM, Li
Agostino MJ,
Fechtel K, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SESSIPS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SESSTPS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 AA;
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                                                                                                                                                                                                                                                    2000US-0539330
2000US-0729674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                               Lavallie E, (
J, Steininger
                                                                                                                                                 Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Pred. No.
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                                                                                                                                                               Collins-racie LA, r RJ, Spaulding V,
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). 17;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary confidences. The proteins are also useful in the treatment of diseases cand disorders including tissue, skin and organ transplantation and in cc and disorders including tissue, skin and organ transplantation and in cc graft-versus-host diseases (GYHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, con the treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by cinflammatory processes, diseases of the peripheral nervous system, alzheimer's, Parkinson's disease, Huntington's disease, camylotrophic lateral sclerosis, and Shy-Drager syndrome, infections, confiarction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration. The contract partial contract of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The
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Best Local :
07-JAN-1998;
08-JAN-1998;
13-JAN-1998;
22-JAN-1998;
                                                                                                                                                                                                                                                                                                                                   Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer: tumour; autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; Crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis,
                                                                            02-JAN-1998
                                                                                              04-DEC-1997;
20-DEC-1997;
                                                                                                                                                                              04-DEC-2000;
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                                                                                                                                       10-APR-1997;
                                                                                                                                                                                                                                                         US2001039335-A1
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
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                                                                                                                                                                              2000US-0729674
                                                     97US-067454P.
97US-068379P.
98US-070346P.
98US-070643P.
98US-070755P.
98US-071304P.
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b. 17;
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cell proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic, anti-inflammatory, immunomodulator, vulnerary, incomposition of the polyment of th
                                                                                                                                                                                 Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55890-ABB55800), especially polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and proteins SEQ ID NO 2 (ABB55698-ABA90876) and SEQ ID NO 20 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 are deposited with the American Type Culture Collection (ATCC) with accession number 98599. The polynucleotides and encoded polypeptides have cytostatic, anti-inflammatory, immunomodulator, vulnerary, respectives activing the polynucleotides and encoded polypeptides have cytostatic, anti-inflammatory, immunomodulator, vulnerary.
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18-FEB-1998;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                              injury, endotoxin lethality, arthritis, inflammatory bowel disease or Crohn's disease; or tumours or cancers, pemphiqus valoario or foliaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New secreted proteins and encoding polynucleotides, useful in gene therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations
                                                                                                                                                                                                                                                                            Sequence
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Merberg D, Treacy
Wong GG, Clark H,
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N-PSDB; ABA90890.
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(COLL/)
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STEININGER R J.
SPAULDING V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLARK H.
FECHTEL K.
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COLLINS-RACIE L A.
EVANS C.
                                                                                                                                                                                 Similarity 100 7; Conservative
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TREACY M.
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                                                                                                                                   SESSTPS 10
                                                                                      SESSTPS 129
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Treacy M, Agostino MJ,
Clark H, Fechtel K;
                                                                                                                                                                                                                                                                            186
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98US-075038P.
2000US-0539330.
98US-0197886.
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Steininger RJ, Spaulding V;
                                                                                                                                                                                                      DB 23; Length 186;
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Minimum DB
Maximum DB
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1 SFQSESSTPSTGGF
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/ACTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                                                 US-09-772-647-4
US-08-968-747-5
US-09-025-151-14
US-09-637-240-14
US-09-637-240-14
US-09-637-240-14
US-09-252-991A-26885
US-09-252-991A-28280
US-09-732-210-1144
US-08-044-547-1
US-08-044-547-1
US-09-252-991A-28280
US-09-252-991A-30898
US-09-252-991A-30898
US-09-252-991A-30898
US-09-258-991A-30898
US-09-248-588-4
PCT-US-96-10602-12
US-07-739-642-8
US-07-739-642-8
US-07-739-642-8
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365.801 Million cell updates/sec
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Sequence 27, Appl
Sequence 4, Appli
Sequence 5, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 37, Appl
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3, Appli
2,820, A
1, Appli
58, Appl
58, Appl
30898, A
20, Appli
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26885, A
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 35 amino acid
                                                                                  NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/335-1729
                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/84
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Abbott
CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/065,383 FILING DATE: CLASSIFICATION:
                                                       TELEX:
                                                                      TELEFAX: 847/938-2623
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Sequence	Sequence	Sequence	Seguence	Sequence	Patent No	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
12, Appl	59, Appl	4411, Ap	4, Appli	3, Appli	. 5196194	20225, A	21, Appl	18, Appl	2, Appli	6, Appli	6, Appli	10, Appl	8, Appli	4, Appli	2, Appli	10, Appl	8, Appli

ALIGNMENTS

Sequence 29, Applicat Patent No. 6391543 GENERAL INFORMATION: APPLICANT: RUSSEL, JOHN C. APPLICANT: STROUPE, STEPHEN D. TITLE OF INVENTION: REAGENTS AND M TITLE OF INVENTION: FOR DETECTING NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: ADDRESSEE: Abbott Laboratories APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Application US/09065383 KLASS, MICHAEL R. KRATOCHVIL, JON D. ROBERTS-RAPP, LISA ROBERTS-RAPP, LISA RUSSELL, JOHN C. STROUPE, STEPHEN D. FRIEDMAN, PAULA N. HODGES, STEVEN C. KLASS, MICHAEL R. GRANADOS, COHEN, MAURICE BILLING-MEDEL, JULIAN FOR DETECTING DISEASES OF THE PROSTATE 33 REAGENTS AND METHODS USEFUL Park Road EDWARD N. PATRICIA

USA

35 amino acide

29:

08/842,385

6084.US.P1

amino acid

single

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                                              ; TOPOLOGY: 1; MOLECULE TYPE: US-09-065-383-27
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US-09-065-383-27
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: 08/842
APPLICATION UNMBER: 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
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APPLICANT:
APPLICANT:
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100.0%;
108 35; Conservative
                                                                                                        TYPE: amino acids
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TOPOLOGY: 1
                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                           NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                    TELEFAX: 847/938-2623
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RUSSELL, JOHN C.
STROUPE, .STEPHEN D.
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
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                                                            No. 6391543e
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Pred. No. 6.4e-29;
Score 35; DB 4;
Pred. No. 7.8e-28;
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              Length 518;
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 737
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/772,647
CURRENT FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Verma, Ajit K
APPLICANT: Reddig, Pete
APPLICANT: Jansen, Aaro
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jansen, Aaron P
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: TOTHER INFORMATION: mouse protein kinase C epsilon coding
                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,747
                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: FRAGER, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08
                                                                                                                                                                                                                                                                                                                                                      ADDATE: 222
STREET: 222
CITY: Boston
TAME: MA
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Scaglioni et al.
TITLE OF INVENTION: INHIBIT
                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                      FILING DATE: 03
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & .....
STREET: 225 Franklin Street
                                                TELEFAX:
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                                                    617/542-8906
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Pred. No.
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RESULT 6
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; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-025-151-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-025-151-14
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US-09-637-240-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Legrain, Pierre
APPLICANT: Fromont, Micheline
APPLICANT: Fromont, Micheline
APPLICANT: Rain, Jean-Christophe
APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: PAST AND EXHAUSTIVE METHOD FOR SELECTING A PREY
TITLE OF INVENTION: INTEREST: APPLICATION TO THE CONSTRUCTION OF MAPS OF
TITLE OF INVENTION: INTERACTORS POLYPEPTIDES
FILE REFERENCE: 03495-0164
CURRENT APPLICATION NUMBER: US/09/025,151
CURRENT APPLICATION NUMBER: US/09/025,151
CURRENT FILING DATE: 199-02-18
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
                                                   SEQ ID NO 14
LENGTH: 76
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Matches 6; Conserva
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                                                                                     CURRENT APPLICATION NUMBER: US/09/637,240
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 09/025,151
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                  APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: FAST AND EXHAUSTIVE METHOD FOR SELECTING A PREY
TITLE OF INVENTION: POLYPEPTIDE INTERACTING WITH A BAIT POLYPEPTIDE OF
TITLE OF INVENTION: INTEREST: APPLICATION TO THE CONSTRUCTION OF MAPS OF TITLE OF INVENTION: INTERACTORS POLYPEPTIDES
FILE REFERENCE: 03495-0164
                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
APPLICANT: Legrain, Pierre
APPLICANT: Fromont, Michel
APPLICANT: Rain, Jean-Chri
           ORGANISM: Saccharomyces cerevisiae
                                   TYPE: PRT
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No. 6187535
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o. 6531284
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100.0%; Pr
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100.0%; Pred. No. 26;
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                                                                                        Sequence 2, Application Patent No. 5939316
GENERAL INFORMATION:
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Patent No. 6111089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPARTIBLE
COMPUTER: IBM PC COMPARTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,599A
FILING DATE: 28-FEB-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/317,522
FILING DATE: 04-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2256
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
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           APPLICANT: Chen, Hong
APPLICANT: Friemer, N
TITLE OF INVENTION: T
TITLE OF INVENTION: T
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                           Application US/08828008
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4370 La Jolla Village Drive,
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Hong
mer, Nelson, B.
ON: METHODS AND COMPOSITIONS FOR
ON: THE DIAGNOSIS AND TREATMENT
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                               OF NEUROPSYCHIATRIC
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                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1995-02-18
PRIOR APPLICATION NUMBER: US 66/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 66/094,190
PRIOR PRIOR PRIOR DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26885
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Best Local Similarity
Matches 6; Conserv
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                  Matches
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                                                   Query Match
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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FILING DATE: 27-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                     ENGTH: 105
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LENGTH: 94 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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              Local Similarity
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TOPOLOGY: linear
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1155 Avenue of the Americas
            17.1%; Score 6; DB 4 ilarity 100.0%; Pred. No. 36. Conservative 0; Mismatches
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100.0%; Pred. No.
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o. 32;
                                                   DB 4;
                                                   Length 105;
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US-08-044-547-3
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Sequence 3, Application US/08044547
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; ORGANISM: Chlorella vulgaris
US-09-732-210-1144
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US-09-252-991A-18728
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                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO.1144
LENGTH: 123
                                                                   Best Local Similarity
Matches 6; Conserv
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 1071
                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                               APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 6; Conserv
109 DRSQSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1144, Application US/09732210
5. 6573361
                               24 DRSQSR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 SSTPST 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 SSTPST 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
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                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09252991A
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1998-02-18
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                   17.1%; Score 6; DB . 100.0%; Pred. No. 41 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.1%; Score 6; 100.0%; Pred. No.

 Mismatches

                                                                                     DB 4;
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                                                                                                    Length 123;
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                                                                    Indels
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Patent No. 5324715

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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-252-991A-28280
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Best Local Similarity
Matches 6; Conserva
                                                                                                                                                       SEQ ID NO 28280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28280, Application US/09252991A
-09-252-991A-28280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/:
FILING DATE: 09-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Parr, Richard S.
REGISTRATION NUMBER: 32,58:
REFERENCE/DOCKET NUMBER: 11
                        LENGTH: 140
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,547
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Connolly, Thome APPLICANT: Keller, Paul M. TITLE OF INVENTION: ProtesTITLE OF INVENTION: Collac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (908) 594-4958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
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TYPE: amino acid
STRANDEDNESS: unkr
TOPOLOGY: unknown
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OPERATING SYSTEM: PC-DOS/MS-DOS
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P.O. Box 2000
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ilarity 100.0%; Pred. No.
Conservative 0; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas M.
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Query Match
Best Local Similarity
Thes 6; Conserve
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                                                                                                                                                                                 US-09-886-319A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-044-547-1
                                                                                                                                                                                                                    RESULT 15
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Patent No. 5324715
GENERAL INFORMATION:
APPLICANT: Connolly, Thomas
APPLICANT: Keller, Paul M.
                                                                                          GENERAL INFORMATION:
                                                                                                                    Sequence 58, Application US/09886319A
Patent No. 6586185
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parr, Richard S.
REGIERATION NUMBER: 32,586
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/594,917
FILING DATE: 09-0CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Parr, Richard S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,547
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 147 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,586
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Pred. No. 49;
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APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
ITITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
ITITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
ITITLE OF INVENTION: Healing and for the Identification of Pharmacologically
ITITLE OF INVENTION: Active Substances
ITITLE OF INVENTION INVEST: US/09/886,319A
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58
LENGTH: 151
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-319A-58
Search completed: July 24, 2003, 12:28:38 Job time : 5.04832 secs
                                                                                                                                                                                                                                                       Query Match 17.1%; Score 6; DB 4; Length 151; Best Local Similarity 100.0%; Pred. No. 50; Matches 6; Conservative 0; Mismatches 0; Indels
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Maximum DB seq length: 200000000
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Perfect score:
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Match
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      Published_Applications_AA: *
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/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
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/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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      US-09-815-242-10932
1 US-09-974-879-143
1 US-09-305-736-142
US-09-729-674-30
                                                 US-09-738-626-4170

US-09-946-374-243

US-10-096-867-100

US-10-052-586-310

US-10-063-547-100

US-10-176-758-310

US-10-176-758-310

US-10-175-737-310
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                     US-10-063-616-100
US-10-173-706-310
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Sequence 143, App
Sequence 142, App
Sequence 30, App
Sequence 243, App
Sequence 100, App
Sequence 100, App
Sequence 310, App
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                                                                                                                                                                                                                         Sequence 10932,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10932, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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Zyskind, Judith W.
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0-174-585-	US-10-174-576-310	0-173-705-3	-10-173-697-31	0-173-695-31	76-991-31	-10-184-658-31	0-176-993-31	US-10-176-992-310	-10-176-987-31	-10-176-985-3	-10-176-750-3	0-176-747-3	-10-176-492-	10-176-488-3	10-175-743-3	0-175-740-3	10-175-739-3	-10-174-588-3	74-582-3	79-3	0-174-572-	°	-10-063-502-10	US-10-180-557-310	0-180-552-	-10-176-913-3	-10-176-757-31	2-3	US-10-175-752-310
e 310,	Sequence 310, App	310,	•	310,	e 310,	e 310,	æ	e 310,	e 310,	e 310,	e 310,	310,	310,	•	310,	•	310,	e 310,	e 310,	e 310,	e 310,	e 310,	e 100,	310,	Sequence 310, App	310,	31	310,	Sequence 310, App

ALIGNMENTS

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FILE OF INVENTION: FILVACE
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLNG DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/223,625
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-12-22
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
PRIOR FILLING DATE: 2001-02-16
NUMBER OF SEG ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEG ID NO 10932
LENGTH: 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
ORGANISM: Enterococcus faecalis
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Best Local S
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                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                         LENGTH: 121
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/064,988 FILING DATE: 1997-11-07
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FILING DATE: 1997-11-07
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                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/066,090
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TLING DATE: 1997-11-07
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                                              SCKETPS 21
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o. US20030028003A1
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                                                                                           20.0%; Score 7; 1
100.0%; Pred. No.
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US-09-305-736-142
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 142
LENGTH: 122
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                                                                                                           Sequence 30, Application US/09729674 Patent No. US20010039335A1
                                                                                                                                                                                                                                                             Matches
                                                                         APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                            INFORMATION:
Collins-Racie, Lisa A.
Evans, Cheryl
Merberg, David
                                              LaVallie, Edward R.
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; OTHER INFORMATION: US-09-305-736-142
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 612
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                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE:
                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/066,090
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EARLIER APPLICATION NUMBER: 60,066,095
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                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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70 SGKETPS
                              15 SCKETPS 21
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                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                             LING DATE: 1997-11-17
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TING DATE: 1997-11-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATION NUMBER: 60/064,983
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                                                                Conservative
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                                                                                20.0%; Score 7;
100.0%; Pred. No.
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                                                                  <u>.</u>
                                                                  Mismatches
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5. 8.5;
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                                                                                                Length 122;
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John M.

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Treacy,

Maurice

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Query Match
Best Local Similarity
Yatches 7; Conserve
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                                                                                                                                     ; ORGANISM: Corynebacterium glutamicum 
US-09-738-626-4170
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US-09-738-626-4170
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-729-674-30
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                     SOPTWARE: PatentIn ver. 3.0
SEQ ID NO 4170
LENGTH: 342
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.0%; Score 7; DB 9
Best Local Similarity 100.0%; Pred. No. 12
Matches 7; Conservative 0; Mismatches
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APPLICANT:
APPLICANT:
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APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6085-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/539,330 PRIOR FILING DATE: 2000-03-30 NUMBER OF SEQ ID NOS: 283
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316 STPSTGG 322
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YOKOI, HARUHIKO
TATEISHI, NAOKO
OFNOH, AKIHIRO
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                                STPSTGG 13
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OCHIAI, KEIKO
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Steininger II, Rober
Spaulding, Vikki
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                                                                20.0%; Score 7; DB lilarity 100.0%; Pred. No. 21 Conservative 0; Mismatches
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SEIKO
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RESULT 6
US-09-946-374-243
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PRIOR FILING DATE: 1998-09-01
PRIOR PELING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/09883
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
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PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
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CURRENT FILING DATE: 2001-09-04
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                                                                                                                                                 OR APPLICATION NUMBER: 60/099741
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099754
OR APPLICATION NUMBER: 60/099763
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099792
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099808
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099808
OR APPLICATION NUMBER: 60/099812
OR APPLICATION NUMBER: 60/099812
DR FILING DATE: 1998-09-10
DR APPLICATION NUMBER: 60/099815
DR FILING DATE: 1998-09-10
DR APPLICATION NUMBER: 60/099816
DR FILING DATE: 1998-09-10
DR APPLICATION NUMBER: 60/100385
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Hillan, Kenneth J.
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Grimaldi, Christopher
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FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/100684

APPLICATION NUMBER: 60/100683 FILING DATE: 1998-09-16 APPLICATION NUMBER: 60/100664 APPLICATION NUMBER: 60/100662

FILING DATE: 1998-09-16

FILING DATE: 1998-09-

PRIOR

APPLICATION NUMBER: 60/100661 FILING DATE: 1998-09-16

APPLICATION NUMBER: 60/100584 FILING DATE: 1998-09-16

FILING DATE: 1998-09-

APPLICATION NUMBER: 60/100627

FILING DATE: 1998-09-16

APPLICATION NUMBER: 60/100388 FILING DATE: 1998-09-15 APPLICATION NUMBER: 60/100390

PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

APPLICATION NUMBER: 60/100848 FILING DATE: 1998-09-18

FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/100711

APPLICATION NUMBER: 60/100849

APPLICATION NUMBER: 60/100710 FILING DATE: 1998-09-17

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FILING DATE: 1998-09-18 APPLICATION NUMBER: 60/ FILING DATE: 1998-09-17

60/100919

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US-10-006-867-100
Sequence 100, Application US/10006867
Publication No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
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Best Local
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FILING DATE: 1998-10-07
APPLICATION NUMBER: 60/103401
FILING DATE: 1998-10-07
APPLICATION NUMBER: 60/103449
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APPLICATION NUMBER: 60/105000
FILING DATE: 1998-10-20
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FILING DATE: 1998-10-08
APPLICATION NUMBER: 60/103678
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FILING DATE: 1998-10-07
APPLICATION NUMBER: 60/103395
FILING DATE: 1998-10-07
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APPLICATION NUMBER: 60/
FILING DATE: 1998-10-22
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APPLICATION NUMBER: 60/105694
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APPLICATION NUMBER: 60/105693
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APPLICATION NUMBER: 60/105266
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FILING DATE: 1998-10-20
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FILING DATE: 1998-10-07
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FILING DATE: 1998-10-07
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FILING DATE: 1998-09-30
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APPLICATION NUMBER: 60/102570
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APPLICATION NUMBER: 60/102331 FILING DATE: 1998-09-29 APPLICATION NUMBER: 60/102484

PRIOR PRIOR PRIOR

FILING DATE: 1998-09-29 APPLICATION NUMBER: 60/: FILING DATE: 1998-09-29

60/102330

APPLICATION NUMBER: 60/102307

FILING DATE: 1998-09-29 APPLICATION NUMBER:

60/102240

PRIOR PRIOR PRIOR

FILING DATE: 1998-09-24
APPLICATION NUMBER: 60/102207
FILING DATE: 1998-09-29

APPLICATION NUMBER: 60/101916 FILING DATE: 1998-09-24

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FILING DATE: 1998-09-24 APPLICATION NUMBER: 60/101915 APPLICATION NUMBER: 60/101743 FILING DATE: 1998-09-24 FILING DATE: 1998-09
APPLICATION NUMBER:

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APPLICATION NUMBER: 60/ FILING DATE: 1998-09-23

60/101479 60/101477 60/101476

APPLICATION NUMBER: 60/101738

1998-09-24

60/101741

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APPLICATION NUMBER: FILING DATE: 1998-09

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FILING DATE: 1998-09-23

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APPLICATION NUMBER: 60/101474 FILING DATE: 1998-09-23 APPLICATION NUMBER: 60/101475 FILING DATE: 1998-09-23

PRIOR PRIOR PRIOR

FILING DATE: 1998-09-23 APPLICATION NUMBER: 60/101472

APPLICATION NUMBER: 60/101471 FILING DATE: 1998-09-22 APPLICATION NUMBER: 60/101279 FILING DATE: 1998-09-18 APPLICATION NUMBER: 60/101071

FILING DATE: 1998-09-23

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FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/101068
FILING DATE: 1998-09-18 FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/101014

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APPLICATION NUMBER: 60/100930

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	; PRIOR FILING DATE: 1998-08-26 ; PRIOR APPLICATION NUMBER: 60/097979 ; PRIOR FILING DATE: 1998-08-26 ; PRIOR APPLICATION NUMBER: 60/098749 ; PRIOR FILING DATE: 1998-09-01 ; PRIOR APPLICATION NUMBER: 60/099763 ; PRIOR APPLICATION NUMBER: 60/099763 ; PRIOR PILING DATE: 1998-09-10 ; PRIOR APPLICATION NUMBER: 60/099792

APPLICATION NUMBER: 60/113430

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US-10-052-586-310
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                          Sequence 310, A Publication No.
                                                                                                                                           GENERAL INFORMATION:
APPLICANT:
                                                                                          APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
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APPLICATION NUMBER: 60/199397
FILING DATE: 2000-04-25
APPLICATION NUMBER: 09/380139
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APPLICATION NUMBER: 60/129122
FILING DATE: 1999-04-13
APPLICATION NUMBER: 60/129674
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FILING DATE: 1999-06-09
APPLICATION NUMBER: 60/144791
FILING DATE: 1999-07-20
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APPLICATION NUMBER: 60/119549
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FILING DATE: 1999-02-10
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APPLICATION NUMBER: 60/113621
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FILING DATE: 1999-01-20
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FILING DATE: 1998-12-30
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                                            Godowski, Paul J. Gurney, Austin L.
Smith, Victoria
Watanabe, Colin
                                                                             Goddard, Audrey
                             Pan, James
                                                                                               Desnoyers, Luc
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FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-08

NUMBER: 60/081049

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CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR PRIOR APPLICATION NUMBER: 60/069266
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
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PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-28
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PRIOR APPLICATION NUMBER: 60/063540
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
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DR FILING DATE: 1998-03-31

OR APPLICATION NUMBER: 60/080194

DR FILING DATE: 1998-03-31

DR APPLICATION NUMBER: 60/080327

DR FILING DATE: 1998-04-01

DR APPLICATION NUMBER: 60/080333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/064103
FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
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APPLICATION NUMBER: 60/
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FILING DATE: 1997-12-12
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/078939
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APPLICATION NUMBER: 60/081070 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-09

PRIOR PRIOR

APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28

FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
FILING DATE: 1998-04-22

APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-1 APPLICATION NUMBER:

60/081838

FILING DATE: 1998-06-05

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APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRATITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 9239RIC1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrappes
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-10-063-547-100
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Best Local S
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff
APPLICANT: Gerritsen
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OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/08861
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088863
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088876
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089090
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089105
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089105
OR FILING DATE: 1998-06-12
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OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088326
OR APPLICATION NUMBER: 60/088655
OR FILING DATE: 1998-06-09
OR APPLICATION NUMBER: 60/088655
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088722
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088738
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088740
OR FILING DATE: 1998-06-10
OR FILING DATE: 1998-06-10
OR FILING DATE: 1998-06-10
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OR FILING DATE: 1998-06-16
DR APPLICATION NUMBER: 60/089514
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089538
OR FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
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FILING DATE: 1998-66-10
APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089598
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7; Conserv
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher
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                                                                                                TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ING THE SAME
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PRIOR PRIOR

R FILING DATE: 1998-06-R APPLICATION NUMBER: 6 R FILING DATE: 1998-06-R APPLICATION NUMBER: 6

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60/087759 60/087609 60/087208

60/087827

APPLICATION NUMBER: FILING DATE: 1998-01 APPLICATION NUMBER:

1998-05-28

DR FILING DATE: 1998-06-03

WE APPLICATION NUMBER: 60/01

WE APPLICATION NUMBER: 60/01

WE APPLICATION NUMBER: 60/01

WE FILING DATE: 1998-06-04

WE APPLICATION NUMBER: 60/01

WE FILING DATE: 1998-06-04

WE APPLICATION NUMBER: 60/01

60/088033 60/088029 60/088028 60/088025

60/088167

60/088202

PRIOR PRIOR PRIOR

FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/086486
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/087098
FILING DATE: 1998-05-28

PRIOR PRIOR

R FILING DATE: 1998-05 R APPLICATION NUMBER: 0 R FILING DATE: 1998-05 R APPLICATION NUMBER: 0

60/086392 60/086023

1998-05-15 1998-05-18

DR APPLICATION NUMBER: 60/085579
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085580
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085582
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085700

R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-05-07

60/084640 60/084639 60/084414 60/084366

60/084643

APPLICATION NUMBER: 60/085573 FILING DATE: 1998-05-15

FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/0
FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/0

FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083499 FILING DATE: 1998-04-29

APPLICATION NUMBER: 60/083496 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29

60/083495

APPLICATION NUMBER: 60/083559

FILING DATE: 1998-09 APPLICATION NUMBER:

1998-05-06

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US-10-174-590-310
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-547-100
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LENGTH: 596
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Matches 7; Conserv
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Publication No. US20030008353A1
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LENGTH: 596
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                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/174,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C42
                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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ORGANISM: Homo Sapien
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                                                                       Watanabe, Colin K. Wood, William I.
                                                                                                                                   Godowski, Paul J. Gurney, Austin L.
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                                                                                                                                                                                Chen, Jian
Desnoyers, Luc
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                                                            Zhang, Zemin
                                                                                                       Smith, Victoria
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NUMBER: US/10/176,758
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RESULT 13
US-10-063-616-100
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-310
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US-10-175-737-310
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; ORGANISM: Homo Sapien
US-10-176-758-310
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Best Local
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 310
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Best Local
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          APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: P3430R1C50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
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Prior Application removed - See
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                           APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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Godowski, Paul
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o. US20030013153A1
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ION: ACIDS ENCODING P3230R1C1
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    See File Wrapper or Palm

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Pred. No.
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RESULT 15
US-10-175-738-310
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US-10-173-706-310
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CURRENT FILING DATE: 2002-05-03;
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
SEQ ID NO 100
LENGTH: 596
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-616-100
                                                                                                  APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Andrey
APPLICANT: Godowski, Paul
                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.0%; Score 7; DB: Best Local Similarity 100.0%; Pred. No. 35 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative (
                                                                                                                                                                                          GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 310, A Publication No.
                                                                                                                                                                                                         Sequence 310, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C7 CURRENT APPLICATION NUMBER: US/10/173,706

CURRENT FILING DATE: 2002-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
                                                     PPLICANT
                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                               123 SESSTPS 129
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                                                                                                                                                                                                                                                                                                                                             4 SESSTPS 10
                                                                    Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith, Victoria Watanabe, Colin K. Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desnoyers, Luc
Goddard, Audrey
                 Smith, Victoria Watanabe, Colin K. Wood, William I.
                                                                                                                                        Desnoyers, Luc
Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10173706
                                                                                                                                                                                                                         Application US/10175738
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                                                                                                                                                                                                         US20030022294A1
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; . Length 596;
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                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 ; SEQ ID NO 310 ; LENGTH: 596 ; TYPE: PRT ORGANIZM: Homo Sapien US-10-175-738-310
                                                                     밁
Search completed: July 24, 2003, 12:48:28 Job time : 6.94436 secs
                                                                                                     Ś
                                                                                                            Query Match
Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C45
CURRENT APPLICATION NUMBER: US/10/175,738
CURRENT FILING DATE: 2002-06-19
CURRENT FILING DATE: 2002-06-19
                                                                   123 SESSTPS 129
                                                                                                     4 SESSTPS 10
                                                                                                                                                       20.0%;
                                                                                                                                     s; Score 7; DB 1
s; Pred. No. 35;
0; Mismatches
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                                                                                                                                                                     Length 596;
                                                                                                                                       Indels
                                                                                                                                       0,
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Result
No.
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Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                              Score
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Match Length DB
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                                                                                                                                                                                                                            / Cgn2_6/ptodata/1/paa/USO6_COMB.pep:*
/ Cgn2_6/ptodata/1/paa/USO7_COMB.pep:*
/ Cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
/ Cgn2_6/ptodata/1/paa/USO82_COMB.pep:*
/ Cgn2_6/ptodata/1/paa/USO82_COMB.pep:*
/ Cgn2_6/ptodata/1/paa/USO82_COMB.pep:*
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/ Cgn2_6/ptodata/1/paa/USO86_COMB.pep:*
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/ Cgn2_6/ptodata/1/paa/USO89_COMB.pep:*
/ Cgn2_6/ptodata/1/paa/USO90_COMB.pep:*
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/ Cgn2_6/ptodata/1/paa/USO94_COMB.pep:*
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    US-08-842-385-8
US-09-991-681-29
                                                                                                                       SUMMARIES
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                                                        Description
Sequence 8, Appli
Sequence 29, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-842-385-8
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Sequence 160845,	מווסחרם אח	equence 30.	e 10,	10,	30,	255	equence 28292	equence 25948	e 142,	equence 142,	quence 1	Sequence 1592	equence	equence 143,	equenc	equence 4149,	equence 256,	equenc	equence 1661,	equence 5962,	equenc	equence 5963;	equence 166960.	equence 57375.	Seguence 10932. A	Semience 10932, a		0 4554,	3553,	equence 77	30, Ag	Sequence 30, Appl	400	32,	equence 499	e 495,	40087	e 44,	4	e 27,	•

ALIGNMENTS

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SSULT 1

S-08-842-385-8

Sequence 8, Application US/08842385

Sequence 8, Application US/08842385

Sequence 8, Application US/08842385

Sequence 8, Application:
APPLICANT: Russell, John
APPLICANTON TYPE: Abbott Park Road

STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,385
FILING DATE:
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

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RESULT 2
US-09-991-681-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: 09/065,383
PILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 36,441
REFERENCE/DOCKET NUMBER: 6084.US
TELECOMMUNICATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 35 amino acids
TYPE: amino acid
                                                                                                                                             APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-Nov-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRATOCHVIL, JON D.

ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BILLING-MEDEL, COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
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                                                                                                                                                                                                                                                                                                                                                                             CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COHEN, MAUKICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                             60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                   100 Abbott Park Road
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Pred. No. 1.8e-27;
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                                      6084.US.P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                            ; MOLECULE TYPE: None US-08-842-385-6
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                                                                             Query Match
Best Local (
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                                                              Matches
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                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,385
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Russell, John APPLICANT: Colpitts, Tra
                                                                                                                                                           TOPOLOGY:
                                                                             Local Similarity
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                         TELEX:
                                                                                                                                                                                                                                                                        TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                        LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
232 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abbott Park
                             SFOSESSTPSTGGFSGKETPSEDDRSOSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08842385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                                                              Conservative
                                                                                                                                                                          single
                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 25; 100.0%; Pred. No. 1.8e-27;
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                                                                                                                                                                                                                                                                                                                       6084.US.01
                                                                             Score 35; DB 12;
Pred. No. 2.3e-26;
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                                                             Mismatches
                                                                                            DB 12;
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                                                                                           Length 467;
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US-09-991-681-27; Sequence 27, Applicati; GENERAL INFORMATION:
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                                                                                                 Sequence 44, Application PC/TUS0301943
GENERAL INFORMATION:
APPLICANT: ORIGENE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                          Matches
                  APPLICANT: ORIGENE TECHNOLOGIES INC
TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
RIOR APPLICATION NUMBER: US 10/054,935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PASESEQ for Windows Version 2.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-Nov-2001
CLASSIFICATION UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                          283 SFOSESSTPSTGGFSGKETPSEDDRSOSREHMGES 317
                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                1 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 6084.US.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 518 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HODGES, STEVEN C.
KLASS, MICHAEL R.
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                                                                                                                                                                                                                                                                                                                      Score 35; DB 25;
Pred. No. 2.6e-26;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens PCT-US03-01943-44
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PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/117,229
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/197,824
PRIOR FILING DATE: 2002-07-19
PRIOR FILING DATE: 2002-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44, Application US/10144198
GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
                                                      NUMBER OF SEQ ID
SOFTWARE: Custom
SEQ ID NO 40087
                                                                                                                                                                                                                                                                                                          Sequence 40087, Application PC/TUS0108631 GENERAL INFORMATION:
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Best Local Similarity
Matches 35; Conserv
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                                                                                                                    PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                              APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                         ENGTH: 1807
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les 35; Conserv
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100.0%; Pred. No. 8.6e-26;
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PCT-US01-42950-495
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Sequence 495, Application US/10416993
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
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CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
SOFTWARE: Patentin version 3.0
SEQ ID NO 495
SEQ ID NO 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 495, Application PC/TUS0142950
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
                                                                Query Match
Best Local Similarity
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SEQ ID NO 495
                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/416,993
CURRENT FILING DATE: 2003-11-16
PRIOR APPLICATION NUMBER: 09/714,936
                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Helper component proteinase domain identified by PFam, OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (941)..(950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX, OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw sc
                                                                                                                                                                        LENGTH: 1839
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SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
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                                                    Conservative
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                                                                                                                                                                                                     version 3.0
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Pred. No. 8.9e-26;
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                                                                  Score 35; DB 30;
Pred. No. 8.9e-26;
                                                    Mismatches
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PCT-US03-04508-32
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; LENGTH: 1872
; TYPE: PRT
                                                    Best Loc
Matches
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Best Local
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                                                                                                                                                                                                                                                                      FEATURE:
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; ORGANISM: Homo sapiens
PCT-US03-04508-32
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NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 037003/0301985
CURRENT APPLICATION NUMBER: PCT/US03/04508
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: IDEC PHARMACEUTICALS APPLICANT: GATELY, DENNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/540,217 PRIOR FILING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                   NAME/KEY: DOMAIN
LOCATION: (11). (25)
OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX,
OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/649,167
                                                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (1065)..(1074)
OTHER INFORMATION: Helper component proteinase domain identified by PFam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam score
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                                             Similarity
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SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
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Pred. No. 9.6e-26;
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Pred. No. 9.1e-26;
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1686 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 1720

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US-10-221-279-7783

Sequence 7783, Application US/10221279

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2221
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-198-30
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US-10-144-198-30
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                                                                                                                     RESULT 14
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PRIOR APPLICATION NUMBER: US 10/054,935
PRIOR PILING DATE: 2002-01-25
PRIOR PPLICATION NUMBER: US 60/356,130
PRIOR PPLICATION NUMBER: US 10/102,946
PRIOR PILING DATE: 2002-02-14
PRIOR PPLICATION NUMBER: US 10/102,946
PRIOR PILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/117,229
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR PILING DATE: 2002-04-08
PRIOR PILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR APPLICATION NUMBER: US 10/197,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/10144198
GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prostate Cance Genes
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Best Local Similarity
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SEQ ID NO 30
LENGTH: 2221
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Best Local
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TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
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NUMBER OF SEQ ID NOS: 102
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Pred. No. 1.1e-25;
; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/221,279
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 12360
SOPTWARE: CUSTOM
SEQ ID NO 7783
LENGTH: 141
                                                                                                             Query Match
Best Local Similarity
""" B; Conserve
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; OTHER INFORMATION: Xaa = any amino acid or nothing US-10-221-279-7783
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Search completed: July 24, 2003, 12:45:55
Job time : 53.7306 secs
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US-09-134-000-3553
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CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 3553
LENGTH: 270
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS TITLE OF INVENTION: FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 21272-046
                                                                                                                                                                                                              ORGANISM: Enterococcus faecalis
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Pred. No.
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o. 21;
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Result
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Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                  is derived by analysis of the total score distribution.
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Match
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140.227 Million cell updates/sec
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| Cgm2_6/ptcdata/2/paa/PCT_NEW_COMB.pep:*
| Cgm2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*
| Cgm2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*
| Cgm2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
| Cgm2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
| Cgm2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
| Cgm2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
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 GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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US-10-243-739A-4
US-10-243-739A-6
US-10-243-739A-6
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US-10-243-739A-6
US-10-243-739A-6
US-10-243-739A-6
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US-10-465-811-24
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US-10-465-811-35
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4400 4400	App	App	Appl	App	App	App	App	App	App	, Apj	App	App	App	App	App	App	App	App	

ALIGNMENTS

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RESULT 2
US-10-462-850-3684
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; ORGANISM: Homo sapiens
US-10-367-978-32
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GENERAL INFORMATION:
APPLICANT: GATELY, DENNIS
TITLE OF INVENTION: PROSTATE SPECIFIC GENES
TITLE OF INVENTION: OR THERAPBUTICS
FILE REFERENCE: 037003-0301988
CURRENT APPLICATION NUMBER: US/10/367,978
CURRENT FILING DATE: 2003-02-19
                                 APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/10/462,850
CURRENT FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3684
LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                    Sequence 3684, Appli GENERAL INFORMATION:
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PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
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               ORGANISM: Homo Sapiens
FEATURE:
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US-10-369-060A-111
; Sequence 111, Application US/10369060A
; GENERAL INFORMATION:
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US-10-462-850-3685
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                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 111
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SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3685
                                                          Query Match
Best Local Similarity
Matches 6; Conserv
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GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
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Best Local
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PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 09/556,605
                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: TRIPEP.020CP1C1
CURRENT APPLICATION NUMBER: US/10/369,060A
CURRENT FILING DATE: 2003-02-14
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sallberg, Matti
TITLE OF INVENTION: SYNTHETIC PEPTIDES
TITLE OF INVENTION: HEPATITIS B VIRUS
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CURRENT APPLICATION NUMBER: US/10/462,850
CURRENT FILING DATE: 2003-06-17
                                                                                                                                          OTHER INFORMATION: Mus musculus
                                                                                                                                                              FEATURE:
                                                                                                                                                                        ORGANISM: Artificial Sequence
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les 6; Conservative
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6; Conserv
RSQSRE 20
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                                                                                                   Sequence 39, Application US/10243739A GENERAL INFORMATION:
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SOFTWARE: PatentIn version
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/10243739A
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version
SEQ ID NO 33
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GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen
TITLE OF INVENTION: Immune Responses Induced by V
FILE REFERENCE: 1700.0210001
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CURRENT APPLICATION NUMBER: US/10/243,739A
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/318,967 PRIOR FILING DATE: 2001-09-14
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TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
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TYPE: PRT
ORGANISM: Hepatitis B virus
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ORGANISM: Hepatitis B virus
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Pred. No.
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Mismatches
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Particles
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US-10-243-739A-42
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LENGTH: 183
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                         Sequence 44, Application US/10243739A GENERAL INFORMATION:
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                          APPLICANT: Bachmann, Martin F.
APPLICANT: Scorni, Tazio
APPLICANT: Scorni, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Accivation of Antigen Presenting Cells for Enhancement of
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739A
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.1
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APPLICANT: Storni, Tazio
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739A
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR APPLICATION DATE: 2001-09-14
SUDTMARE: Patentin version 3:1
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CURRENT APPLICATION NUMBER: US/10/243,739A
CURRENT FILING DATE: 2002-09-16
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PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 143
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TYPE: PRT
ORGANISM: Hepatitis B virus
                      ID NO 44
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Local Similarity 100.0%; Pred. No. 11;
hes 6; Conservative 0; Mismatches
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RESULT 10
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                       Query Match
Best Local Similarity
Matches 6; Conserv
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APPLICANT: Storni, Tazio
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739A
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 46
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APPLICANT: Storni, Taxio
APPLICANT: Storni, Taxio
APPLICANT: Storni, Taxio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739A
CURRENT FILING DATE: 2002-09-16
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PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR FILING DATE: 2001-09-14
                                                                                                                            LENGTH: 183
TYPE: PRT
ORGANISM: Hepatitis B virus
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TYPE: PRT
ORGANISM: Hepatitis B virus
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ORGANISM: Hepatitis B virus
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175 RSQSRE 180

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RESULT 14
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APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739A
CURRENT FILING DATE: 2002-09-16
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APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
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                                        APPLICANT: Bachmann, Martin F. APPLICANT: Storni, Tazio APPLICANT: Lechner, Franziska
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PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 143
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PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 143
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CURRENT FILING DATE: 2002-09-16
ITILE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement
ITILE OF INVENTION: Immune Responses Induced by Virus Like Particles
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TYPE: PRT
ORGANISM: Hepatitis B virus
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TYPE: PRT
ORGANISM: Hepatitis B virus
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Lechner, Franziska
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                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
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CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 143
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APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
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CURRENT APPLICATION NUMBER: US/10/243,739A
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/318,967
PRIOR FILING DATE: 2001-09-14
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                       TYPE: PRT ORGANISM: Hepatitis B virus
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TYPE: PRT
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175 RSQSRE 180
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Maximum DB seq length: 2000000000
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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R; Becker, M.; Bradshaw, H.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A; Description: The sequence of C. elegans cosmid F32D1.
A; Reference number: Z15134
A; Accession: T03915
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                                                                                       A; Map position: V
A; Introns: 29/3; A; Note: F32D1.6
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
T03915
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Best Local Similarity
Watches 8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, A;Reference number: Z19578
A;Accession: T22540
Query Match
Best Local Similarity
""" Conserve
                                                                                                                                                             A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-164 <BEC>
A;Cross-references: EMBL:AF016427;
                                                                                                                                                                                                                                                                                                                                 hypothetical protein F32D1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T03915
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A;Introns: 38/1; 103/1; 192/2; 239/1; 268/2; 300/3; 532/2; 546/1
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A;Experimental source: clone F53B6
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               20.0%; So ilarity 100.0%; For Conservative 0;
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0; Mismatches
                                 Score 7;
Pred. No.
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                                                                                                                                                                 NID:g2291228; PIDN:AAB65349.1; PID:g2291230
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N;Alternate names: protein F26K9.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-200
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C;Keywords: copper binding; transmembrane protein
F;66,107,112,117/Binding site: copper (His, Cys, F;79-113/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 136, 79-85, 1993
A;Title: A negatively light-regulated gene A;Reference number: I39698; MUID:94124044; A;Accession: I39698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blue copper binding protein homolog [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 21-Oct-2002 C;Accession: T51838
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R;Van Gysel, A.; Van Montagu, M.; Inze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blue copper-binding protein, 20K - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Datc: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change
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                                                    RING-H2 zinc finger protein ATL5
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: Characterization
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A;Residues: 1-196 <RES>
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;Date:
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Science 294, 849-852, 2001
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maduendok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, A; Title: Comparative genomics of Listeria species.
A; Title: Comparative AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hembry, C.
submitted to the EMBL Data
A;Status: p.-.
A;Molecule type: DNA
A;Residues: 1-571 <GLA>
A;Residues: 1-571 <GLA>
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C;Superfamily: Arabidopsis hypothetical protein
F;109-160/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                      C;Date: 27-Nov-2001 #sequenc
C;Accession: AB1274
R;Glaser, P.; Frangeul, L.;
; Dominguez-Bernal, G.; Duc
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R;Bloecker, H.; Mewes, H.W.; Rudd, submitted to the Protein Sequence
                                                                                                A; Reference number: AB1077; A; Accession: AB1274
                                                                                                                                                                                                                                                                                             C; Species: Listeria monocytogenes
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A;Experimental source: cultivar Columbia;
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A; Residues: 1-257 <BLO>
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tive 0; Mismatches
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2000
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·Boland, J.
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Voss, H.; Wehland,
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PID:g16411023; GSPDB:GN00177

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F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zinc-binding repeat homology <KZI>F:243-292/Domain: protein kinase C zinc-binding repeat homology <KZZ>
F:406-668/Domain: protein kinase C zinc-binding motif
F:414-422/Region: protein kinase homology <KIN>
F:414-422/Region: protein kinase ATP-binding motif
F:170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:256,259,281,284/Binding site: Lys, Glu, Asp, Lys #status predicted
F:703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation)
protein kinase C (EC 2.7.1.-) epsilon - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change C;Accession: S02270 R;Schaap, D.; Parker, P.J.; Bristol, A.; Kriz, R.; Knopf, J. FEBS Lett. 243, 351-357, 1989 A;Title: Unique substrate specificity and regulatory properties A;Reference number: S02270; MUID:89137541; PMID:2917656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
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A;Residues: 397-447,'GQRGLHDDREEDFGSGAET',467,'LSNPTLLLLPDQGPPLLRQ',487-545,'C',547-636
A;Cross-references: GB:M15523; NID:g206192; PIDN.AAA41877.1; PID:g206193
C;Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene &
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A; Molecule type: DNA
A; Residues: 1-737 < ONO>
A; Cross-references: GB.M18331; NID: 9206182; PIDN: AAA41872.1; PI
R; Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.;
Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
A; Title: Isolation of cDNA clones encoding protein kinase C: ev
A; Reference number: A94145; MUID: 87147193; PMID: 3469647
A; Accession: B26408
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A;Title: The structure, expression, and properties of additional members of the
A;Reference number: A92717; MUID:88198270; PMID:2834397
A;Accession: B28163
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J. Biol. Chem. 26
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;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
;Accession: B28163; B26408; S00216
;Cono, Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igarashi, K.; Nishizuka, Y.; Cono, Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igarashi, K.; Nishizuka, Y.; Diol. Chem. 263, 6927-6932, 1988
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t; Pred. No. 16;
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A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A; Note: activity is calcium-independent, phospholipid-dependent, and activated by diacytic C; Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; protein kinase C zinc-binding repeat binding; phospholipid by F;156-161/Region: pseudophosphorylation; duplication; phorbol ester binding; phospholipid by F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ1>F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>F;406-668/Domain: protein kinase C zinc-binding repeat homology <KZ2>F;414-422/Region: protein kinase homology <KIN>F;414-422/Region: protein kinase ATP-binding motif F;170,201,204,220/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted F;437,456,532,534/Active site: Lys #stat
A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-1693 <GEB> A;Cross-references: EMBL:U73199; N A;Experimental source: brain
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                                                                                                                                                            R;Gebbink, M.F.B.G.; Poland, M.; Kranenburg, submitted to the BMBL Data Library, October 1 A;Reference number: 220911
A;Accession: T30867
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A; Residues: 1-783 < MUR>
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Matches
                                                                                                                                                                                                                                                                                             ;Species: Mus musculus (house mouse)
;Date: 22-Oct-1999 #sequence_revision
;Accession: T30867
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                                     NID:g1657834; PID:g1657835; PIDN:AAB18197.1
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snRNP protein SMX4 - yeast (Saccharomyces cerevisiae)
N,Alternate names: protein YLR438c-a; small nuclear p
C;Species: Saccharomyces cerevisiae
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A;Title: Expressed var genes are found in Plasmodium falciparum subtelomeric regions. A;Reference number: Z20483; MUID:97154495; PMID:9001213
A;Accession: T28161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein FCR3-varT11-1 - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Decies: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T28161
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                                                         S78568
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C;Accession: T28157
R;Yang, S.O.; Wollish, W.S.; Gut, J.; Wu, submitted to the EMBL Data Library, July 1
A;Description: The molecular cloning and 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erythrocyte membrane protein 1 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
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                                                                      RESULT 14
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A;Experimental source: strain FCQ27/PNG
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A; Cross-references: EMBL
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A; Accession: T28157
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Note: FCR3-varT11-1
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A;Gene
A;Map
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A;Cross-references: MIPS:YLR438c-a; SGD:S0006434
A;Map position: 12L
C;Keywords: nucleus
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                                                                                                                                                                                                                                                                                                                                                      R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein - Deinococcus radiodurans (strain R1) C;Species: Deinococcus radiodurans C;Deceies: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 C;Accession: H75281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U21094; GSPDB:GN00012; MIPS:YLR438c-a, A;Experimental source: strain S288C (AB972) C;Genetics:
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A; Accession: S78568
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A;Experimental source: strain R1
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A; Residues: 1-93 <WHI>
                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: H75281
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TRPF_CAUCR
CHLT_CHLRE
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CHIX_PEA
RT01_YEAST
H12R_RAT
AR13_NEUCR
VG07_VACCCC
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PIR; T51838; T51838

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InterPro; IPR000923; BlueCu 1.

InterPro; IPR0003245; Plcyanin like.

Pfam; PF02298; Cu_bind_like; I.

ProDom; PD003122; Plcyanin like; 1.

PROSITE; PS00196; COPPER_BLUE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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EMBL; AF296825; -; NOT ANNOTATED CDS
EMBL; AY052681; AAK96585.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein (Probable).
DEVELOPMENTAL STAGE: MAXIMUM LEVELS ARE FOUND IN 35 DAY OLD
PLANTLETS WHEN THE ROSETTE IS MATURE, CONSISTING OF 8-10 FULL
EXPANDED LEAVES, AND AS THE FLORAL STEM STARTS TO FORM. THIS
REMAINS CONSTANT DURING THE FURTHER LIFE SPAN OF THE PLANT.
INDUCTION: BY DARK ADAPTATION. THIS GIVES A 20-FOLD INCREASE
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01-APR-1990 (Rel. 14, Las
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Protein kinase C, epsilor
PRKCE OR PKCE OR PKCEA.
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Mushinski J.F.;
"The catalytic domain of PKC-epsilon, in reciprocal PKC-delta
"The catalytic domain of PKC-epsilon conferring tumorgenicity
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NIHST3 cells, whereas both regulatory and catalytic domains of
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                                                                                                                MGD;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P16054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98127436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                   GO:0004699; F:calcium
                                                                                                                                                                                                                                                                                                                                                                     mitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIFID-DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.

SERINE- AND THEONINE-SPECIFIC ENZYME.

FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES A PHOSPHOR FOR PHONDIES. STEELS, A CLASS OF TUNG PROMOTERS. THE RECEPTOR FOR PHOREOL ESTERS, A CLASS OF TUNG PROMOTERS.
                                                                                                                                                                                                                                                                                                                               binding domains.
SIMILARITY: Contains
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                   PKC
                                                                                                                MGI:97599; Prkce.
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, Goodnight J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epsilon type (EC
                         ; DAG_PE-bind.
; Pkinase_C.
; Prot_kinase.
; Ser_thr_pkinase.
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Last annotation updat
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                                                                                                   independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ion update)
2.7.1.-) (nPKC-epsilon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  737
                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                  FAMILY OF
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properties
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PRODOM; PD000vv.,
SMART; SM00109; C1; 2.
SMART; SM00239; C2; 1.
SMART; SM00239; C2; 1.
SMART; SM00239; STKC; 1.
R SMART; SM00220; STKC; 1.
JR PROSITE; PS50004; C2 DOMAIN 2; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
CR PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
CR PROSITE; PS00108; PROTEIN KINASE DOM; 1.
CR PROSITE; PS00108; PROTEIN KINASE; Phosphorylation; Repeat; ATP-binding; Transferase; Phorbol-ester binding; Zinc.
C2 DOMAIN.
C2 DOMAIN.
C3 DOMAIN.
C4 SMART; SM00109; PO0109; PROTEIN KINASE; Phorbol-ester binding; Zinc.
C2 DOMAIN.
C3 DOMAIN.
C4 SMART; SM00239; C2; 1.
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Matches 7
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Pfam; PF00433; pkinase_C; 1.
PRINTS; PR00008; DAGPEDOMAIN.
ProDom; PD000001; Prot_kinase; 1
SMART; SM00109; C1; 2.
SMART; SM00239; C2; 1.
SMART; SM00133; S_TK_X; 1.
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NP BIND
BINDING
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MOD RES
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                                                                                                                                                                                                                                                                   SEQUENCE OF 135-297 FROM N.A.
MEDILINE=88083621; PubMed=3691811;
Ono Y., Fujii T.; Ogita K., Kikkawa U., Igarashi K.,
"Identification of three additional members of rat pi
family: delta, epsilon- and zeta-subspecies.";
FEBS Lett. 226:125-128(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPCE_RAT
P09216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ono Y., Fujii T., Ogita K., Kikkawa U., Igo "The Structure, expression, and properties the protein kinase C family.",
J. Biol. Chem. 263:6927-6932(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88198270; PubMed=2834397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                             FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDEN SERINE- AND THREONIUS-SPECIFIC ENZYME.
FUNCTION: PKC IS ACTIVATED BY DIACYLGIXCEROL WHICH IN TURN PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
SIMILARITY: Contains 2
binding domains.
SIMILARITY: Contains 1
SIMILARITY: BELONGS TO
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0; Mismatches
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BY SIMILARITY.
                                     domain.
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      SER/THR FAMILY OF
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5. 7.2;
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                                                                                       phorbol-ester and
                                                                                                                                                                                                                                          PHOSPHOLIPID-DEPENDENT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of additional members
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      PROTEIN KINASES
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ALSO SERVES AS
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Best Local S
Matches 7
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ProDom; PD000001; Prot_kinase; 1.

SMART; SM00109; C1; 2.

SMART; SM00139; C2; 1.

SMART; SM00239; C2; 1.

SMART; SM00230; S_TKC; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PSS0004; C2 DOWAIN 2; 1.

PROSITE; PSS00479; DAG PE BIND DOM 1; 2.

PROSITE; PSS00479; DAG PE BIND DOM 2; 2.

PROSITE; PSS00107; PROTEIN KINASE DOM; 1.

PROSITE; PSS00107; PROTEIN KINASE DOM; 1.

PROSITE; PSS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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                                                                                Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schiz
                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00069; pkinase; 1.
Pfam; PF00433; pkinase_C; 1.
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InterPro; IPR002290; Ser thr pl
Pfam; PF00130; DAG_PE-bind; 2.
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InterPro; IPR002219; DAG_PB-bind.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                    Schizosaccharomyces.
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  SEQUENCE
                                       NCBI_TaxID=4896;
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PHORBOL-ESTER AND DAG BINDING 1.
PHORBOL-ESTER AND DAG BINDING 2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
MW; 6AD6999EFDD2659F CRC64;
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0; Mismatches
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Phorbol-ester binding;
                                                                                                                                                                                     ation update) chromosome I
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5. 7.2;
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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Comnor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Simmonds M., Squares S., McDonald S.,
RA Richerford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rodward J., Vonstreels E., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gobel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gerzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
"The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415: 817.180 (2002)
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Best Local
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Houssa B., Moolenaar
"Identification of a
                                                              MEDLINE=97344280; PubMed=9199174; Gebbink M.F.B.G., Kranenburg O.,
                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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30-MAY-2000
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SEQUENCE 7
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783 AA; 8
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                                                          Kranenburg O.,
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      novel, putative Rho-specific GDP/GTP exchange
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le exchange factor (Rho-interacting
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                                                              Poland M., van Horck F.P.G.
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Best Local
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PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50010; DH_2; 1.
Guanine-nucleotide releasing factor; Cc DOMAIN 99 266
                                                                                                                                                         TSM3_YEAST STANDARD; PRT; 89
P57743; Q05176; Q06759;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence updat
15-SEP-2003 (Rel. 42, Last annotation upd
U6 sNRNA-sasociated Sm-like protein LSm3
LSM3 OR SMX4 OR USS2 OR YLR438C-A.
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SEQUENCE
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SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEF; 1.
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DOMAIN
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                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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MGD; MGI:1346016; Rgnef.
InterPro; IPR002219; DAG PE-bind.
Tresponding CDS_CDC24.
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                MEDLINE=95262648;
                                     SEQUENCE FROM N.A.,
                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
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Pfam; PF00169; PH; 1.
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InterPro; IPR000219;
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1522
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PHORBOL-ESTER AND DAG BINDING.

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COILED COIL (POTENTIAL).

5 MW; 4E96087C449FF14C CRC64;
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Nuclear protei
RNA-binding,
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MEDLINE-97313/67; PubMed-9169871;

Johnston M., Hillier L., Riles L., Dubois E., Duesterhoeft A.,

Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,

Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,

Entian K.-D., Floeth M., Goffeau A., Hilger F., Kleine K., Koetter P.,

Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

Mueller-Auer S., Nentwich U., Ober-mier B., Piravandi E., Pohl T.M.,

Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,

Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,

Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the Ewropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
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                                                                                                         PIR; S78568; S78568.

SGD; S0006434; LSM3.
GO; GO:0017070; F:U6 snRNA binding ac GO; GO:0006371; P:mRNA splicing; IPI.
InterPro; IPR001163; snRNP_Sm.
Pfam; PF01423; Sm; 1.
                                                                                                                                                                                                                                                                       EMBL; Z30582; CAA83056.1; -.
EMBL; X06790; CAA29948.1; -.
EMBL; U21094; -; NOT_ANNOTATED_CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional analysis of the regulatory region adjacent to the cargB gene of Saccharomyces cerevisiae. Nucleotide sequence, gene fusion experiments and cis-dominant regulatory mutation analysis."; Eur. J. Biochem. 169:193-200(1987).
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an email to license@isb-sib.ch).
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                                              protein; Ribonucleoprotein; mRNA splicing; mRNA processing;
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P56354;
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SEQUENCE FROM N.A.
STRAIN-IAM C-27 / Tamiya;
STRAIN-IAM C-27 / Tamiya;
MEDLINE=97303241; PubMed=9159184;
Wakasugi T., Nagai T., Kapoor M.,
Tsudzuki J., Nakashima K., Tsudzu
                                                                                                                                    Eukaryota; Viridiplantae;
Chlorellaceae; Chlorella.
NCBI_TaxID=3077;
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Hypothetical protein.
SEQUENCE 115 AA; 1
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Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
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PIR; T07237; T07237;

HAWAP; MF 00403; -; 1

InterPro; IPR006032; Ribosomal S12_23.

InterPro; IPR005679; S12 bact chlorpl.

Pfam; PP00164; Ribosomal S12_2.

PRINTS; PR01034; RIBOSOWALS12.

PRODOM; PD000576; RIBOSOWALS12_23; 1.
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"Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella vulgaris: the existence of genes possibly involved in chloroplast division.";

Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).

-i- FUNCTION: With S4 and S5 plays an important role in translational accuracy. Located at the interface of the 30S and 50S subunits (B)
use by
                                                                                                                              TISSUE=Salivary gland;

MEDLINE=9220247; PubMed=1551898;

Keller P.M., Schultz L.D., Condra C., Karczewski J., Connolly T.M.

"An inhibitor of collagen-stimulated platelet activation from the salivary glands of the Haementeria officinalis leech. II. Cloning the CDNA and expression.";

J. Biol. Chem. 267:6899-6904(1992).
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Rhynchobdellida; Glossiphoniidae;
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PROSITE; PS00055; RIBOSOMAL S12; 1.

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SEQUENCE 123 AA; 13678 MW; F5DBCA65206664BD CRC64;
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              ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restriction by non-profit institute.
                                                                                        FUNCTION: AN INHIBITOR OF COLLAGEN-AGGREGATION, DENSE GRANULE RELEASE SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE S12P FAMILY OF RIBOSOMAL PROTEINS
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RESULT 11
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01-OCT-1996 (
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Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                               Vanderleyden J., Desair J., de Meirsman C., Michiels K., van Gool A.P., Chilton M.-D., Jen G.C.; "Nucleotide sequence of an insertion sequence (IS) element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumefaciens Plasmid pTiT37.
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01-NOV-1988 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; 3D-structure.
SIGNAL 1 2
                                                                                                                                                                                                                     Hypothetical 
SEQUENCE 1
                                                                                                                                                                                                                                            EMBL; X04282; CAA27829.1; -. PIR; S07372; S07372.
                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Rhizobiaceae; Rhizobium/Agrobacterium group; A
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PDB; 118N; 08-AUG-01.
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                                                                                                                                                                                                                                                                                                                                                                                                    in the T-DNA region of a spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86312927; PubMed=3018677;
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                                                                                                                       SSTPST 138
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Conservative
                                                                                                                                                                                                                    il protein; Plasmid;
159 AA; 16934 MW;
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(Rel. 34, Last sequence update)
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protein C6C3.02c in chromosome I
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                                                             STANDARD;
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IS136 hypothetical 16.9 kDa
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100.0%; Pred. No.
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ANTI-PLATELET PROTEIN
                                                                                                                                                                                                                    Transposable element.
EF0158ECE821EE6B CRC64;
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Asgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mngall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Skelton J., Simmonds M., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Berz P., Zimmermann W., Wedler H., Wambutt R., Punnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
"The genome sequence of Schizosaccharomyces pombe.";
"The genome sequence of Schizosaccharomyces pombe.";
"The SIMILARITY SOMP"
RESULT 12
CORA HPBV4
ID CORA H
AC P03150
DT 21-JUL
DT 01-FEB
DE Core a
GN C:
OS Hepati
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Best Local :
                                                                              CORA HPBV4 STANDARD;

P03150; P03151;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequent of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GeneDB_SPombe; SPAC6C3.02c;
InterPro; IPR007017; DUF657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z69731; CAA93615.1; -. PIR; T39026; T39026.
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Hepatitis B virus (subtype adr4)
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                                                              antigen
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RESULT 13
CORA HPBVJ
ID CORA HPE
AC P17391;
DT 01-AUG-1
DT 01-FEB-1
DE Core ant
OS Hepatiti
OC Viruses;
OX NCBI Tax
RN [1]
RR SEQUENCE
RA MEDLINE-
RA Okamoto
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SEQUENCE
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EMBL; X01587; CAA55745.1; -.
EMBL; D00331; -; NOT ANNOTATED_CDS.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes.";
J. Gen. Virol. 69:2575-2583(1988).
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Hepatitis B virus (subtype adw / strain Indonesia/pIDW420).
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10409, 106820, 10412;
MEDLINE=89010694; PubMed=3171552;
Okamoto H., Tsuda F., Sakugawa H.
                       SEQUENCE FROM N.A. MEDLINE=89010694;
                                                                                                                                                  Hepatitis B virus
                                                                                                                                                                            Core antigen.
                                                                                                                                                                                                    01-FEB-1991
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01-AUG-1990
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Miyakawa Y., Mayumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89010694; PubMed=3171552;
Okamoto H., Tsuda F., Sakugawa H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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"The complete nucleotide sequences of the cloned hepatitis B virus
DNA: subtrome adrand adw ".
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(Rel. 17, Last ann
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                                                                                                                                                                                                                                                                                                       STANDARD;
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Sakugawa H.,
                                                                                                                          Hepadnaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ED2DA1DB07FB596D CRC64;
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                  / strain Japan/pJDW233).
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InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
Core protein; Repeat.
REPEAT 162 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89010694; PubMed=3171552; Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; "Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes."; J. Gen. Virol. 69:2575-2583(1988).
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                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                             Core protein; Repeat.
REPEAT 162 16
REPEAT 170 17
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D00330; -; NOT_ANNOTATED_CDS.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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J. Gen. Virol. 69:2575-2583(1988).
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                                                                                                                                       Local Similarity
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21-JUL-1986
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EMBL; X02496; -; NOT_ANNOTATED_CDS.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
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Bichko V., Pushko P., Dreilina D., Pumpen P., Gren E.;
"Subtype ayw variant of hepatitis B virus. DNA primary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.; "Nucleotide sequence of the hepatitis B virus genome (subtype ayw) cloned in E. coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus (subtype ayw).
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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REPEAT 1
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Nature 281:646-650(1979).
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177
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80 A -> I (IN STRAIN LATVIA)
21116 MW; EOD9D9763F24E958 CRC64;
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Sp bacteria

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Sp human:*

Sp human:*

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Q9HHM3
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Q9H629
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Q8EWP2
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Q9EXP6
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OBn4y4 homo sapien
Q96ch9 homo sapien
Q9ulh6 homo sapien
Q9wn2 caenorhabdi
Q9hhm3 halobacteri
O16292 caenorhabdi
Q9hi4 thermoplasm
Q8h620 phytophthor
Q8ewp2 mycoplasma
Q9xf64 arabidopsis
Q9t1z6 arabidopsis
Q9t1z6 arabidopsis
Q8tlm7 methanosarc
Q8mr74 drosophila
Q8mr74 drosophila
Q8mr74 genorhabdi
Q9ims8 cherry mott
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hepatitis	hepatitis	hepatitis	hepatitis	Q8qp11 hepatitis b	hepa	Q8bwa6 mus musculu	Q8cft8 mus musculu	σ	ct	Q8f9t3 leptospira	3 methano		Q40111 lycopersico		hepatitis		Q8bk88 mus musculu	caenc	Q9uig2 homo sapien	plasm		O55597 garlic viru		Q9vx63 drosophila			œ	Q8tfy2 aspergillus

ALIGNMENTS

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SEPPPE
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Best Local Similarity 100.0%; Pred. No. 5:
Matches 35; Conservative 0; Mismatches
                                Q96CH9
Q96CH9;
Q1-DEC-2001
01-DEC-2001
01-OCT-2002
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033191; AAH33191.1; -.
NON TER 1
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SEQÜENCE 589 AA; 66086 MW; 8041EEA348DE65F7 CRC64;
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O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to KIA1244 protein (Fragment).
 Hypothetical
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Colon;
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(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
1 protein (Fragment).
s (Human).
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Q9XVN2;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
Submitted [2]
                                White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "KIĀA1244 as a novel distantly related member (BIG3) of the subfamily of ARF GEFs."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF413080; AAL04174.1; -. InterPro; IPR000904; Sec7. SMART; SM00222; Sec7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ULH6; Q96P46;
01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                   SEQUENCE FROM N.A.
                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Mammalia; Eutheria;
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Mammalia; Eutheria;
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llarity 100.0%;
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Primates;
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01-JAN-1998
01-MAR-2003
                                                                                                            016292
016292;
   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                            F32D1.6 protein.
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VNG6325H.
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01-MAR-2001
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Science 282:2012-2018(1998).
EMBL; Z81086; CAB03116.1; -.
                                 F32D1.6.
                                                                                                                                                                                                                                                                                                                                             Plasmid;
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Halobacteriaceae; Haloba
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88 AA; 9956 MW;
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Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Dale H., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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Pfam; PF00100; zona pellucida; 1.
SMART; SM00241; ZP; 1.
SEQUENCE 610 AA; 66585 MW; 09819
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Chromadorea; Rhabditida;

Rhabditoidea;

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EMBL; AL445067; CAC12486.1;
HSSP; P28692; 1EJO.
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20479972; PubMed=11029001; Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasm acidophilum.";
                                                                                                                                                                                    Hypothetical SEQUENCE 2
                                                                                                                                                                                                                     InterPro; IPR002877; FtsJ.
InterPro; IPR000051; SAM_bind.
Pfam; PF01728; FtsJ; 1.
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STRAIN=DSM 1728;
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01-MAR-2001
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Submitted (JUN-1999)
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"The sequence of C. elegans cosmid F32D1.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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cl protein; Complete proteome.
205 AA; 23194 MW; 96EB170D8CD6D8E1 CRC64;

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protein Tal365.
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01-NOV-1999
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Q8H6Z0;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.; "The complete genomic sequence of Mycoplasma penetrans, intracellular bacterial pathogen in humans."; Nucleic Acids Res. 30:5293-5300 (2002).

EMBL; AP004170; BAC43952.1; -.
Hypothetical protein; Complete proteome.
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                                                                                                                           Q9XF64
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
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"EST Mining and Functional Expression Assays Identify Extracellular Elicitor Proteins from Phytophthora.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Hypothetical protein.

Phytophthora infestans (Potato late blight fungus).

Phytophthora infestans (Potato late blight fungus).
                                                                                             Q9XF64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma penetrans. Bacteria; Firmicutes;
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01-MAR-2003
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MEDLINE=22354719; PubMed=12466555;
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SEQUENCE 208 AA; 23390 MW;
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7; Conserv
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o. 14;
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RESULT 11

Q9LZJ

Q9LZJ

D7 Q9LZJ

D7 01-Q0

D7 01-Q0

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                                                                                           Matches
                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/Ge
-: SMILLARITY: CONTAINS 1 RING-TYP
EMBL; AL162651; CABB3119.1; -
InterPro; IPRO01841; Znf ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS50089; ZF RING 2; 1.
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 257 AA; 28592 MW; B6B7
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Metal-binding; Zinc;
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Q9LZJ6;
01-OCT-2000
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-! SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AF132015; AAD33583.1; -.
InterPro; IPR001841; Znf ring.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
Metal-binding; Zinc-finger.
Metal-binding; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RING-H2 zinc finger
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                                                                                      Conservative
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28608 MW; 0
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1 RING-TYPE ZINC FINGER.
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dons; core eudicots; Rosidae;
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RESULT 12
Q8TLM7
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Best Local S
Matches
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01-JUN-2002
01-OCT-2002
FlyBase;
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00795; CN hydrolase; Hydrolase; Complete proteome. SEQUENCE 309 AA; 34100 MW.
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                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoā; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                              Submitted (JUN-2002) to the EMBL; AY122081; AAM52593.1;
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                    FROM N.A.
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arcinaceae; Methanosarcina.
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     341
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2 (TrEMBLrel. 21,
2 (TrEMBLrel. 22,
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  ΑA,
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PubMed=11932238;
     38533 MW;
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34100 MW;
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100.0%; Pred. No. 18
tive 0; Mismatches
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23,
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Last annotation updat
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                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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     EC614C84C65208CB CRC64;
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5. 18;
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                                                                                                            databases
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RESULT 15
Q21298
ID Q2129
AC Q2129
AC Q2129
DT 01-NE
DT 01-MA
DE K07F5
GN K
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QBNSR
ID QBNSR
AC COCYM
CGL GRACTE
OC COCYM
OX 
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Q8NSR7;
01-OCT-2002
01-OCT-2002
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                                                                                                                                                                                               "Genome sequence of the nematode C.elegans: A platform for investigating biology,"; Science 282:2012-2018 (1998).
EMBL; Z70284; CAA94285 4; --
WormPep; K07F5.14; CE29594.
SEQUENCE 422 AA; 48674 MW; 62F033819A0937A6 CRC64;
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Hypothetical protein; Complete proteome.
SEQUENCE 342 AA; 35227 MW; BCAB356CAA77F36B CRC64;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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K07F5.14.
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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     h 20.0%; Score 7; DB 5;
Similarity 100.0%; Pred. No. 24;
7; Conservative 0; Mismatches
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Similarity 100.0%; P
7; Conservative 0;
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(TrEMBLrel. 22, Last sequence update)
(TREMBLEL. 22, Last annotation update)
protein Cgl0601.
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f; Pred. No. 20;
O; Mismatches
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                                                                                                     Length 422;
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          Indels
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A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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180
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		180							Score
33.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query
1061	1982	1839	1807	518	518	518	35	35	Query Match Length DB
22	22	23	22	23	23	19	23	23	
ABB59318	ABG09731	ABP64835	ABG09728	AAM50809	AA019165	AAW85472	AAM50811	AA019167	ID
Drosophila melanog	Novel human diagno	Human protein SEQ	Novel human diagno	PS118 prostate mar	Human prostate-spe	PS118 protein enco		Human prostate-spe	Description

45		43	42	41 .	40	39	38	37	36	<u>ა</u>	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	. 16	15	14	13	12	11	10
53.5	54	54	54	54	54.5	54.5	54.5	4.	54.5	54.5	54.5	4.	4	٠.	4.	Α.	4.	۵.	55	55.5	56	56	56	56	56	56	56	56	56	56	57	57	58	59	59
29.7	30.0	30.0			•					•		•						٠	30.6		•	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	•	31.7	•	32.8	
542	712	600	351	337	2514	2514	2048	938	721	721	721	721	694	568	546	524	230	147	89	490	2047	102	102	102	102	102	102	102	102	102	530	345	73	1403	253
22	22	22	23	23	24	21	21	24	20	20	20	20	24	22	19	22	20	21	24	22	23	23	22	22	22	22	22	22	22	22	24	22	22	22	22
ABG21248	AAY97665	ABB63003	ABP28729	ABG32877	ABU06028	AAY75097	AAY75096	ABU06027	AAY38759	AAY38758	AAY38756	AAY38755	ABP79036	ABB59306	AAW78756 .	AAB47131	AAY38757	AAB33115	ABU02866	ABB44563	AAU75883	ABG37933	AAM03917	AAM28677	AAM16187	AAM68370	AAM56001	ABB20603	ABB29997	ABG50041	ABR40769	ABB70235	AAU42806	ABB60540	ABG06957
Novel numan diagno	dopsi	Drosophila melanog	prococcus pol	Frog zinc finger p	N. meningitidis va	B seria	Neisseria gonorrhe	N. lactamica vacci	N. gonorrhoeae ant	۳.	N. gonorrhoeae ant	Neisseria gonorrho	N. gonorrhoeae ami	Ħ	Human EYA3. Homo	CDIFF-10, Incyte I	Neisseria meningit	us radiata	S. pneumoniae type	Human wound healin		Human peptide enco	Peptide #2599 enco	#2714	Peptide #2621 enco		brain ex	Protein #2602 enco	Α.	Human liver peptid	Glycine max oil tr	Drosophila melanog	Propionibacterium	Drosophila melanog	Novel human diagno

ALIGNMENTS

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RESULT 1
AAO19167
 (BILL/)
(COHE/)
(COLP/)
(FRIE/)
(GORD/)
(GRAN/)
(HODG/)
(KLAS/)
                                                                                                                                                                     Human; prostate; prostate-specific sequence; prostate cancer; PS118; EST; expressed sequence tag; cytostatic; gene therapy.
                                                                                                                                                                                                                                  AA019167;
                                                                                                                                                                                                                                                   AAO19167 standard; Peptide; 35
                                                                           23-APR-1998;
23-APR-1997;
                                                                                                                     04-JUL-2002.
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                Human prostate-specific PS118 protein fragment
                                                                                                                                                                                                                 27-NOV-2002 (first entry)
                                                                                                    26-NOV-2001; 2001US-0991681.
                                                                                                                                     US2002086316-A1.
COLEN M.
COLPITTS T L.
FRIEDMAN P N.
GORDAN J .
GRANADOS E N.
HODGES S C.
KLASS M R.
                                                           BILLINGEL P A.
                                                                           98US-0065383.
97US-0842385.
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RESULT 2
AAM50811
          В
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Best Local
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      Billing-Medel
Granados EN,
                                                                                                                                                                                                               US2001055758-A1
                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                  PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                              PS118 prostate
                                                                                                                                                                                                                                                                                                                  01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                          AAM50811 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-665429/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Granados EN,
Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Billingel PA,
                                                                   (BILL/)
(COHE/)
(COPL/)
(FRIE/)
(GORD/)
(GRAN/)
(HODG/)
                                                                                                                                                    23-APR-1997;
                                                                                                                                                                       23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KRAT/)
(ROBE/)
(RUSS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                  sapiens
                                                            FRILL...
GORDON J.
GRANADOS E N.
TONGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) KRATOCHVIL J
) ROBERTS-RAPP
) RUSSELL J C.
) STROUPE S D.
                                     KLASS M R.
KRATOCHVIL J D.
ROBERTS-RAPP L.
                                                                                                                                BILLING-MEDEL
                                                                                                             COPLPITTS T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                      COHEN
                                                                                                                                                                                                                                                                                                                                                                                                           SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                             SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stroupe
                                                                                                                                                                                                                                                                                                                 (first entry)
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Hodges
        PA, Cohen
Hodges SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                             marker immunogenic
                                                                                                                                                    97US-0842385
                                                                                                                                                                        98US-0065383
                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58pp; English
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IM,
Klass
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Klass MR,
                                                                                                                                                                                                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
        Coplpitts TL, Friedman ass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 180; DB 23;
Pred. No. 1.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                              polypeptide
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       PN, Gordon J
Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gordan J;
Roberts-Rapp
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RESULT 3
AAW85472
ID AAW8
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of an immunogenic polypeptide comprising amino acids 283-317 of human prostate-specific PS18 polypeptide (see AM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, polymucleotides, antibodies, agonists and inhibitors are useful for detecting, antibodies, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostateic hyperplasia, prostateitis, prostatetatitis, prostatate, such as benign prostateic hyperplasia, prostaticis, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
WPI; 1998-610000/51
N-PSDB; AAV82812.
                                           Billing-medel PA,
Granados EN, Hod
Russell JC, Stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                    EST clone; PS118; prostate tumour tissue; prostatic disease;
                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                           AAW85472;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW85472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 44; 57pp;
                                                                                                                                     23-APR-1997;
                                                                                                                                                                                               29-OCT-1998
                                                                                                                                                                                                                           WO9848054-A1
                                                                                                                                                                                                                                                                                                                  PS118 protein encoded by consensus sequence
                                                                                                                                                                                                                                                                                                                                               25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-187683/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Russell JC,
                                                                                                        (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; ilarity 100.0%; Conservative 0;
                                           1 PA, Cohen M, Colpitts TL, Hodges SC, Klass MR, Krat Stroupe SD;
                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                    97US-0842385.
                                                                                                                                                                   98WO-US08239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 180; DB 23;
Pred. No. 1.2e-18;
; Mismatches 0;
                                                            3 TL, Friedman
Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35
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Best Local
                                 Billingel
Granados E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a cDNA library made from prostate tumour tissue. Recombinant PS118 protein is used to detect PS118-specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is
                                                                                                              (FRIE/)
(GORD/)
(GRAN/)
(HODG/)
(KLAS/)
                                                                                                                                                                     (COLP/)
                                                                                                                                                                                                                  23-APR-1998;
23-APR-1997;
                                                                                                                                                                                                                                                  26-NOV-2001; 2001US-0991681
                                                                                                                                                                                                                                                                          04-JUL-2002
                                                                                                                                                                                                                                                                                               US2002086316-A1
                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                          Human; prostate; prostate-specific sequence; prostate cancer; EST; expressed sequence tag; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                            Human prostate-specific PS118 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            AA019165
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO19165 standard; Protein; 518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostatic disease, particularly cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New P118 nucleic acid and proteins - used for diagnosis and treatment of prostatic disease, especially cancer, and also
                                                                                         (KRAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on 25-MAR-2003 to correct PI field.)
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2002-665429/71
                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                      COLPITTS T L.
FRIEDMAN P N.
GORDAN J.
GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Н
                JEN,
                                                                  ROBERTS-RAPP |
RUSSELL J C.
STROUPE S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 100.0%;
Similarity 100.0%;
35; Conservative (
                                                                                                                                                                                 BILLINGEL COHEN M.
                                                                                                  KLASS M R.
KRATOCHVIL J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                          PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 93-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518
                     Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                 Cohen
Hodges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş,
                                                                                                                                                                                                               98US-0065383.
97US-0842385.
                                                                                                                                                                                           PA.
                     SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117pp;
                                Colpitts TL,
Klass MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 180; DB 19;
Pred. No. 2.8e-17;
; Mismatches 0;
                                Friedman
Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317
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                                Roberts-Rapp L;
                                           Gordan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subjects at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for drug
                                                                                                                                                                                                                                                                                                                                                       PS118;
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RESULT 5
AAM/5080
ID AAM/508
XX AAM/508
XX AAM/508
AC AAM/5
XX AAM/508
XX PS11
XX PS12
XX PS12
XX PS13
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Best Local
                                                                                                                                                                                                            Billing-Medel PA,
Granados EN, Hod
Russell JC, Stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a
                        preventing or treating or disease -
                                          Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                   (COHE/)
(COPL/)
(FRIE/)
(GORD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS118; prostate; marker; prostate cancer; tumous benign prostatic hyperplasia; prostatic intraeps prostatitis; human; diagnosis; therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring prognosticating, preventing, treating, or determining predisposition individual to diseases and conditions of prostate, e.g. prostrate
                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 42-43;
                                                                                                                                                                                                                                                                                                                                       (KLAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                        (HODG/)
                                                                                                                                                                                                                                                                                                                                                                                                               (GRAN/)
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                                                                                                                                              2002-187683/24.
DB; ABA91651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
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                                                                                                                                                                                                                                                                                                           FRIEDMAN P N.
GORDON J.
GRANADOS E N.
HODGES S C.
KLASS M R.
KRATOCHVIL J D
ROBERTS-RAPP I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BILLING-MEDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COHEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 AA;
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                                                                                                                                                                                                                    Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                 PA, Cohen M, Coplpitts TL, Frid Hodges SC, Klass MR, Kratochvil Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0842385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0065383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marker; prostate cancer; tumour; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 518
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Pred.
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No. 2.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intraepithelial neoplasia;
                                                                                                                                                                                                                                        Friedman PN, Gordon J;
hvil JD, Roberts-Rapp L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
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                                                                     prognosticating,
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Best Local S
Matches 35
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo
                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                               Drmanac RT,
                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #9719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and reagents of the invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate than in non-prostate tissue. PS118 polypeptides, including derivatives of the present sequence, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostatic intraepithelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polynucleotides in transfected host cells. The methods
                                                                   Claim 20;
                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG09728 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of a human prostate-specific PS118 polypeptide, as predicted from a partial comeansus CDNA sequence (see ABA91651), and lacking the N-terminal region. The PS118 consensus sequence is found at least 12 times more often in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 42-43; 57pp; English
                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                 2001-639362/73.
DB; AAS73915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                 SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                               Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 1807
                                                              40087; 103pp;
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Pred. No. 2.8e-17;
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                                                                English.
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CC diagnostic amino acid sequences of the invention.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coaquiation disorder; nootropic; antiallergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide; immunostimulant; cerebroprotective.
                                                       New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders invaberrant protein expression or biological activity -
                                                                                                                                        WPI; 2002-590824/63.
N-PSDB; ABQ99421.
                                                                                                                                                                                                                                                                                                       17-NOV-2000; 2000US-0714936
                                                                                                                                                                                                                                                                                                                                                16-NOV-2001; 2001WO-US42950.
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35; Conserv
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ue AJ, Yang
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Pred. No. 1.2e-16;
                                                                                                                                                                                                   Zhou P, Asundi V,
an T, Drmanac RT;
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Claim 20; SEQ

ID 495;

394pp; English

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CC Note: The sequence data for this patent did not form part of the printed or ar fern winc nint much, while isolated on a segmence of the company of the printed of the printe
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Matches 35
                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167.
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     biodiversity
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                                                                                                                                                                                                                                                                                        WPI; 2001-639362/73.
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Pred. No. 1.2e-16;
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Best Local :
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                                                                                                                          WPI; 2001-656860/75
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11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 4746.
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                                                          New isolated nucleic acid
genes from Drosophila and
                                                                                                           N-PSDB; ABL03421.
                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                   27-SEP-2001.
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                                                          detection reagent for detecting 1000 for elucidating cell signalling and c
                                                                                                                                                                                                                                                                                                                                                                                                           biology; cell signalling; insecticide;
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Pred. No. 1.3e-16;
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Disclosure;

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4746; 21pp

+ Sequence Listing; English

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Query Match
polypeptide (II) sequences. (I) is useful as hybridisation prover, polypeptide (II) sequences. (I) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 37316; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167.
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Pred. No. 8.7;
4; Mismatches
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                                                                    capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABB73737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostics forensics, gene mapping, identification of mutations responsible for genetic disorders or client traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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11-JUL-2000;
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                           specification, but was obtained in electronic
at ftp.wipo.int/pub/published_pct_sequences.
                                          The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                       Disclosure; SEQ ID NO 8412; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                              genes from Drosophila
                                                                                                                                                                                                                                                                New isolated nucleic
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                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent
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15; Conser
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                                                                                                                                                                                                                                                 detection reagent for detecting for elucidating cell signalling
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Pred. No. 3.2;
5; Mismatches
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RESULT 12
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                                                                                                                                                                 C polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, CC pustulosis, hypertosis and osteomyelicis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes polypeptides and ct. therefore treat P. acnes infections. The antibodies may also be used as CC diagnostic agents for determining P. acnes presence, for example, by
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                                                                                  diagnostic agents for determining P. acnes press enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
      Sequence
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02-JUN-2000;
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, Jen S, Carter D
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5; Mismatches
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Query Match

32.2%;

Score

58;

DB

22;

Length

73;

RESULT 14 ABR40769

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ABR40769;

ABR40769

standard;

Protein; 530

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                                           Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG1840-ABL16175) and the encoded proteins
                                                                                                   Sequence
                                                                                                                                    (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
genes from Drosophila and
                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 37497; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABL14338.
                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 37497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
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                                                                                                                                                                                                                                                                                                           interactions
                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY.
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KESTGNSGGFAPTQVPQTDKVDQSSGHMDTS
                      ESSTPSTGGFSGKETPSEDDRSQSREHMGES
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                                                                                                   345 AA
                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental biology; cell signalling; insecticide;
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2000US-0614150.
                                                           31.7%;
38.7%;
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                                                           Score 57; I
Pred. No. 8.
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                                               Mismatches
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                                                         DB
1.9;
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                                                                         Length 345
                                                 Indels
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RESULT 15
ABG50041
ID ABG50
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AC ABG50
XX
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                                                                                                                                                                                                                                                            CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP) kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC cativity and CKC-like transcription factor activity. Also described:
CC (1) complement (II) of (I); (2) a chimeric construct (III) comprising (I)
CC or (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (Y); and
CC (5) oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC canola, Brassica, sorghum, sunflower or ACC00868 and ABR40591 to
CC CRARA0879 represent segments used in the account of the account.
                                                                                                                                                                                            Query Match
Best Local S
Matches 12
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shen
               ABG50041;
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 377-379; 542pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering oil phenotypes in plants such as sunflower, coconut, soybean, wheat a
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                                               ABG50041 standard;
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TJ, Kinney AJ,
B, Tarczynski MC;
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PIONEER HI-BRED INT INC.
                                                                                                                                                                                                             Similarity
                                                                                                                               NSTLPIGGLSGKNKNSTDSASESKSH 347
                                                                                                                                                           SSTPSTGGFSGKETPSEDDRSQSREH 31
                                                                                                                                                                                                                                                                                                           represent
                                                                                                                                                                                                                                                            530
                                                                                                                                                                                               Conservative
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                                               Peptide; 102
                                                                                                                                                                                                                                                                                                          sequences used
                                                                                                                                                                                                           31.7%;
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Klein
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epelbaum S, Famodu OO, Ha
Li C, Oliveira IC, Sakai
                                                                                                                                                                                                             DB 24; Length 530;
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Search completed: July 24, Job time: 14.3763 secs

2003, 11:53:40

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                                                                                                                   The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                         Matches
                                                                       Best Local
                                                                                  Query Match
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful analysing gene expression in human adult liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn
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03-AUG-2000;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000;
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                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC.
                          QSESSTPSTGGFSGKETPSEDDRSQSREHM 32
QNESQSPQ----EPEEGPSEDDKAEGEEEM
                                                                                                                   102 AA;
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000GB-0024263.
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2000US-0236359
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2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                          ID No 28689; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DK,
                                                                    31.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                      Score 56; DB Pred. No. 3; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28689.
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                                                                                     Length 102;
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                                                         Gaps
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Result
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Maximum |
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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52.5
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length: 2000000000
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180
1 SFQSESSTPSTGGFS
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1: /cgn
2: /cgn
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4: /cgn
5: /cgn
6: /cgn
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
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    GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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US-09-772-647-4
US-09-9772-647-4
US-08-910-925-1
US-08-93-118-10
US-08-645-1678-20-24
US-08-68-25-20-24
US-09-066-2818-10
US-09-107-5328-6475
US-09-107-5328-52
US-09-107-5328-52
US-09-107-5328-52
US-09-107-5328-20
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US-09-107-105-20
US-09-108-20-20-20
US-09-108-20-20-20
US-09-108-20-20-20
US-09-108-20-4120-357
US-09-528-419-30781
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US-09-526-4120-199
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20, Appl
1, Appli
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30781, App
195, App
195, App
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179, App
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27, Appl
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46.5	46.5	46.5	46.5	47	47	47	47	47	47.5	47.5	47.5	48	48	48.5	48.5	48.5	48.5
25.8	25.8	25.8	25.8	26.1	26.1	26.1	26.1	26.1	26.4	26.4	26.4	26.7	26.7	26.9	26.9	26.9	26.9
98	98	98	98	2509	2265	1704	365	300	590	590	590	714	432	568	568	568	335
2	N	N	N	N	N	w	N	4	4.	ω	w	4	4	σ	w	۲	4.
US-08-485-862B-50	US-08-486-756A-50	US-08-477-504A-50	US-08-481-658B-50	US-08-149-097D-35	US-08-149-097D-36	US-08-485-355B-40	US-08-481-814A-10	US-09-277-078-2	US-09-052-753B-2	US-08-821-818-2	US-08-893-852A-4	US-09-347-878-16	US-09-252-991A-31253	PCT-US94-04496-30	US-08-545-860D-30	US-08-320-559-30	US-09-106-872A-17
Sequence 50, Appl	Sequence 50, Appl	Sequence 50, Appl	Sequence 50, Appl	Sequence 35, Appl	Sequence 36, Appl	Sequence 40, Appl	Sequence 10, Appl	-	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 16, Appl	25	Sequence 30, Appl	Sequence 30, Appl	•	Sequence 17, Appl

ALIGNMENTS

LENGTH: 35 amino acida
8
; TELEPHONE: 847/935-1729
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REFERENCE/DOCKET NUMBER: 6084 US P1
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Y/AGENT INFORMAT
23-APR-
PRIOR APPLICATION DATA:
; CLASSIFICATION:
LICATION DATA:
COMPOURK: IBM COMPACIBLE
Bd
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: IL
Abbott Park
00 Abbott
ADDRESSEE: Abbott Laboratories
DENCE ADDRESS
R OF SEQUENCES: 33
OF INVENTION: FOR DETECTING DISEASE
NVENTION: REAGENTS
. APPLICANT: STROUBE STROUGN D
: ROBERTS-R
: KRATOCHVIL, JO
: KLASS, MICHAEL
: HODGES, STEVEN C.
GORDON, JULIAN
; APPLICANT: COLPITTS, TRACEX L.
: COHEN, MAURICE
: BILLING
GENERAL INFORMATION:
; bequeice 49, Applicación 68/09065365
201-1
10 00 00 100 30

amino acid

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RESULT 2
US-09-065-383-27
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                                                     US-09-065-383-27
*Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                   RECISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
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                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: REAGENTS AND MITTLE OF INVENTION: FOR DETECTING NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Abbott Park
                                                                                                                                                                                                     TELEFAX: 847/938-2623
                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                    amino acid
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                                                                                                                                518 amino acids
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RUSSELL, JOHN C.
STROUPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GORDON, JULIAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
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                                                                   No. 6391543e
                                                                                                    single
   100.0%;
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CTING DISEASES OF THE PROSTATE
   Score 180; DB 4;
Pred. No. 3.3e-17;
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                 Length 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
LENGTH: 737
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 1, Application US/08910925
Patent No. 6162601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Verma, Ajit K.
APPLICANT: Reddig, Peter J
APPLICANT: Jansen, Aaron P
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
FILE REFERENCE: 960296.97613
FILE REFERENCE: 960296.97613
CURRENT APPLICATION NUMBER: US/09/772,647
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Bandman
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                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,925
FILING DATE: Herewith
                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HU
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                 E: Incyte Pharmaceuticals, 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bandman,
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 PF-0365 US
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Pred. No. 26;
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Query Match 27.8 Best Local Similarity 42.4 Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5750395
GENERAL INFORMATION:
                                                                                                                                                                                                                                                        SOFTWARE: PATENTIN Release #1.0, Vers:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
PRIOR APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATMELE, STEVEN W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                           NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line
IMMEDIATE SOURCE:
LIBRARY: FIBRN
CLONE: 53219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amendations)
                                                                                                                                                                                                                            TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Enwarca
CITY: San Francisco
                                                                                                      TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                         TYPE: amino acid
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TELEFAX: 650-845-4166
                                                                                                                                                         ENGTH:
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Similarity 41.2%;
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amino acid
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                                                                                                                                                       309 amino acids
                                                                                                                                                                                                             415-576-0300
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                                                                                                          linear
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                  27.8%;
42.4%;
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 4; Mismatches
                  Score 50; DB 1; Length 309; Pred. No. 28;
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 13;
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; Sequence 10, Application US/08845528C
                                                                                                                                                                                                                    RESULT 7
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                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/845,528
FILING DATE: APPLICATION:
APPLICATION NUMBER: US/08/845,528
FILING DATE: APRIOR
APPLICATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5455
TELECOMMUNICATION INFORMATION:
                                                                        GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie,
APPLICANT: DE SMET, Charl
APPLICANT: BOON FALLEUR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LUCAS, Sophie;
APPLICANT: DE SMET, Charle;
APPLICANT: DE SMET, Charle;
APPLICANT: BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS;
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids STRANDEDNESS: single stranded TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                            27.8%;
                                                                                           Charles;
                ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES THEREOF
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                                                                             Thierry
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Pred. No. 28;
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Matches 14; Conserv
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FILING DATE: April 25, 1997
CLASSIFICATION: 4335
ATTORNEY/AGENT INFORMATION:
NAME: MARY Anne Schofield
REGISTRATION NUMBER: 56,669
REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 838-3884
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sinc
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-Apr-1996
CLASSIFICATION: -Unknown>
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fikes, John D.
                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE COMPLETE MAGE 1 GENE
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
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               APPLICATION NUMBER: US/08/103,623 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                              STATE: CA
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                                                                                                                                                                                                                                                                                               CITY: San Francisco
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805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Livingston, Brian D. Sette, Alessandro D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single stranded
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Pred. No.
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Query Match
Best Local Similarity
Matches 14; Conserv
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Best Local Similarity 42.4%;
Matches 14; Conservative
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                                                                                                                                                                                      TELEFAX: (212) 752-5958 INFORMATION FOR SEQ ID NO: :
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LUCAS, SC
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Lb.,
COMPUTER: Lb.,
OPERATING SYSTEM: PC-LC
OPERATING SYSTEM: PC-LC
OPERATION DATA:
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5455.2 US - JEL/MAS
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: April 24,
CLASSIFICATION:
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Filbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 318-3100
                                                                                                           TYPE: amino acids
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York City
                                                                                                                                                 ENGTH:
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TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 QGASAFPTTINFTRQRQPSEG--SSSREEEGPS 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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 Conservative
                                                                                              linear
                                                                                                         single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
: ISOLATED NUCLEIC ACID MOLECULE CODING
: FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
                 27.8%;
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                   Score 50; DB 4;
Pred. No. 28;
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Pred. No. 28;
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 Mismatches
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                                     Length 309;
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 Indels
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US-09-107-532A-6475
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                                                                         Sequence 5, Application US/08549004A Patent No. 5969101
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                        Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6475:
                   APPLICANT: PENDERGAST, APPLICANT: DAI, ZONGHAN TITLE OF INVENTION: ABL-
 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598

PILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

PILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...333
SEQUENCE DESCRIPTION: SEQ ID NO: 6475:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICATION NUMBER: US/09/107,532A
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                          162 STSSESSTENTSGESSTESTSSESSTENTSSESSTES 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCE CHARACTERISTICS:
LENGTH: 333 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                        27.8%;
40.5%;
ABL-INTERACTOR PROTEIN
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD/ROM IS09660
                                                         ANN MARIE
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                                                                                                                                                                                                                                                                                                        Score 50; DB
Pred. No. 30;
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                         DB 4; Length 333;
                                                                                                                                                                                                                                                                                      15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diak
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,004A
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
       COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,982A
FILING DATE: 08-JUL-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-193

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09051982A
Patent No. 6255074
GENERAL INFORMATION:
APPLICANT: PENDERGAST, ANN MARIE
APPLICANT: DAI, ZONGHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ABL-INTERACTOR PROTEIN
                                                                                                                                                                                                                                                                                                                     STREET: 1100 NOI
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 SVNQRNRTYSSSGSSGPSHPS--SRSSSRENSG
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                                                                                                                                                                                                                                                                                                                                                           E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
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(703) 816-4000
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linear
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Pred. No. 38;
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US-09-208-742-4
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                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 11
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Best Local S
Matches 14
                                                                                                                                                                                                APPLICANT: KAUfmann, Joerg
TITLE OF INVENTION: CIF130 INHIBITS CELL CYCLE PROGRESSION
FILE REFERENCE: 200130.456 / 1513.003
CURRENT APPLICATION NUMBER: US/09/332,295
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1261
TYPE: PRT
ORGANISM: human
S-09-208-742-4
                                                                   Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09332295
Patent No. 6303372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09208742
Patent No. 6174679
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kaufmann, Joerg
TITLE OF INVENTION: CIF150/hTAFII150 is Necessary for Cell
TITLE OF INVENTION: Cycle Progression
FILE REFERENCE: 1453.002
CURRENT APPLICATION NUMBER: US/09/208,742
CURRENT FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5;
SEQUENCE CHARACTERISTICS;
LENGTH: 401 amin.
                                                                                                                                                LENGTH: 1261
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 27.8%;
Local Similarity 36.7%;
les 11; Conservative
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mes 14; Conserv
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
840 NSREGTGGSNGKRERYTENRGSSRHSHGET 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                              840 NSREGTGGSNGKRERYTENRGSSRHSHGET 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 SVNORNRTYSSSGSSGPSHPS--SRSSSRENSG 212
                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 SSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMG 33
                               SSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                 27.8%;
36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.8%; Score 50; 42.4%; Pred. No.
                                                               Score 50; DB 4;
Pred. No. 1.5e+02;
5; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 3;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 401;
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                                                                                                 Length 1261;
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Search completed: July 24, Job time: 4.12592 secs

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US-09-709-979-2
                                                                                                                                                                                                                                                                                                                                                                PATENT NO. INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kaufmann, Joerg
APPLICANT: Kaufmann, Joerg
TITLE OF INVENTION: CIF130 INHIBITS CELL CYCLE PROGRESSION
FILE REFERENCE: 200130.456 / 1513.003
FILE REFERENCE: 200130.456 / 1513.003
FULL REPERENCE: 20010.1513.003
FULL REPERENCE: 20010.11-09
FULL REPERENCE: 2000-11-09
                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 1261
                                                                                     Query Match 27.8%;
Best Local Similarity 36.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09709979 Patent No. 6423822
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/332,295
PRIOR FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                      TYPE: PRT
840 NSREGTGGSNGKRERYTENRGSSRHSHGET 869
                                            6 SSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                          5
                                                                                        Score 50; DB 4;
Pred. No. 1.5e+02
5; Mismatches 1
                                                                                               14;
                                                                                                                                         Length 1261;
                                                                                             Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
Published Applications AA:*

1: /cgm2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgm2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgm2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgm2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*

6: /cgm2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

6: /cgm2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

7: /cgm2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgm2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgm2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

11: /cgm2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

12: /cgm2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

13: /cgm2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

14: /cgm2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

15: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

18: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

19: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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Gapop 10.0 , Gapext 0.5
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180
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15	14	13	12	11	10	9	80	7	თ	u	4	ω	N	مــو ،	Result No.
50	50	51	51	51	51	51	51	51	51	51	51	52.5	53.5	56	Score
27.8	27.8	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	29.2	29.7	31.1	Query Match
253	212	758	105	105	89	. 80	79	77	65	65	42	91	737	102	Length
9	11	9	10	10	10	10	10	10	10	10	10	14	15	9	BB
US-09-864-761-37733	US-09-764-891-4686	US-09-904-987-5	US-09-955-807-14	US-09-955-807-2	US-09-955-807-15	US-09-955-807-16	US-09-955-807-3	US-09-955-807-4	US-09-955-807-10	US-09-955-807-5	US-09-955-807-9	US-10-090-035-16	US-10-228-931-4	US-09-864-761-35901	ID
Sequence 37733, A	Seguence 4686, Ap	Sequence 5, Appli	Sequence 14, Appl	Sequence 2, Appli	Sequence 15, Appl	Sequence 16, Appl	Sequence 3, Appli	Sequence 4, Appli	Sequence 10, Appl	Sequence 5, Appli	Sequence 9, Appli	Sequence 16, Appl	Sequence 4, Appli	Sequence 35901, A	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	. 27	26	25	24	23	22	21	20	19	18	17	16
48	48	48	48	48.5	48.5	49	49	49	49	49	49	49	49	49.5	49.5	49.5	49.5	49.5	49.5	50	50	50	50	50	50.	50.	50	50	50
26.7	26.7	26.7	26.7	26.9	26.9	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.5	27.5	27.5	27.5	27.5	27.5	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8
699	444	324	121	724	550	2011	1776	821	683	489	331	331	331	2022	1908	737	515	232	99	1770	1261	1261	1031	856	428	413	309	309	275
15	10	15	11	10	15	15	φ	9	9	9	9	9	9	15	15	10	10	15	9	9	15	14	9	10	15	9	14	10	9
US-10-198-070-85	US-09-738-626-6577	-761	US-09-764-891-4135	US-09-925-300-1053	US-10-156-761-14105	US-10-176-847-56	US-09-841-132-179	US-09-841-132-195	US-09-841-132-357	US-09-876-889-350	US-09-815-242-13146	US-09-815-242-12872	US-09-815-242-5912	US-10-128-714-8475	US-10-128-714-3475	US-09-771-161A-195	US-09-801-368-384	US-10-156-761-12867	US-09-216-393-20	US-09-841-132-444	US-10-338-279-2	US-10-147-268-2	US-09-815-242-10932	US-09-738-626-3515	US-10-156-761-11846	US-09-801-574-2	US-10-085-108-10	US-09-766-889A-2	US-09-755-456-9
Sequence 85, Appl	657	Sequence 9761, Ap	4135,	•	Sequence 14105, A	e 56,	Sequence 179, App	195,	Sequence 357, App	•		Sequence 12872, A	5912,	Sequence 8475, Ap	3475,	195,	Sequence 384, App	e 128	Sequence 20, Appl	Sequence 444, App	'n	Sequence 2, Appli	10932,	Sequence 3515, Ap	Sequence 11846, A		_	Sequence 2, Appli	Sequence 9, Appli

ALIGNMENTS

APPLICANT: Rank, David K. APPLICANT: Harzel, David K. APPLICANT: Chen, Mensheng TITLE OF INVENTION: HUMAN EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1 CURRENT APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2001-05-23 PRIOR FILING DATE: 2000-02-04 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-27 PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00667 PRIOR APPLICATION NUMBER: PCT/US01/00667 PRIOR APPLICATION NUMBER: PCT/US01/00669 PRIOR APPLICATION NUMBER: PCT/US01/00669 PRIOR APPLICATION NUMBER: PCT/US01/00669 PRIOR APPLICATION NUMBER: PCT/US01/00669 PRIOR APPLICATION NUMBER: PCT/US01/00665 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00665 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00666	RESULT 1 US-09-864-761-35901 ; Sequence 35901, Application US/09864761 ; Patent No. US20020048763A1 ; GENERAL INFORMATION
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US-10-228-931-4
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APPLICANT: Verma, Ajit K
APPLICANT: Reddig, Peter J
APPLICANT: Jansen, Aaron p
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
FILE REFERENCE: 960296.97613
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US/10/228,931
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US/09/772,647
PRIOR FILING DATE: 2001-01-30
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 737
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Publication No. US20030051258A1
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SEQ ID NO 35901
LENGTH: 102
                                                                                                                                                      Matches
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NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: MAP TO AL096678.8
OTHER INFORMATION: EXPRESSED IN BT0417
OTHER INFORMATION: EXPRESSED IN BONE
THE THREE 
                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: T7 tag and OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/608,408
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327 AESPQPASG----NSPSEDDRSKS 346
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                                                       SESSTPSTGGFSGKETPSEDDRSQS
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N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

N: EXPRESSED IN LUNG, SIGNAL = 1.7

N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.96

N: EXPRESSED IN PLACTURA, SIGNAL = 0.96

N: EXPRESSED IN PLACTURA, SIGNAL = 0.98

N: EXPRESSED IN HELART, SIGNAL = 2.1

N: EXPRESSED IN HELAR, SIGNAL = 2.1

N: EXPRESSED IN HELA, SIGNAL = 1.2

N: EXPRESSED IN HELA, SIGNAL = 1.2
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                                                                                                                                                                                 Score 53.5;
Pred. No. 1.
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                                                                                                                                                  Mismatches
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RESULT 5
US-09-955-807-5
; Sequence 5, Ap
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US-10-090-035-16
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US-10-090-035-16
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                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 9
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CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 91
                                                                                                                                                                        Query Match
Best Local Similarity
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Matches 18; Conserv
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                                                                                                                                                        Matches
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Patent No. US20020132996A1
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                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Secretory Protein-48
FILE REFERENCE: 98-17C1
CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR PILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lok, Si
APPLICANT: Sheppa:
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                                                                                                                                                                                                                                                                           ENGTH: 42
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                                                                                      17 PAVTGFTGDSGAKETVSQDKRSQ 39
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                                                                                                                      9 PSTGGFSG----KETPSEDDRSQ 27
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                                                                                                                                                        Conservative
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Pred. No. 10;
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Pred. No. 1
                                                                                                                                                         Mismatches
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GENERAL INFORMATION: APPLICANT: Lok, Si

Sheppard, Paul O.

Sequence 5, Application US/09955807 Patent No. US20020132996A1

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RESULT 7
US-09-955-807-4
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-09-955-807-5
                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-955-807-10
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                                                    Sequence 4, Application US/09955807
Patent No. US/0020112996A1
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Sheppard, Paul O.
APPLICANT: Kindervogel, Wayne
APPLICANT: Bort, Susan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 65
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APPLICANT: Shepp
APPLICANT: Kinds
APPLICANT: BOTT,
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TITLE OF INVENTION: Secretory Protein-48 FILE REFERENCE: 98-17C1 CURRENT APPLICATION NUMBER: US/09/955,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Secretory Protein-48
FILE REPERENCE: 98-17C1
CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
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CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FITLE OF INVENTION: Secretory Protein-48
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Local Similarity 52.2%;
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                              Local
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5. US20020132996A1
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                                                                                                                                                                                                                                                                                                                           12; Conservative
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Similarity 52.2%;
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Kindsvogel, Wayne
Bort, Susan J.
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                                                  Kindsvogel, Wayne
Bort, Susan J.
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; Pred. No. 17;
3; Mismatches
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; Pred. No. 17;
3; Mismatches
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; SEQ ID NO 3
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-807-3
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PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 17
SOPTWARE: FASTSEQ for Windows Version 3.
SEQ ID NO 4
LENGTH: 77
APPLICANT: Lok, Si
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Wayne
APPLICANT: Kindsvogel, Wayne
APPLICANT: Bort, Susan J.
TITLE OF INVENTION: Secretory Protein-48
FILE REFERENCE: 98-17C1
CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
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US-09-955-807-3
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Best Local Similarity
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Patent No. US20020132996A1
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Best Local Similarity
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CURRENT FILING DATE: 2001-09-19
FRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
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APPLICANT: Sheppard, Paul O.
APPLICANT: Kindsvogel, Wayne
APPLICANT: Bort, Susan J.
TITLE OF INVENTION: Secretory Protein-48
FILE REFERENCE: 98-17C1
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52.2%;
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Pred. No. 21;
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Pred. No. 20;
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US-09-955-807-16
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TITLE OF INVENTION: Secretory Protein-48
FILE REFERENCE: 98-17C1
CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
SEQ ID NO 2
LENGTH: 105
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Best Local Similarity
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 80
TYPE: PRT
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APPLICANT: Lok, Si
APPLICANT: Sheppar
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LENGTH: 89
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Best Local Similarity
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                                                                                                      FILE REFERENCE: 98-17C1
CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
                                   SOFTWARE: FastSEQ
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NUMBER OF SEQ ID NOS: 17
                                                      NUMBER OF SEQ ID NOS:
                                                                                      PRIOR APPLICATION NUMBER: 09/410,603
                                                                                                                                                                                                TITLE OF INVENTION: Secretory Protein-48
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                                                                     PRIOR FILING DATE: 1999-10-01
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                                                                                                                                                                                                               Kindsvogel, Wayne
Bort, Susan J.
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Bort, Susan J.
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                                   for Windows Version 3.0
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Pred. No. 24;
3; Mismatches
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Pred. No.
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RESULT 13
US-09-904-987-5
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US-09-955-807-14
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                                                                         US-09-904-987-5
                                                                                                                                                                                                                     FILE REFERENCE: 42108/26146
CURRENT APPLICATION NUMBER: US/09/904,987
CURRENT FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: No. US20020037908Alactyl, Inc.

TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepathorititle OF INVENTION: Protein Assembly or Aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 14
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                                    Query Match
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CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
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                                                                                                                                               TYPE: PRT
ORGANISM: homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lok, Si
APPLICANT: Sheppa:
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                                                                                       DATABASE ACCESSION NUMBER: NCBI ENTREZ / NM_016835
DATABASE ENTRY DATE: 2001-02-13
RELEVANT RESIDUES: (1)..(758)
                                                                                                                                                                                                       ENGTH: 758
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Local Similarity 27.3
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les 12; Conserv
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Bort, Susan J.
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                 28.3%;
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 Mismatches

                 Score 51; DB 9; Length 758; Pred. No. 2.5e+02;
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Pred. No. 28;
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; OTHER INFORMATION: X
; NAME/KEY: SITE
; LOCATION: (205)
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US-09-764-891-4686
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US-09-764-891-4686
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SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 4686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37733, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserva
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                                                                                                                                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERNCE: Acendica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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TYPE: PRT
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                                   APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
                                                                            APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                 FILING DATE: 2000-10-04
  APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION
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Search completed: July 24, 2003, 12:18:18 Job time : 6.24832 secs

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NUMBER OF SEQ ID NOS: 49117
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LENGTH: 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
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APPLICATION NUMBER: US 60/234,687
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203 SDEQTPSRDDDSQSR 217
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                                                                     SGKETPSEDDRSQSR 29
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: EXPRESSED IN HBL100,
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ED IN HELA, SIGNAL = 1.9
ED IN PLACENTA, SIGNAL = 1.3
ED IN HEART, SIGNAL = 1.7
ED IN BT474, SIGNAL = 1.4
ED IN FETAL LIVER, SIGNAL = 1.7
ED IN BONE MARROW, SIGNAL = 1.4
ED IN LUNG, SIGNAL = 4.6
ED IN BRAIN, SIGNAL = 2.8
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US-09-991-681-29
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Sequence 8, Appli
Sequence 29, Appl
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CC	1378 1403 1403 1403 1403 73 73 73 245	200001229	467 518 1770 1770 1807 1839 1839 1839
30 30 30 31 31 31 31 31 31 31 31	31 31 31 28 28 30	1 27 28 20 20 31 31 31 31	12 25 1 27 1 1 30
US-09-708-427-73150 US-10-437-963-119781 US-09-791-537-48904 US-10-438-246-10453 US-10-438-246-10307 US-60-312-544-563 US-09-614-150-37497 US-60-191-637-37111 US-60-191-637-37111 US-60-191-681-28918 US-10-155-881-18359 US-10-155-881-18359 US-10-155-881-18358	US-60-167-217-8500 US-09-614-150-8412 US-60-173-464-6811 US-60-191-637-8436 US-60-191-681-6552 US-60-191-681-6552 US-00-978-825-4001 US-09-978-825-4001 US-10-057-498-4001 US-10-425-114-6612	-US01-08631-400 -US03-01943-30 -10-144-198-30 -10-221-279-778 -09-614-150-474 -60-167-217-486 -60-173-464-393 -60-191-637-476 -60-191-631-376 -00-191-631-376	-08-842-385-6 -09-991-681-27 -US03-01943-44 -10-144-198-44 -US01-08631-4008 -US01-42950-495 -10-416-993-495
Sequence 13150, A Sequence 119781, A Sequence 14904, A Sequence 10453, A Sequence 30307, A Sequence 37497, A Sequence 37497, A Sequence 3711, A Sequence 3711, A Sequence 31359, A Sequence 31359, A Sequence 3142, A Sequence 3143, A Sequence 3143, A Sequence 3143, A Sequence 3143, A Sequence 3794, Ap Sequence 40793, A Sequence 7974, Ap Sequence 18358, A	Sequence 8500, Sequence 8412, Sequence 8411, Sequence 8436, Sequence 6552, Sequence 4001, Sequence 4001, Sequence 5380, Sequence 5380,	e 4000 e 30, ce 30, ce 770 ce 474 ce 480 ce 480 ce 480 ce 470 ce 470 ce 373	Sequence 6, Sequence 27 Sequence 44, Sequence 400 equence 400 equence 495 Sequence 495

ALIGNMENTS

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RESULT 1

US-08-842-385-8

(Sequence 8, Application US/08842385

GENERAL INFORMATION:

APPLICANT: Russell, John
APPLICANT: Colpitts, Tracey
ITILE OF INVENTION: FOR DETECTING DISEASE OF THE PROSTATE

CORRESPONDENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA
ZIP: 6064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION NUMBER: US/08/842,385

FILING DATE:
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 100.0%; Score 180; DB 12; Local Similarity 100.0%; Pred. No. 9.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                           OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/991,681
FILING DATE: 26-Nov-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                    ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
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                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Abbott Park
                                                                                                                        APPLICATION NUMBER: 09/065,383 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                   STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRANADOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COHEN; MAURICE
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                                          6084.US.P1
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US-08-842-385-6
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                                                                                                                               US-08-842-385-6
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APPLICANT: Russell, JAPPLICANT: Colpitts,
                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 35; Conserv
                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,385
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
                                                                                                                                           TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                       LENGTH: 467 amino acids
                                                                                                                                                                                                                                                          TELEX:
                                                                                                                                                                                                                                                                         TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Abbott Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: None
232 SFOSESSTPSTGGFSGKETPSEDDRSOSREHMGES 266
                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60064-3500
                                                                                                                                                                                        amino acid
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                  SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08842385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 Abbott Park Road
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                                                               Conservative
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                                                                                                                                                            linear
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                                                                                                                                                                         single
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Pred. No. 9.3e-16;
); Mismatches 0;
                                                                             Score 180; DB 12;
Pred. No. 2.4e-14;
                                                               Mismatches
                                                                                              DB 12;
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                                                                                                                Sequence 44, Application PC/TUS0301943 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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Sequence 27, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               Matches
              APPLICANT: ORIGENE TECHNOLOGIES INC
TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
RIOR APPLICATION NUMBER: US 10/054,935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: line MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRATOCHVIL, JON D.

ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                    283 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                         1 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-NOV-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 847/938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 518 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09991681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRANADOS, EDWAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                           Score 180; DB 25;
Pred. No. 2.8e-14;
Mismatches 0;
                                                                                                                                                                                                                                    317
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                                                                                                                                                                                                                                                                                                               Indels
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                                                        PRIOR FILING DATE:
NUMBER OF SEQ ID NO:
SOFTWARE: Custom
SEQ ID NO 40087
                                                                                                                                                                                                                                                                                                                                        PCT-US01-08631-40087
                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-144-198-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                  Sequence 40087, Application PC/TUS0108631 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/10144198 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
                                                                                                                                         PRIOR APPLICATION NUMBER: 09/649,167
                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                      APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 10/197,824 PRIOR FILING DATE: 2002-07-19 NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 10/144,198 PRIOR FILING DATE: 2002-05-14
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PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/117,229
PRIOR FILING DATE: 2002-04-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                       ENGTH: 1807
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les 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/356,130
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                                                                                                   SEQ ID NOS:
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                                                                                                                      2000-08-23
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Pred. No. 1.3e-13;
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GENERAL INFORMATION:

APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: US/10/416,993
CURRENT FILING DATE: 2003-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-416-993-495
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Best Local Similarity
                                                             Matches
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Best Local Similarity
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SEQ ID NO 495
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LENGTH: 1839
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CURRENT APPLICATION UNMBER: PCT/US01/42950
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION UNMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
SOFTWARE: Patentin version 3.0
                                                                                                                                                                           LENGTH: 1839
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Helper component proteinase domain identified by PFam, OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Pusion glycoprotein F0 domain identified by eMATRIX, OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw score
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LOCATION: (941)..(950)
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SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
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                                                                          Score 180; DB 30;
Pred. No. 1.4e-13;
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PCT-US03-04508-32
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PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 40090
                                                                    Matches
                                                                                                          Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 037003/0301985
CURRENT APPLICATION NUMBER: PCT/US03/04508
CURRENT FILING DATE: 2003-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hyseq, Inc
                                                                                                                                                                 NAME/KEY: DOMAIN
LOCATION: (1065)..(1074)
OTHER INFORMATION: Helper component proteinase domain identified by PFam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (11)..(25)
OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX,
OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw sc
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 1982
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35; Conserv
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                                                                                      Similarity
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SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
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                                                                  Score 180; DB 1;
Pred. No. 1.5e-13;
Mismatches 0;
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Pred. No. 1.4e-13;
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Sequence 30, Application US/10144198
GENERAL INFORMATION:
APPLICANT: OFIGENE Technologies Inc
ITILE OF INVENTION: Regulated Prostate Cance Ger
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
RESULT 14
US-10-221-279-7783
; Sequence 7783, Application US/10221279
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: Novel Nucleic Acid
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-198-30
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US-10-144-198-30
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PRIOR APPLICATION NUMBER: US 10/054,935
PRIOR FILLING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/356,130
PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR FILLING DATE: 2002-02-14
PRIOR FILLING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/117,229
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR FILLING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/197,824
PRIOR FILLING DATE: 2002-07-19
PRIOR FILLING DATE: 2002-07-19
PRIOR FILLING DATE: 2002-07-19
PRIOR PRILING DATE: 2002-07-19
PRIOR FILLING DATE: 2002-07-19
PRIOR FILLING DATE: 2002-07-19
PRIOR FILLING DATE: 2002-07-19
PRIOR FILLING DATE: 2002-07-19
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LENGTH: 2221
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FILE REFERENCE: 3U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ORIGENE TECHNOLOGIES INC
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                                                                                                                                                                                      1986 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cn 100.0%; Score 180; DB 1; 1 Similarity 100.0%; Pred. No. 1.7e-13; 35; Conservative 0: Mismathham
                                                                                                                                                                                                                                                                                 35;
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                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                 Conservative
Novel Nucleic Acids and Polypeptides
                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                            Score 180; DB 27; Pred. No. 1.7e-13; ); Mismatches 0;
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; FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(141)
OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-221-279-7783
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GENERAL INFORMATION:
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SOFTWARE: Custom
SEQ ID NO 7783
                                                                             Matches
                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                  SEQ ID NO 4746
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                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/614,150 CURRENT FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DETECTION KIT, SUCH AS TITLE OF INVENTION: ARRAYS, FOR DETECTING TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Venter, J. Craig APPLICANT: et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/519,705 PRIOR FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/221,279
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 21272-046
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/173,383 PRIOR FILING DATE: 1999-12-28
                                                                                                                                                                                                LENGTH: 1
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                          ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/175,693 FILING DATE: 2000-01-12
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  39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 79.4%;
l Similarity 96.4%;
27; Conservative
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                                SESSTPSTGGFSGKETPSEDDRSQSRE 30
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SKSSRPSSAGVVIDETQSEEEESQSSE
                                                                             Conservative
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                                                                                             33.9%;
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                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 143; DB 28;
Pred. No. 3.6e-10;
0; Mismatches 1;
                                                                                             Score 61; DB 20;
Pred. No. 2.3e+02;
65
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EXPRESSION OF 10,000 OR MORE
                                                                                                               Length 1061;
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Search completed: July 24, 2003, 12:15:13 Job time: 53.7306 secs

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB DB
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                                                                                                           44.5
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length: 2000000000
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140.227 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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180
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(cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*
(cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*
(cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*
(cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
(cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
(cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
(cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
  SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
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                                                           US-10-367-978-32

US-10-370-480-28

US-60-479-073-296

PCT-US02-35624-173

US-10-273-573-890

US-10-294-433-286

US-10-294-433-289

US-10-273-573-10678

US-10-273-573-10878

US-10-273-573-10878

US-10-273-573-10878

US-10-372-209-13

US-10-372-209-13

US-10-372-209-13

US-10-372-209-13

US-10-373-573-6327

US-10-373-573-6327

US-10-294-433-293

US-10-294-433-396

PCT-US02-1683-15

US-10-294-433-396

PCT-US03-1694-15
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                                       32, Appl
296, Appl
296, Appl
9796, Appl
8906, Appl
10678, Appl
3144, Appl
3144, Appl
118, Appl
118, Appl
118, Appl
118, Appl
12, Appl
13, Appl
1623, Appl
623, Appl
623, Appl
623, Appl
6423, Appl
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	41.5	41.5	42	. 42	42	. 42	42	42.5	42.5	42.5	42.5	42.5	42.5	42.5	43	43	43	43.5	43.5
•	23.1	23.1	23.3	23.3	23.3	23.3	23.3	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.9	23.9	23.9	24.2	24.2
	282	152	1627.	787	630	140	74	793	753	609	439	402	131	131	2041	1994	937	846	250
	δ	σ	σ	σ	7	δ	δ	_	7	7	7	v	6	6	σ	6	7	7	σ
	US-10-273-573-8747	US-10-294-433-849	US-10-433-757-5	US-10-372-227-43	US-60-478-196-3344	US-10-273-573-10371	US-10-273-573-7515	PCT-US03-11867-4	US-60-479-073-437	US-60-479-073-439	US-60-478-196-3261	US-09-635-359B-19	US-10-273-573-7876	US-10-273-573-7534	US-10-294-433-338	US-10-294-433-339	US-60-478-196-3207	US-60-478-196-3082	US-10-273-573-7905
	Sequence 8747, Ap	Sequence 849, App	Sequence 5, Appli	Sequence 43, Appl	Sequence 3344, Ap	Sequence 10371, A	Sequence 7515, Ap	Sequence 4, Appli	Sequence 437, App	Sequence 439, App	Sequence 3261, Ap	Sequence 19, Appl	Sequence 7876, Ap	Sequence 7534, Ap	Sequence 338, App	Sequence 339, App	Sequence 3207, Ap	Sequence 3082, Ap	Sequence 7905, Ap

ALIGNMENTS

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APPLICANT: Hitachi LTD.
TITLE OF INVENTION: ADDB INTERACTING PROTEINS ANI
FILE REFERENCE: HITA.0167
CURRENT APPLICATION NUMBER: US/10/370,480
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 60/358,319
PRIOR PILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/407,252
PRIOR APPLICATION NUMBER: US 60/407,252
PRIOR APPLICATION NUMBER: US 60/407,252
PRIOR FILING DATE: 2002-09-03
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-10-367-978-32
; Sequence 32, Application US/10367978
; GENERAL INFORMATION:
; APPLICANT: GATELY, DENNIS
; APPLICANT: GATELY PROSTATE SPECIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 1872
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-978-32
                                                                                                                                                                                                                                                                                                                                                                                                              US-10-370-480-28
                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/10370480 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 180; DB 6; Best Local Similarity 100.0%; Pred. No. 1.4e-16; Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
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CURRENT APPLICATION NUMBER: US/10/367,978
CURRENT FILING DATE: 2003-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1637 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 1671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-273-573-9796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-60-479-073-296
                                                                                                                                         ; SOFTWARE: Custom
; SEQ ID NO 9796
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-573-9796
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                                                                                                                                                                                                                                                                                                                                 Sequence 9796, Application US/10273573
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.2
SEQ ID NO 296
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                                                                                          Best
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TITLE OF INVENTION: Amino acid sequences useful for developing compounds
TITLE OF INVENTION: prevention and/or treatment of metabolic diseases an
TITLE OF INVENTION: sequences encoding such amino acid sequences.
FILE REFERENCE: D00590.70042.US
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
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CURRENT FILING DATE: 2003-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Saunders, Michael John Scott
APPLICANT: Logghe, Marc Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: De Wilde, Gert Jules Hector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2047
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                                                                                          Local
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                                                                                        Similarity
                                  ESSTPSTGGF-----SGKETPSEDDRSQSREHMGE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSESSTPSTGGFSGKETPSEDDRSQSREHM 32
EPPTPGDGGCVPRSGSRPRDAQEAPNPDIRSQHKVHTNE
                                                                     Conservative
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                                                                                        28.1%;
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Pred. No.
                                                                                      Score 50.5;
Pred. No. 3.
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                                                                     Mismatches
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                                                                                                        DB 6; Length 233;
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PCT-US02-35624-173
                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Custom
SEQ ID NO 8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 12; Conserv
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SEQ ID NO 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 173, Application PC/TUS0235624 GENERAL INFORMATION:
                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: PCT/US02/35624
CURRENT FILING DATE: 2003-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Skeiky, Yasir A. W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Corixa Corporation APPLICANT: Maisonneuve, Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 10994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hyseq,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(817)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                                                                                         OTHER INFORMATION: Elongation factor 1 beta/beta'/delta chain proteins domain OTHER INFORMATION: identified by eMATRIX, accession number BL00824B, p-value=7.130e-OTHER INFORMATION: 10, raw score of 9.21
                                                                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (478)..(498)
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 817
                                                                                             Local Similarity
329 SESEGPOKGPASDSETEDASRHKOKPESDDDS-DRENKGE 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    704 SSESGSSTPQDGGAASSGAPSGDQSISANACLAKS 738
                                                                             16;
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                                     SESSIPSIGGESGKET--
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Probst, Peter
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                                                                           Conservative
                                                                                           27.2%;
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Pred. No. 29;
                                     ----PSEDDRSQSREHMGE 34
                                                                                             Score 49; DB Pred. No. 22;
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                                                                         Mismatches
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                                                                                                            Length 817;
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                                                                             Indels
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RESULT 8
US-10-273-573-10678
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US-10-294-433-286
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CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/US01/14826
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/989,600
PRIOR APPLICATION NUMBER: 09/989,600
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR APPLICATION NUMBER: 10/115,831
                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                        SEQ ID NO 10678
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                                                                 Matches
                                                                                                                                        ORGANISM: Homo sapiens
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILLING DATE: 2002-10-18
CURRENT FILLING DATE: 2002-10-18
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PRIOR FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/775,330
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 864
SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-294-433-286
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PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
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                                                                                                                                                                                                                                            SOFTWARE: Custom
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                                                                                                                                                                                    TYPE: PRT
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TYPE: PRT
                                                                                 Local
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APPLICATION NUMBER: 09/715,869
FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 10/115,831
FILING DATE: 2002-04-02
APPLICATION NUMBER: 09/677,298
FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/695,781 FILING DATE: 2000-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402
ch 26.1%; l Similarity 38.5%; 10; Conservative
                                                                                                                                                                                                       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10273573
                                                          ; Score 47; DB
; Pred. No. 13;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 6; Length 402; Pred. No. 13;
                                                                                                  DB 6; Length 301;
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                                                            10; Indels
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RESULT 11
PCT-US02-18638A-188
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                                                                                                                                                                                                                                                                                                APPLICANT: Hu, Wengi
APPLICANT: Hu, Wengi
APPLICANT: Roemer, Terry
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF ASPERGILLUS FUMIGATUS AND ME
TITLE OF INVENTION: USB
TITLE OF INVENTION: USB
FILE REFERENCE: 10182-026-888
CURRENT APPLICATION NUMBER: US/60/478,196
CURRENT FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 4000
SOFTWARE: Patentin version 3.1
SEQ ID NO 3.14
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SOFTWARE: Custom
SEQ ID NO 8991
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Best Local (
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                 LENGTH: 42
TYPE: PRT
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LOCATION: (649)..(669)
COTHER INFORMATION: CORONAVIRUS NUCLEOCAPSID PROTEIN domain identified by
OTHER INFORMATION: eMATRIX, accession number DM01206B, p-value=4.646e-09,
OTHER INFORMATION: 10.69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 1189
                                                                                                                                                 Local Similarity
nes 13; Conserv
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ilarity 39.4%;
Conservative
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Pred. No. 60;
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Pred. No. 23
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Sequence 188, Application PC/TUS0218638A GENERAL INFORMATION:

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Best Local Similarity
Matches 10; Conserv
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SEQ ID NO 12
LENGTH: 186
                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 13
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LENGTH: 743
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                                                                                                                  APPLICANT: Hitachi, Ltd.
TITLE OF INVENTION: RBM5-INTERACTING PROTEINS AND USE THEREOF FILE REFERENCE: HITA.0169
CURRENT APPLICATION NUMBER: US/10/372,209
CURRENT FILING DATE: 2003-02-25
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TITLE OF INVENTION: RBM5-INTERACTING PROTEINS AND USE THEREOF
FILE REFERENCE: HITA.0169
CURRENT APPLICATION NUMBER: US/10/372,209
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/358,723
PRIOR PLING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
                                                        PRIOR APPLICATION NUMBER: US 60/358,723
PRIOR FILING DATE: 2002-02-25
NUMBER OF SEQ ID NOS: 19
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PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
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CURRENT APPLICATION NUMBER: PCT/US02/18638A
CURRENT FILING DATE: 2002-06-12
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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 282
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US-10-380-565-34
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LENGTH: 282
TYPE: PRT
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LENGTH: 565
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CURRENT APPLICATION NUMBER: US/10/372,209
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/358,723
PRIOR FILING DATE: 2002-02-25
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/380,565
CURRENT FILING DATE: 2003-06-17
PRIOR APPLICATION NUMBER: PCT/GB01/04053
PRIOR FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                               APPLICANT: Cooper, Joseph I
APPLICANT: Naylor, Martin
TITLE OF INVENTION: Method and primers for detecting viral genes
FILE REFERENCE: 0380-P03334USO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hitachi, Ltd.
TITLE OF INVENTION: RBM5_INTERACTING PROTEINS AND USE THEREOF
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                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: GB 0022505.2
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ORGANISM: Homo sapiens
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33.3%;
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ALIGNMENTS

RESULT A40580

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hypothetical protein F7A7.180 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T48187 C;Accession: T48187 R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAIternate manees: probable nucleoside triphosphate binding protein lodestar (Species: Drosophila melanogaster)

NAIternate names: probable nucleoside triphosphate binding protein lodestar (Species: Drosophila melanogaster

C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 21-Jul-2000

C;Accession: A40580; S19008

R;Girdham, C:H.; Glover, D.M.

Genes Dev. 5, 1786-1799, 1991

A;Reference number: A40580; MUID:92009170; PMID:1916263

A;Accession: A40580
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                                                                                       A; Map position: 5
A; Introns: 65/3; A; Note: F7A7.180
                                                                                                                                                                       A;Reference number: Z24487
A;Accession: T48187
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-621 <BEV>
A;Cross-references: EMBL.AL161946
A;Experimental source: cultivar Columbia; BAC clone F7A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: lodestar
A;Cross-references: FlyBase:FBgn0002542
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A; Residues: 1-974 <GIR>
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Query Match
Best Local Similarity
Matches 12; Conserv
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Best Local :
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mes 14; Conserv
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                                                                                                            263/3; 289/3; 403/1; 469/3; 495/2; 529/2; 592/3
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    Conservative
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51.9%;
                    31.1%;
Score 56; DB Pred. No. 20; 6; Mismatches
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Pred. No. 7.2;
4; Mismatches
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x;rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Pet on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, I nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus, A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Raccession: B95010
A;Raccession: B95010
hemagglutinin/hemolysin-related protein NMB1768 [imported] - Neisseria meningitidis (str
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: F81045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, A; Title: Genome of the Bacterium Streptococcus pneumonia A; Reference number: A97872; MUID:21429245; PMID:11544234 A; Accession: H97881
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A;Residues: 1-89 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK74275.1; PID:g14971554; GSPDB:GN00164;
A;Experimental source: strain TIGR4
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A; Residues: 1-89 < KUR>
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Best Local S
Matches 10
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Pred. No. 3.8;
9; Mismatches
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E.J.; Lu, J.; Matsushima, P.; McAhren,
                                                                                                                                                                                                                                                                                                                                       DB 2;
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pneumoniae St
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                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 11-Jun-1999
C;Accession: B28163; B26408; S00216
R;Ono, Y; Fujii, T; Ogita, K; Kikkawa, U; Igarashi, K; Nishizuka, Y.
J. Biol. Chem. 263, 6927-6932, 1988
A;Title: The structure, expression, and properties of additional members of
                                                                                                                                                                                                                       protein kinase C (EC 2.7.1.-) epsilon - rat
C;Species: Rattus normali---
  A; Molecule type: DNA
A; Residues: 1-737 < O
                                               A; Accession: B28163
                                                                   A;Title: The structure, expression, and properties of additional members of A;Reference number: A92717; MUID:88198270; PMID:2834397
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ri, H.; Qin, H.; Vamathevan, V., Vandathevan, V., Vandath
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A;Molecule type: DNA
A;Residues: 1-715 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Theologis, A.; Ecker, J.R.; Palm,
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A; Residues: 1-2514 < TET>
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    SASSSTSSPTIGGLSLLFSGASVKSSSSSSSSHPSVGE
                                                                         SFQSESSTPSTGG----FSGKETPSEDDRSQSREHMGE 34
                                                                                                                                                           Conservative
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B, strain MC58
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                                                                                                                                                                                                  Score 54;
Pred. No.
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.;
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                                                                                                                                                                                                  DB
42;
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strain MC58.
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; Dewar, K.;
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A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl C;Superfamily; protein kinase C delta; protein kinase C zinc-binding repeat homology; processes: Aff; autophosphorylation; duplication; phorbol ester binding; phospholipid by F;156-161/Region: pseudophosphorylation motif F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>F;443-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>F;406-668/Domain: protein kinase C zinc-binding repeat homology <KZ2>F;404-422/Region: protein kinase homology ctills
F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Hstatus predicted F;183,186,209,212/Binding site: zinc (His, Cys, Cys, Hstatus predicted F;256,259,281,284/Binding site: zinc (His, Cys, Cys, Hstatus predicted F;356,329,281,284/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted F;303,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
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F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZI>
F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;403-668/Domain: protein kinase c zinc-binding metif
F;414-422/Region: protein kinase homology <KINN
F;414-422/Region: protein kinase ATP-binding motif
F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,209,212/Binding site: zinc (Gys, Cys, His, Cys) #status predicted
F;243,273,276,292/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted
F;2437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F;703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase C (EC 2.7.1.-) epsilon - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
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A;Residues: 397-447,'GQRGLHDDREEDFGSGAET',467,'LSNPTLLLLPDQGPPLLRQ',487-545,'C',547-636.
A;Cross-references: GB:M15523; NID:g206192; PIDN:AAA41877.1; PID:g206193
C;Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene a
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R;Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
A;Title: Isolation of cDNA clones enco61109 protein kinase C: evidence for a protein kina A;Reference number: A94145; MUID:87147193; PMID:3469647
A;Accession: B26408
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A; Residues: 1-737 <SCH>
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A;Accession: S02270
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A, Title: Unique substrate specificity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic
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Best Local
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                                                                        l Similarity
12; Conser
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SESSTPSTGGFSGKETPSEDDRSQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.J.; Bristol, A.; Kriz, R.; Knopf, J.
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Pred. No. 50;
5; Mismatches
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                                                                    <u>ن</u>
                                                                                                          Score 53.5;
Pred. No. 50;
                                                                        Mismatches
28
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A;Reference number: G08875
A;Accession: G01936
A;Status: preliminary; translated fi
A;Molecule type: mRNA
A;Residues: 1-390 <REN>
A;Cross-references: EMBL:U31089; NII
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Lennard, N.
submitted to the EMBL Data
submitted to the EMBL Data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein K11D2.4 - C;Species: Caenorhabditis elega C;Date: 15-Oct-1999 #sequence_r C;Accession: T23604; T26115
                                                                                                                                                                                                                                                                                                                                                Abl binding protein 3 - human C;Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence C;Accession: G01936
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                                                                                                                                                                A;Gene: AblBP3
C;Superfamily: SH3
F;335-382/Domain:
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A; Introns: 46/1; 103/1;
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RESULT 11
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A; Cross-references: EMBI
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A;Accession: T23604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:U31089; NID:g987264; PID:g987265
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13; Conserv
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                                                                        SFQSESSTPSTGGFSGKETPSEDDRSQSREHMG
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                                                                                                       Conservative
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                                                                                                                    29.4%;
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                                                                                                                    Score 53;
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Pred. No.
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hypothetical

protein

Y38H6C.14

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Caenorhabditis elegans

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RESULT 13
C86337
R?Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Waiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A;Cross-references: EMBL:Y16563; NID:g3413503; PIDN:CAA76287.1; PID:g3413504
A;Experimental source: strain Sprague Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: brain-specific synapse-associated protein C;Species: Rattus norvegicus (Norway rat) C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T26702
                                                                                                                                                                                                                                    hypothetical protein P14O10.5 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002 C;Accession: C86337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A;Reference number: Z22249; MUID:98345363; PMID:9679147 A;Accession: T42761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, J. Cell Biol. 142, 499-509, 1998
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A; Residues: 1-814 <WIL>
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A;Experimental source: clone Y38H6C
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Pred. No.
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    Query Match
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-775 <YAM>
C;Superfamily: collagen a:
C;Keywords: coiled coil; (
                                                                             Invest. Ophthalmol. Vis. Sci. 32, 2924-2930, 1991
A;Title: Cloning of alpha1(IV) and alpha2(IV) collagen cDNAs
A;Reference number: A61228; MUID:92010685; PMID:1717398
A;Recession: A61228
                                                                                                                                                                                                                                                         RESULT 15
A61228
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S51037
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A;Accession: S06565
                                                                                                                                                                             collagen alpha 2(IV) chain precursor - rabbit C;Species: Oryctolagus cuniculus (domestic rab C;Date: 12-May-1994 #sequence_revision 12-May-C;Accession: A61228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 85-448,'K',450-613 <NIE>
A;Experimental source: clone XlcGF20-1
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C;Keywords: DNA binding; zinc finger
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R;Nietteld, W.; El-Baradi, T.; Mentzel, H.;
J. Mol. Biol. 208, 639-659, 1989
A;Title: Second-order repeats in Xenopus lac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: not compared with conceptual translation
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A;Molecule type: DNA
A;Residues: 1-675 <SCH>
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C;Accession: S51037; S06565
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C; Superfamily: mitochondrial inner membrane protein TIM17
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J. Biochem. 226, 567-576, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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7; Mismatches
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Pred. No. 71;
8; Mismatches
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Knoeche

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Score Pred.

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Length

Page 5

Search completed: July Job time : 5.86969 secs	Qy Db 1	Matches
leted 5.869	9 PS 	15;
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11:5	QKGEI	ω ~:
58:05	SEDDRSQSREHMGE 34 : : : PYALSEEDRDRYRGEIGE 18	3; Mismatches
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Query Match
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Matches 14
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01-JUN-1994
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SITE
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SEQUENCE
Mueller-Taubenberger A.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E1).

-i- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                          P36413;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dihydrolipoamide acetyltransferase component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ODP2
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EMBL; AE003576; AAF54167.1; -
FlyBase; FBgn0002542; Ids
GO; GO:0008094; F:DNA dependent aden
GO; GO:0006353; P:transcription term
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                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=AX2;
                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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SMART; SM00490; HELICC;
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InterPro; IPR001650; Helicase C.
InterPro; IPR00130; SNP2 N.
Pfam; PF00271; helicase C; 1.
Pfam; PF00176; SNP2 N; 1.
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SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00364; biotin lipoyl.

Pfam; PF00364; biotin lipoyl; 2.

Pfam; PF02817; e3 binding; 1.

ProDom; PD001115; 20xoacid_dh; 1.

TIGRPAMS; TIGR01349; PDHac_trf_mito; 1.

PROSITE; PS00189; LIPOYL; 2.

Glycolysis.
                                                                                                                     MDN1 HUMAN STANDARI
Q9NU72; C1501;
28-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, I
28-FEB-2003 (Rel. 41, I
                                                                                                                                                                                    HUMAN
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TRANSIT
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                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                           Midasin (MIDAS-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001078; 20xoacid_dh.
InterPro; IPR0006257, Acef long.
InterPro; IPR000089; Biotin lipoyl.
InterPro; IPR0004167; E3_binding.
InterPro; IPR003016; Lipoyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U06634; AAA16511.1; -. HSSP; P10515; 1FYC. DictyDb; DD05070; dlaA.
                                           NCBI_TaxID=9606;
                                                                                  Homo sapiens (Human)
                                                                                                MDN1 OR KIAA0301.
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COFACTOR: THE E2 COMPON
COFACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: 20 TO 30 ALPHA(2)-BETA(2) TETRAMERS OF E1 + 6 HOI OF E3 + 60 COPIES OF E2.
SUBCELLULAR LOCATION: Mitochondrial matrix.
SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY SIMILARITY: Contains 2 lipoyl-binding domains.
                                                                                                                                                                                                                                    262
                                                                                                                                                                                                                                                           ۳
                                                                                                                                                                                                                                                                                  l Similarity
14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide; Lipoyl.
                                                                                                                                                                                                                                  SSSSQESTPSSSSSSSSSSSSSSSSSQQTTRKSGE
                                                                                                                                                                                                                                                           SFQSESSTPSTGGFSGKE-TPSEDDRSQSREHMGE
                                                           Eutheria;
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592
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158
258
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360
82
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64424
                                                            Primates;
                                                                      Chordata;
                                                                                                                                                                                                                                                                                              31.9%;
40.0%;
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                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                     MW.
                                                                                                           protein)
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E3 BINDING SITE (BY SIMILA
CATALYTIC (BY SIMILARITY).
LIPOYL (BY SIMILARITY).
LIPOYL (BY SIMILARITY).
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۲۰
                                                                                                                                                                                                                                                                                  Score 57.5; DE Pred. No. 6.3; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           LIPOYL BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                              DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION
                                                           Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                     30D0989F88D55BB7 CRC64;
                                                                                                                                                                          5596
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                                                                                                                                                                        A
                                                            Hominidae;
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EMBL; AL096678; CAB86660.1; -.

EMBL; AL096678; CAB86661.1; -.

EMBL; AB00229; BAA20761.1; -.

Genew; HGNC:18302; MDN1.

GO; GO:0005634; C:nucleus; NAS.

GO; GO:0016867; F:ATPase activity; NAS.

GO; GO:001687; F:Chaperone activity; NAS.

GO; GO:0003754; F:chaperone activity; NAS.

GO; GO:0003754; AAA, ATPase.

InterPro; IPR002035; VWF A.

Ffam; PF00004; AAA; 1.
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BMC Genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N. Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain code for large proteins in vitro."; DNA Res. 4:141-150(1997).
                                                                                                                                                                        NP_BIND
                                                                                                                                                                                                                                                                           Pfam; PF00004; AAA; 1.
SMART; SM00382; AAA; 7.
SMART; SM00327; VWA; 1.
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                                                                                         SEQUENCE
                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tracey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1255-2356 AND 3550-5596 TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garbarino J.E., Gibbons I.R.; "Expression and genomic analysis conserved AAA protein distantly BMC Genomics 3:18-18(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97349984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 3550-5596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSUE=Brain;
4932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear (By 8 SIMILARITY: Contains 1 VWFA domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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12; Conserv
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QNESQSPQ----EPEEGPSEDDKAEGEEEM
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                                          Score 56; DB
Pred. No. 1.3e
6; Mismatches
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related to dy
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RESULT
FXN3_HU
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Riting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
Thuman and mouse cDNA sequences.",
Tat Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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000409; Q961
30-MAY-2000
   EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROWEN L., Madan A., Qin S., Abbasi N., Baradarani L., Birditt B., Bloom S., Dors M., Dickhoff R., Fleetwood P., Harrison G., James Kaur A., Madan A., Owen M.P., Rattcliffe A., Shaffer T., Hood L.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR THAT MAY BE INVOINT DNA DAMAGE-INDUCIBLE CELL CYCLE ARRESTS (CHECKPOINTS).
                                                                                                              between the Swiss Institute of Bioinformatics and the It the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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30.-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Checkpoint suppressor 1 (Forkhead box protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                         Note=No experimental confirmation available; -!- SIMILARITY: Contains 1 fork-head domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2;
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U68723; AAB58252.1; -.
BC007506; AAH07506.1;
AC007263; AAF18259.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=000409-2;
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RA WOOD V., Gwilliam R., Rajandréam M.A., Lyne M., Lyne R., Stewart A.,
RA WOOD V., Gwilliam R., Rayles J., Basham D., Bowman S.,
RA Sqouros J., Peat N., Hayles J., Basker S., Basham D., Bowman S.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Huntt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moseft D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galbert F., Aves S.J., Xiang Z.; Hunt C., Moore K., Hurst S.M.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galbert M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Crutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR GO; GO:0003700; F:transcription factor activity; TAS.

R GO; GO:0000077; F:DNA damage checkpoint; TAS.

R GO; GO:0000055; F:G2 phase of mitotic cell cycle; TAS.

R InterPro; IPR001766; TF Fork head.

Pfam; PF00250; Fork head; 1.

R PRINTS; PR00053; FORKHEAD.

R PROSITE; PR000425; TF Fork head; 1.

R PROSITE; PS00657; FORK HEAD_1; 1.

R PROSITE; PS00657; FORK HEAD_2; 1.

R PROSITE; PS00658; FORK HEAD_2; 1.

R PROSITE; PS00658; FORK HEAD_3; 1.

R PRO
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Best Local
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16-ОСТ-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C543.04 in chromosome II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHPO
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Genew; HGNC:1928; CHES1.
MIM; 602628; -.
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TRANSFAC; T04204; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPBC543.04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.5%;
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Pred. No. 9
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EE07975A592C8C01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPDIDAASAMMLLNTPPEIQAGF -> V (in isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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RESULT
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RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer E.G., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blacy R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blacy R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gherson K.Y., Benos P.V., Berman B.P., Bhandari D., Deviss P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dubbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
Downstream of son
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005365; UPF0171. Pfam; PF03666; UPF0171; 1.
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-i- SIMILARITY: BELONGS TO THE UPF0171 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
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40, Last annotation update)
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46.4%;
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92F53DFB5AC1BE59 CRC64;
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EYA3_HUMAN

EYA3_HUMAN

Q99504; 095463; Q99813;

15-JUL-1998 (Rel. 36, Created)

1 30-MAY-2000 (Rel. 39, Last sequence upda

1 30-MAY-2003 (Rel. 41, Last annotation upda)
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Hypothetical
SEQUENCE 56
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                                                                                                                                                                                                                                                                                                  Abdelhak S., Kalatzis V., Heilig R., C
Vincent C., Weil D., Cruaud C., Sahly
Bitner-Glindzicz M., Francis M., Lacom
Charachon R., Boven K., Bedbeder P., v
Weissenbach J., Petit C.;
"A human homologue of the Drosophila e
branchio-oto-renal (BOR) syndrome and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
"Cloning and characterization Drosophila eyes absent gene."; Genome Res. 7:128-141(1997).
                                                                                         Genin A., Spinner
Bonini N.M.;
                                                                                                             MEDLINE=97202104; PubMed=9049631;
Zimmerman J.E., Bui Q.T., Steingr
Genin A., Spinner N.B., Copeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97172972; PubMed=9020840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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nilarity 36.8%;
Conservative
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568 AA; 6
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Pred. No. 15;
5; Mismatches
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Lacombe D., Vigneron J.,
P., van Regemorter N.,
                                                                      two
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Y I., Leibovici
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                                                                                                             N.A.,
                                                                   homologs of
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a novel gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "EYA4, a novel vertebrate gene related to Drosophila eye
Hum. Mol. Genet. 8:11-23(1999).
-!- FUNCTION: MAY BE INVOLVED IN DEVELOPMENT OF THE EYE.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                      InterPro; IPR005545; EYA.
InterPro; IPR005834; Hydrolase.
Pfam; PF00702; Hydrolase; 1.
TIGRPAMS; TIGR01658; EYA-cons domain;
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EMBL; U81602; AAB42066.1; -.
EMBL; AJ007991; CAA07814.1;
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Banfi S., Gattuso C., Ma:
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                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q99504-2; Sequence=VSP_001493;
Note=No experimental confirmation available;
SIMILARITY: BELONGS TO THE EYA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative
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                   15;
                          Similarity
  SFQSE-----
                                                                                                    Conservative
                                                                                                                                                                                                                                                       protein; Multigene family;

1 126 Missing (in

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P:vision; TAS.
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                                                           62558
                          30.3%;
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Mariani M., Dixon M., Donnai D., Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splicing; Named isoforms=2;
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                         Score 54.5;
Pred. No. 1
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IN REF. 2)
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N REF. 2).
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P. 2).
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                                   BB
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                                                   CRC64;
                                  Length 573;
                   Indels
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Metcalfe K.,
 32
                   15;
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                  Gaps
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MEDLINE=21099286; PubMed=11168356;
Wang Z., Vandenberghe I., Depreitere J., Devreese B., Clerens S.,
Nouwen E.J., Van Beeumen J., De Potter W.;
"Identification and characterization of novel chromogranin B-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., SEQUENCE SPECTROMETRY OF 606-622 (MONG FORMS); 623-656 AND 657-667,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Secretogranin I precursor (SgI) (Chromogranin
Peptide SR-17; Peptide HQ-34; Peptide KR-11).
                                                                                                                 PRINTS; PR00659; CHROMOGRAVII.

PROSITE; PS00422; GRANINS_1; 1.

PROSITE; PS00423; GRANINS 2; FALSE NEG.
Sulfation; Cleavage on pair of basic re
                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptides fom porcine chromaffin granules by liquid chromatography/electrospray tandem MS."; Bur. J. Biochem. 268:235-242(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                         SIGNAL
                                                                                                                                                                                     EMBL; AF284349; AAG13399.1; -. 30; GO:0030141; C:secretory granule; IEP. 30; GO:0006887; P:exocytosis; NAS. InterPro; IPR001819; Chromogranin_AB. InterPro; IPR001990; Granin.
                                                                                                         Phosphor
                                                                                                                                                                             Pfam; PF01271; Granin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Neuroendocrine secretory granule protein, which may the precursor for other biologically active peptides.
SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory
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MASS SPECTROMETRY: MW=2034.04; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granules.
PTM: Peptide SR-17 exists in both monophosphorylated
                                                                                                                                                                                                                                                                                                                                                                                      most probably an artifact of isolation.
                                                                                                                                                                                                                                                                                                                                                                                                  CAUTION: Observed oxidation
                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622 with one phosphate group.

MASS SPECTROMETRY: MW=2115.42; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with two phosphate groups.
S SPECTROMETRY: MW=3815.56; METHOD=Electrospray;
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622
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667
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Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UENCE OF 342-356; 475-492 AND 606-668, MASS (MONOPHOSPHORYLATED AND DIPHOSPHORYLATED
       SECRETOGRANIN I.
SR-17.
HQ-34.
KR-11.
BY SIMILARITY.
SULFATION (BY SIMILARITY).
                                                                                                                      of basic residues;
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                                                                                                                                                                                                                                                                                                                                                                                                   in Ref.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHOD=Electrospray; RANGE=657-
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                                                                                                                   Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                  sulfoxide
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Matches 16
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01-APR-1990 (Rel. 1
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Protein kinase C, 6
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MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98127436; PubMed=9467942; Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H., Mushinski J.F.; Wang Q.J., acs P., Goodnight J., Blumberg P.M., Mischak H., Wushinski J.F.; The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and epsilon chimeras, is responsible for conferring tumorgenicity to NIH3T3 cells, whereas both regulatory and catalytic domains of NIH3T3 cells, whereas both regulatory and catalytic domains of
                                                                                                   use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt
           EMBL; AF028009; AAB84189.1;
EMBL; AF325507; AAG53692.1;
PIR; S02270; KIMSCE.
HSSP; P28867; 1PTQ.
                                                                                                                                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There \varepsilon
                                                                                                                                                                                                                                                                                                                                                                            Wheeler D.L.,
Submitted (DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89137541; PubMed=2917656; Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.; Schaap D., Parker p.J., Bristol A., Kriz R., Knopf J.; "Unique substrate specificity and regulatory properties PKC-epsilon: a rationale for diversity."; FEBS Lett. 243:351-357(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                       or send an
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKC-epsilon contribute to in vitro transformation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein kinase C, epsilon PRKCE OR PKCE OR PKCEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P16054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPCE MOUSE
                                                                                                                                                                                                                                                                            SERINE- AND THREONINE-SPECIFIC ENZYME.
FUNCTION: PKC IS ACTIVATED BY DIACYLLYCEROL WHICH IN TURN
FUNCTION: PKC IS ACTIVATED BY DIACYLLYCEROL WHICH IN TURN
PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES
THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
                                                                                                                                                                                                                                                                                                                                                          nitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT.
                                                                                                                                                                                                                 SIMILARITY: BELONGS PKC SUBFAMILY.
                                                                                                                                                                                                                                  SIMILARITY: Contains 1 C2 domain. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF
                                                                                                                                                                                                                                                             binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93
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16; Conser
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                                                                                       equires a license agreement (S email to license@isb-sib.ch).
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Last annotation update)
ilon type (EC 2.7.1.-) (
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Pred. No. 24;
3; Mismatches
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                                                                                                                        Usage
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RESULT 10

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InterPro; IPR0007290; Ser_thr_pkinase.
InterPro; IPR0002290; Ser_thr_pkinase.
Pfam; PP00168; C2; 1.
Pfam; PP00130; DAG PE-bind; 2.
Pfam; PP00033; pkinase; 1.
Pfam; PP00433; pkinase; 1.
PRINTS; PR000008; Prot_kinase; 1.
PRINTS; PR000008; Prot_kinase; 1.
SMART; SM00109; C1; 2.
SMART; SM00109; C2; 1.
SMART; SM00109; C2; 1.
SMART; SM00109; C2; 1.
SMART; SM00109; C7; 1.
SMART; SM00220; S_TKC; 1.
SMART;
SEQUENCE OF 135-29/ FROM SEQUENCE OF 135-29/ FROM SEQUENCE OF 135-29/ FROM SEQUENCE OF 135-29/ PubMed=3691811;
ONO Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Ono Y., Fujii T., Ono Y., Ono Y.,
                                                                                                                                                                                                                                              MEDLINE-88198270; PubMed=2834397;
Ono Y., Fujii T., Ogita K., Kikkawa U., Iga
"The structure, expression, and properties
the protein kinase C family.";
J. Biol. Chem. 263:6927-6932(1988).
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NP_BIND
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InterPro; IPR002219; DAG PE-bind.
InterPro; IPR000961; Pkinase C.
InterPro; IPR000961; Prot kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPCE_RAT STANDARD; PRT; 737 AA.

P09216;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
PRKCE OR PKCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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Serine/threonine-protein
DOMAIN 1 99
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Rodentia;
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C2 DOMAIN.
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PHOSPHORYLATION (AUTO-)
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Phorbol-ester binding;
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No. 27;
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les of additional members
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RESULT 11

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(Rel. (Rel.

37, Created)
37, Last sequence update)
41, Last annotation update)
AT band 60B (Minifly protei

protein).

STANDARD;

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Matches 12
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R Pfam; PF00433; pkinase C; 1.

R PRINTS; PR00008; DAGPEDOMAIN.

R PRINTS; PR000001; Prot kinase; 1.

R SMART; SM00109; C1; 2.

R SMART; SM00139; C2; 1.

R SMART; SM00239; C2; 1.

R SMART; SM00239; S_TKC; 1.

R SMART; SM00239; S_TKC; 1.

R SMART; SM00249; DGG_PE_BIND_DOM_1; 2.

R PROSITE; PS500047; DGG_PE_BIND_DOM_2; 2.

R PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.

R PROSITE; PS500107; PROTEIN_KINASE_BOM; 1.

R PROSITE; PS500107; PROTEIN_KINASE_BOM; 1.

R PROSITE; PS500108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS500108; PROTEIN_KINASE; Phosphorylation; Serine/threenine-protein kinase; Phosphorylation; Zin Serine-protein kinase; Phosphorylation; Zin Zin Zin Zin Zin 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000719; Prot_kina
InterPro; IPR002290; Ser_thr_p
Pfam; PF00158; C2; 1.
Pfam; PF00130; DAG_PE-bind; 2.
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FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS. SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.

SIMILARITY: Contains 1 C2 domain.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKC SUBFAMILY.
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327
                                                     4
                                                                                                                l Similarity
12; Conserv
                                        SESSTPSTGGFSGKETPSEDDRSQS
AESPOPASG----NSPSEDDRSKS
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IPR000961; Pkinase_C.
IPR000719; Prot_kinase.
IPR002290; Ser_thr_pkinase.
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                                                                                                                Conservative
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83478
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220
292
668
422
437
703
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                                                                                                                                                                                                                                          MW.
                                                                                                                                                                                                                                C2 DOMAIN.

PHORBOL-ESTER AND DAG BINDD
PHORBOL-ESTER AND DAG BINDD
PHORBOL-ESTER AND DAG BINDD
PHOTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (PC
PHOSPHORYLATION (AUTO-) (PC
PHOSPHORYLATION (AUTO-) (PC
PHOSPHORYLATION (AUTO-) (PC)
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Pred. No.
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346
                                                                                                                            3.5;
27;
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                                                                                                                                                                           Length
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RA Adams D.D. (Calniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Kichards S., Assburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Assburner M., Henderson S.N., RA George R.A., Chewis S.E., Richards S., Assburner M., Henderson S.N., RA George R.A., Chewis S.E., Richards S., Assburner M., Henderson S.N., RA Sutton G.G., Wolt G., Baster E.G., G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Bellew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Buch P., Bhandari D., Bolshakov S., Canter A., Chardra I., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Chardra I., Ra Borkova D., Betchan M.R., Bouck J., Brokstein P., Brottier P., Borthies P., Burtis K.C., Chardra I., Cadieu E., Center A., Chardra I., Ra Gebeson K., Doup L.E., Downes M., Dayenport L.B., Davies P., Bartis R.M., Glaster M., Claster S., Klub D., Dew I., Dietz S.M., Dowles P., Bartis R.M., Glaster K., Galbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyawn C., Katchum K.A., Marris M., Kulp D., Lai Z., Kulp D., Lai Z., Ling Y., Lin X., Lia K., Lin X., L
                                               use by
                                                                                                                                                                                       This
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Science 287:2185-2195(2000)
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MEDLINE=99189256; PubMed=10087258;
Giordano E., Peluso I., Senger S., Fu
"minifly, a Drosophila gene required
"minifly, a Drosophila gene required
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MEDLINE=99045289; PubMed=9
Phillips B., Billin A.N.,
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Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE TRUB F/SIMILARITY: Contains 1 PUA domain.
                                                                                                                                                                                                                                                                                  FUNCTION: PLAYS A CENTRAL ROLE IN RIBOSOMAL RNA PROCESSING.
SUBCELLULAR LOCATION: Nuclear; nucleolar.
SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES
                                                                                                             European Bioinformatics Institute.
                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         functions in yeast.";
Gen. Genet. 260:20-29(1998).
       non-profit institutions as long and this statement is not removed requires a license agreement (See
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in A.N., Cadwell C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.";
removed. Usage by and fo
ent (See http://www.isb-sib.
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ed for ribosome biogenesis.";
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RESULT 12
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SEQUENCE FROM N.A.
MEDLINE=95094815; PubMed=8001572;
MEDLINE=95094815; PubMed=8001572;
Schaefer U., Rausch O., Bouwmeester T.
"Sequence-specific recognition of a re
"Sequence-specific recognition of a re-
"Sequenc
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Best Local
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Pfam; PF01509; TruB N; 1.
SMART; SM00359; PUA; 1.
TIGRFAMS; TIGR00425; CBF5; 1
PROSITE; PS50890; PUA; 1.
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SEQUENCE
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as 
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01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Gastrula zinc finger protein XFG20-1 (XLCGF20.1).
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P18714;
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EMBL; AF089837; AAD16092.1; --
EMBL; AE003463; AAF47178.1; --
                                                                                                                       EMBL; X82643;
PIR; S51037; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nietfeld W., El-Baradi T
Poeting A., Knoechel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0023184; Nop60B.
InterPro; IPR004802; Cbf5.
InterPro; IPR002478; PUA.
InterPro; IPR002501; TruB_N.
                                                                                                                                                                                                                 or send an
                                                                                                                                                                                                                                               entities requires
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Nietfeld W., El-Baradi T., Mentzel H.,
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                -order repeats in Xenopus laevis finger proteins."; Biol. 208:639-659(1989).
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294 369 PUA.
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POLY-ALA.
POLY-LYS.
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Pred. No. 23;
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; Pipidae;
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TRANSFAC;

IPR007087; Zn: 0096; zf-C2H2; T02366;

Znf_C2H2. H2; 18.

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Best Local :
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ZN FING
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SMART; SM00355; ZnE
PROSITE; PS00028; 2
PROSITE; PS50157; 2
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=88217329; PubMed=2966922;

Rothwell V.M., Rohrschneider L.R.;

Rothwell V.M., Cloning, sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P09581; Q9DBH9;
01-MAR-1989 (Rel. 10, Created)
01-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Macrophage colony stimulating factor I receptor
(EC 2.7.1.112) (Fms proto-oncogene) (c-fms).
CSFIR OR CSFWR OR FMS.
MEDIJINE-21085660; PubMed=11217851;
MEDIJINE-21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                                                                                                                            STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                       Oncogene
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                             "Reassessment
                                                                                                                                                                                Parseval N., Bordereaux D., Giss eassessment of the murine c-fms peasessment Acids Res. 21:750-750(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
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62 84
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373 395
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5; znf C2H2; 18.
5; znc FINGER C2H2_1; 17.
1028; zINC FINGER C2H2_2; 18.
10157; zINC FINGER C2H2—2; 18.
10157; ביחding; DNA-binding; Repeat.
                                                                                                           N.A.
6J; TISSUE=Liver;
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37.5%;
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Pred. No. 38;
8; Mismatches
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MSD; Pllsb4, — Gefir.

MGD; MGI:1339758; Cefir.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig c2.

R InterPro; IPR003056; Ig MHC.

R InterPro; IPR0000719; Prot kinase.

InterPro; IPR001824; RTKinaseIII.

ThterPro; IPR001245; Tyr pkinase.

NOT_ANNOTATED_CDS

pfam; pF00047; ig; 4.

pfam; pF00069; pkinase; 1.

proDom; pF0000001; Prot kinase; 2.

proDom; pF0000001; Prot kinase; 2.

sNART; SM00408; IGc2; 1.

sMART; SM00219; TYrKc; 1.

pROSITE; pS50835; IG_LIKE; 4.

pROSITE; pS50835; IG_LIKE; 4.

pROSITE; pS500107; pROTEIN KINASE DOM; 1.

pROSITE; pS50011; PROTEIN KINASE TYR; 1.

pROSITE; PS500109; PROTEIN KINASE TYR; 1.

pROSITE; PS001040; RECEPTOR TYR KIN III; 1.

pROSITE; PS00240; RECEPTOR TYR KIN III; 1.

proto-oncogene; Tyrosine-protein kinase; Receptoroncogene; Tyrosine-protein kinase; Re

domain;

Repeat

Receptor; Transmon; ATP-binding;

Transmembrane; nding; Signal;

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Kuehl P., Lewis S., Matsuo Y., NIKALUU I., FUNCTION SCHITMI L.M., Staubli F., Suzuki R., Tomita M., Washio T. Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van der Geer P., Hunter T.;

"Identification of tyrosine 706 in the kinase insert as the major colony-stimulating factor 1 (CSP-1)-stimulated autophosphorylation site in the CSP-1 receptor in a murine macrophage cell line.";

Mol. Cell. Biol. 10:3991-3002(1990)

-i- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTITYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93268269; PubMed=8497248; Yue X., Favot P., Dunn T.L., Cassady A.I., Hume D.A.; "Expression of mRNA encoding the macrophage colony-stirexpression of is controlled by a constitutive prome specific transcription elongation."; [6]. Cell. Biol. 13:3191-3201(1993).
                                                                                                                                                                                                                                                                                                      EMBL; X06368; CAA29666.1; ALT_SEQ.
EMBL; AK004947; BAB23691.1; -.
EMBL; S62219; -, NOT_ANNOTATED_CDS
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                               send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                         European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It een the Swiss Institute of Bioinf.
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                                                                                                                                                                                                                                                                                                                                                                               s requires a license agreement an email to license@isb-sib.c
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CSF-1/PDGF
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RECEPTOR
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RESULT 14
KFMS_RAT
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Matches 12
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Q00495;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
(EC 2.7.1.112) (Fms proto-oncogene) (c-fms).

CSFIR OR CSFMR OR FMS.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Murinae; Rattu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
CARBOHYD
CONFLICT
CONF
                                          STRAIN-Wistar; TISSUE-Skeletal muscle;
MEDLINE-33001225; PubMed=189227;
BOTYCKI A.G., Guillier M., Leibovitch M.P., Lei
"Molecular cloning of CSF-1 receptor from rat m
analysis and regulation during myogenesis.";
Growth Factors 6:209-218(1992).
-i-FUNCTION: THIS PROTEIN IS THE RECEPTOR.
TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
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Mammalia; Eutheria; Rodentia;
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CATALYTIC ACTIVITY: ATP + a protein tyrosine tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
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Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot kinase;
SMART; SM00408; IGC2; 1.
SMART; SM00219; TYTKC; 1.
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InterPro;
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HSSP; P11362; 1FGK.
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SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
L Similarity
12; Conser
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; IPR003598; Ig c2.
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PROTEIN KINASE DOM; 1
PROTEIN KINASE TYR; 1
PROTEIN KINASE TYR; 1
RECEPTOR TYR KIN III;
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IG-LIKE C2-TYPE 1.
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IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
PROTEIN KINASE.
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16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase 15 (EC 3.1.2.15) (Ubiquitin thiolesterase 15) (Ubiquitin-specific processing protease 15)
(Deubiquitinating enzyme 15) (Unph-2) (Unph4).
                                                                                                                                                                                                                  MEDLINE=99375319; PubMed=10444327;
Baker R.T., Wang X.-W., Woollatt E., White J.A., Sutherland G.R.;
"Identification, functional characterization, and chromosomal localization of USP15, a novel human ubiquitin-specific protease related to the UNP oncoprotein, and a systematic nomenclature for human ubiquitin-specific proteases.";
Genomics 59:264-274(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fetal brain;
Kimura Y., Saya H., Nakao M.
"Cloning and identification
Submitted (JUL-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Dermal papilla; Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Cl Hwang S.Y., Im S.U., Jung E.J., Lee J.H., "A catalogue of genes in the human dermal by expressed sequence tags."; Submitted (MAY-1999) to the EMBL/GenBank/
                                             protease Usp15.
                                                                                                                                            ALTERNATIVE SPLICING (ISOFORMS 1 A MEDLINE=22419901; PubMed=12532266;
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"Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w code for large proteins in vitro.";
DNA Res. 5:31-39(1998).
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Nakajima D., Okazaki N., Yamakawa H., Kikuno F
"Construction of expression-ready cDNA clones
curation of 330 KIAA cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                     Angelats C.,
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                                                                           "Isolation and characterization
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  n. Genome 14:31-46(2003)
CATALYTIC ACTIVITY: Ubi
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ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
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Catarrhini;
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1., Kim J.C.
nal papilla
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i; Hominidae;
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                                                                                                                   Jenkins N.A.,
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genes: manual
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Matches 10
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GO; GO:0004843; F:ubiquitin-specific protease activity; TAS
R InterPro; IPR006615; DUSP.
R InterPro; IPR001394; UCH-2.
R Pfam; PF00443; UCH; 1.
R Pfam; PF00443; UCH; 1.
R PROSITE; PS00972; UCH; 2.1; 1.
R PROSITE; PS00973; UCH-2.2; 1.
R PROSITE; PS00973; UCH-2.3; 1.
R PROSITE; PS00973; UC
                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB011101; BAA25455.2; --
EMBL; AF106069; AAD52099.1; --
EMBL; AF153604; AAD41086.1; --
EMBL; AF013990; AAG28973.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; C19.022; -.
Genew; HGNC:12613; USP15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Su or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9Y4E8-3; Sequence=VSP 005260; TISUE SPECIFICITY: Expressed In skeletal muscl placenta, liver, thymus, lung, and ovary, with expression in other tissues.
SIMILARITY: Belongs to peptidase family C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ubiquitin + a thiol.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1;
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655
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EMETDEPDDESSQDQELPSENENSQSEDSVG
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968
981 AA;
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968
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/FTId=VSP_005261.

T -> A (IN REF. 5).

N -> H (IN REF. 5).
                                                                                        7;
                                                                                                              Score 52;
Pred. No.
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                                                                                                                   57;
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Result
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Maximum Match 100%
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Perfect score:
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_plant:*

10: sp_plant:*

11: sp_vertebrate

13: sp_vertebrate

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180
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       Q96tv3 pleurotus o
Q9vj23 drosophila
Q9m010 arabidopsis
Q97t67 streptococc
Q8czc2 streptococc
Q8czc2 streptococc
Q8iwh6 homo sapien
Q963j2 drosophila
Q8ivx7 homo sapien
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ALIGNMENTS

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Q96CH9 Q8CH9 Q8CH9; Q97 AA. Q96CH9; Q96CH9; Q96CH9; Q97 AA. Q98CH9; Q97 AA. Q9
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033191; AAH33191.1; -...
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SEQUENCE 589 AA;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Colon;
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Submitted
SEQUENCE FROM N.A.
STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                          TAHA6D
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9ULH6; Q96P46;
01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=Colon;
                                                                                   Ephydroidea; Drosophilidae; Drosophila.
NCBL TaxID=7227;
                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                Q9VHY1;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "KIĀA1244 as a novel distantly related member (BIG3) of subfamily of ARF GEFs."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF413080; AAL04174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9HTD6
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                        LDS OR
                                                                                                                                                                                                                                 CG2684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
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                                                                                                                                                                                                          CG2684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFOSESSTPSTGGFSGKETPSEDDRSOSREHMGES 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFOSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592 AA; 66400 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           distantly related member (BIG3) of the BIG1/Sec7p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195845 MW;
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13,
22,
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22,
22,
                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 2e-16;
Mismatches
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Pred. No. 5.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                            1061
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RESULT 5
Q9BLU9
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                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00271; helicase C; 1.
Pfam; PF00176; SNP2 N; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00499; HELICC; 1.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 1061 AA; 118374 MW;
                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Cre
01-JUN-2001 (TrEMBLrel. 17, Las
01-JCCT-2002 (TrEMBLrel. 22, Las
Possible SNF2-related helicase.
                                                   Leishmania major.
Eukaryota; Euglenozoa;
                                                                                                                                                                    Q9BLU9;
01-JUN-2001
                                                                                                                                                                                                           Q9BLU9
SEQUENCE FROM N.A.
                               NCBI_TaxID=5664;
                                                                                            L2230.06
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InterPro; IPR000330; SNF2_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro;
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                                                                                                                                                                                                                                                                                                                                          SESSTPSTGGFSGKETPSEDDRSQSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001410; DEAD.
                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 33.9%;
                                                     Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                              Last sequence up
                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 5;
Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                           1252 AA
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                                                                                                                                update)
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RESULT 6
Q9VPA
TO Q9VP
DT 01-W
DT 01-W
DT 01-W
DT 01-W
DT 01-C
CG42
GN CG4
GN CG4
GN CG4
GN CG4
GN CG4
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Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
AR George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
AR George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
AR Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
AR Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
AR Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
AR Sutton G.G., Wortman J.R., Helt G., Champe M., Pfeiffer B.D.,
AR Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
AR Brandon R.C., Baster E.G., Helt G., Champe M., Pfeiffer B.D.,
AR Ballew R.M., Baster E.G., Helt G., Nelson C.R., Miklos G.I.G.,
AR Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
AR Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
AR Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
AR Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
AR Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
AR Ghodson K., Doup S., Dahlke C., Days A.D., Dew I., Dietz S.M.,
AR Durbin K.J., Evangelista C.C., Ferrier S., Dunkov B.C., Dunn P.,
AR Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
AR Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
AR Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
AR Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
AR Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
AR Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
ARA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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01-MAY-2000 (Tre
01-OCT-2002 (Tre
CG4297 protein.
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Q9VPQ4;
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Genome Res. 8:135-145(1998).
EMBL; AL513062; CAC24685.1; -.
InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000330; SNP2_N.

Pfam; PF00271; helicase_C; 1.

Pfam; PF00176; SNP2_N; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00490; HELICC; 1.

ATP-binding; Helicase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG4297
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Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98146435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Friedlin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MAY-2000 (TrEMBLrel.
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S.M., Bagherzadeh A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.1%;
41.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137895 MW;
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13,
22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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Pred. No. 1
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Baldwin D.,
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Zheng X.H., Zhong F.N., Zhong W., Zhau W., Zhau Q., Zheng L., Ra Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., RA Cibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

DR EMBL; AE003389; AAR51491.1; -.

DR FlyBase; FBgn0031258: CG4707
                                                                                               AC DE RAPARA RAP
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl R., Toruno M., Aono H., Baldarelli R., Barsh G.,
A Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Bulking H., Kang K.H., Weitz C., Whittaker C., Wilming L.,
Waynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Query Match
Best Local Similarity
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Best Local (
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01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                               EMBL;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9CXS4;
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                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3110013H01Rik protein.
3110013H01RIK.
                                                                                                                                                       MGD; MGI:1920389; 3110013H01Rik.
InterPro; IPR006913; DUF636.
                                                                                                                                                                                                                                                   Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                    "Functional annotation of a
                                                                                                                                                                                                                                                                                                                  Yayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1104
                                                                                                                                                                                                                     AK014046; BAB29130.1;
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16; Conservative
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1403 AA; 1
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                                                                                               ₽,
                                                                                                                             DUF636;
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                                                                                               27482
32.2%;
45.8%;
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150676 MW;
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                                                                                                                                                                                                                                                                                 full-length mouse cDNA collection.";
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Pred. No.
Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                               FDEADB1DE2A69961 CRC64;
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DB
4.2;
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                             Length 252;
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Q9VJ23
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
NON_TER
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SEQUENCE
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Submitted
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VJ23;
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pleurotaceae; Pleurotus.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical zinc finger pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG15169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG15169 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the edible basidiomycete Pleurotus ostreatus."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases EMBL; AJ417658; CAD10796.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002328; ADH zinc.
InterPro; IPR002893; Znf_MYND.
Pfam; PF01753; zf-MYND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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(OCT-2001)
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118 AA;
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ete Pleurotus ostreatus.";
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McBherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McBherson D.L.,
RA Merkulov G., Milshina N.V., Nobarry C., Morris J., McBherson D.L.,
RA Merkulov G., Milshina N.V., Nobarry C., Morris J., McBherson D.L.,
RA Merkulov G., Milshina N.V., Nobarry C., Morris J., McBherson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shive B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stappleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stappleton M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yeb J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.,
Forence 287.2185-2195(2000)
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Bevan M., Pohl T., Weizenegger T., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/G
                                                    InterPro; IPR006652; Kel
Pfam; PF01344; Kelch; 6.
SMART; SM00612; Kelch; 6
                                                                                                              EU Arabidopsis sequencing proje
Submitted (MAR-2000) to the EMB
EMBL; AL161946; CAB82282.1;
InterPro; IPR006652; Keich rep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabīlopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2003
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                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
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se; FBgn0032734; CG15169.
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12; Conser
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         1 protein.
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ne EMBL/GenBank/DDBJ databases
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Pred. No. 8.2;
5; Mismatches
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         259E20AAF74CE73F CRC64;
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Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C. Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
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Best Local
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Zook C.A., E
Glass J.I.;
FlyBase;
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                  Q963J2 PRELIMINARY; PRT; 656 AA.
Q963JZ:
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Voltage-dependent calcium channel alphal3 subunit (Fragment).
CA-ALPHA-IT OR CG4222 OR CG15899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein NON TER 287 21 SEQUENCE 287 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBIWH6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical SEQUENCE 89
                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein (Fragment).
Homo sapiens (Human).
                                                          "Exon organization of Ca2+ c
Submitted (APR-2001) to the
SMBL; AF371281; AAK54737.1;
                                                                                                                         Mittman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-2002) to the EMBL; BC039706; AAH39706.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE008392; AAK98884.1;
                                                                                                                                            SEQUENCE
                                                                                                                                                                             Ephydroidea; Drc
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003
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J. Bacteriol. 183:5709-5717(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSUE=Bladder;
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                                         FBgn0029846; Ca-alpha-1T
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3 (TrEMBLrel. 23, 0
3 (TrEMBLrel. 23, 0
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Baltz R.H., J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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inkler M.E., Yang Y., Y.
altz R.H., Jaskunas S.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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33143 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.6%;
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e EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       te proteome.
3D2136BE4CC51426
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Pred. No. 13;
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Mismatches
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                                                                                                      genes.";
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Zhao G.
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                                                                                                                        Query Match 30.3%; Score 54.5; DB 4; Length 536; Best Local Similarity 31.9%; Pred. No. 30; Matches 15; Conservative 6; Mismatches 11; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                              Q8IVX7 PRELIMINARY; PRT; 536 AA.
Q8IVX7;
Q8IVX7;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to eyes absent homolog 3 (Drosophila).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUB-Brain;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041667; AAH41667.1; -.
SEQUENCE 536 AA; 58697 MW; 7F502740058138F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                            ICBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 TYGSEKPSVMAPAPAAQRLSSGDPSTSPSLSQTTPSKDTDDQSRKNM 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
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                                                                                            1 SFOSE----
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                                                                                       ----STPSTGGFSGKETPSEDDRSQSREHM 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
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Sequence:
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seq length: 2000000000
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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Match
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41
1 EDDERSTDSSQQCS
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                                     AAO19166
AAM50810
AAW85472
AAO19165
AAM50809
ABG09728
ABF64835
ABF64835
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                                                                                                                                                                                                                                                                                     Description
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l human l human l human n polype n polype	Human 5' EST secre Human OFFX protein Human DITHP intrac Omega-conopeptide Propionibacterium Human polypeptide Propionibacterium Human polypeptide Propionibacterium Human polypeptide Propionibacterium	RATLId6 RATLId6 le #6, ar lein-coup lcidic dc lcidic dc ln inhibi lellar lellar libacter libacter	Human polypeptide Human prostate can Herpes simplex vir Human protein sequ Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Rat UNC-5 homologu Rat netrin binding Rat netrin recepto Proliferation pote PK40 TAU/neurofila PK40 protein kinas Bovine TAU/neurofila Human RATILId6 case

RESULT 1 AAO19166 PAAR PAAR PRESENTATION OF A PARAMETER PRESENTATION OF A PA (BILL/) (COHE/) (COLP/) (FRIE/) (GORD/) 23-APR-1998; 23-APR-1997; 04-JUL-2002. Homo sapiens. Human; prostate; prostate-specific sequence; prostate cancer; PS118; 27-NOV-2002 (first entry) AA019166; AAO19166 standard; Protein; 41 26-NOV-2001; 2001US-0991681. EST; expressed sequence tag; cytostatic; gene therapy. US2002086316-A1 Human prostate-specific PS118 protein fragment GRAN/) COHEN M. COLPITTS T L. FRIEDMAN P N. GORDAN J. GRANADOS E N. HODGES S C. KLASS M R. BILLINGEL P A. 98US-0065383. 97US-0842385. B

AAY48248

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RESULT 2
AAM50810
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Best Local :
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Granados EN,
Russell JC, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived from the human PS118 gene. These can be used in the detection monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
  Billing-Medel
Granados EN,
                                                                                                                                                                         23-APR-1998;
                                                                                                                                                                                               27-DEC-2001.
                                                                                                                                                                                                                  US2001055758-A1
                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                        PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                           01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                     AAM50810 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17;
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                                                                                               (BILL/)
(COHE/)
(COPL/)
(FRIE/)
                                                                                                                                                     23-APR-1997;
                                                                                                                                                                                                                                                                                                    PS118 prostate marker immunogenic
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(ROBE/)
(RUSS/)
                                                                           (GORD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (STRO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                               COPLPITTS T L.
) FRIEDMAN P N.
) GORDON J.
) GRANADOS E N.
) HODGES S C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) KRATOCHVIL J
) ROBERTS-RAPP
) RUSSELL J C.
) STROUPE S D.
                                KLASS M R.
KRATOCHVIL J D.
ROBERTS-RAPP L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                BILLING-MEDEL P
                                                                                                                      COHEN M
                                                                                                                                                                                                                                                                                                                                                                                                                        EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                     EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 43-44;
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 L PA, Cohen I
Hodges SC,
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Hodges
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                                                                                                                                                     97US-0842385
                                                                                                                                                                          98US-0065383
                                                                                                                                                                                                                                                                                                                                                                     Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58pp;
  M, Coplpitts TL, Frie
Klass MR, Kratochvil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 23;
Pred. No. 7.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to a number of prostate-specific sequences gene. These can be used in the detection,
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           Friedman
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PN, Gordon J
Roberts-Rapp
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RESULT 3
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ID AAW8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in non-prostate tissue. PS118 polypeptides, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the prostate, such as benign prostatic hyperplasia, prostatitits, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of immungenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the invention may provide an early means of detecting diseases of the between the clinically important and unimportant prostate cancers without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                  Billing-medel PA, Co
Granados EN, Hodges
            WPI; 1998-610000/51
                                       Granados EN,
Russell JC,
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                          25-MAR-2003
25-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of an immunogenic polypeptide comprising amino acids 184-224 of human prostate-specific PS118 polypeptide (see AMM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 43; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
                                                                                                                     23-APR-1997;
                                                                                                                                              23-APR-1998;
                                                                                                                                                                                                   WO9848054-A1
                                                                                                                                                                                                                                                                                PS118 protein encoded by consensus sequence.
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                                                                                          (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 518
                                                                                                                                                                                                                                                       PS118; prostate tumour tissue; prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative 0;
                                       Stroupe
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(first entry)
                                                                                                                      97US-0842385
                                                                                                                                              98WO-US08239.
                                       Cohen M,
yes SC, . K
ipe SD;
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                                                   M, Colpitts TL,
Klass MR, Krat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 23;
Pred. No. 7.3e-36;
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                                                   S TL, Friedman
Kratochvil JD,
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                                                  PN, Gordon J
Robertsrapp
                                                                                                                                                                                                                                                       disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
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RESULT 4
AAO19165
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AAO19167
AC AAO1
AXX
AC AAO1
AXX
AC Huma
XXX
CS Homc
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PA (GGI)
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Best Local S
Matches 41
                                                                                     Billingel
Granados E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a cDNA library made from prostate tumour tissue. Recombinant PS118 protein is used to detect PS118-specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of profession detection, diagnosis, staging, monitoring and prophecia of profession of detection, diagnosis, staging, monitoring and prophecia of profession and profession of profession and profession of profession and profession of profession and professi
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(COHE/)
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  WPI; 2002-665429/71
                                                       Russell
                                                                                                                                                                                                                                                                                      (HODG/
                                                                                                                                                                                                                                                                                                                                           (GORD/
(GRAN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1998;
23-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                               COLPITTS T L. FRIEDMAN P N. GORDAN J.
                                                                                                                                                                 KLASS M R.
KRATOCHVIL J I
ROBERTS-RAPP I
RUSSELL J C.
STROUPE S D.
                                                    B EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COHEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                             HODGES
                                                                                                                                                                                                                                                                                                                                              GRANADOS
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                                                                                                               PA,
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                                                    Hodges
Stroupe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e; prostate-specific sequence; prostate cancer; PS118; sequence tag; cytostatic; gene therapy.
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97US-0842385
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                                                       SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117pp; English.
                                                                                  Colpitts TL,
Klass MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41;
Pred. No.
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                                                                                  Friedman
Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
6.1e-35;
hes 0;
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                                                                                  'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 518;
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                                                                                                            Gordan J;
                                                                                  Roberts-Rapp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 5
AAMSO809
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XX AAMS
AC AAMS
AC AAMS
XX PS11
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PA (
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring prognosticating, preventing, treating, or determining predisposition individual to diseases and conditions of prostate, e.g. prostrate
                            preventing or disease -
                                            Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                        Billing-Medel PA,
Granados EN, Hoda
Russell JC, Stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COME/)
(COPL/)
(FRIE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS118 prostate marker partial sequence
                                                                                                                                                                                                                                                                                                                                                        (KLAS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                              (GRAN/)
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                                                                                                                                                                                                                                                                                                                                ROBE/)
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                                                                                                                                                  2002-187683/24.
DB; ABA91651.
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                                                                                                                                                                                                                                                                                                                                                                        FRIEDMAN P N.
GORDON J.
GRANADOS E N.
HODGES S C.
KLASS M R.
                                                                                                                                                                                                                                                                                                                              ROBERTS-RAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPLPITTS T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BILLING-MEDEL P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              518 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                             Stroupe
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                                                                                                                                                                                                                           PA, Cohen M, Coplpitts TL, Friedman
Hodges SC, Klass MR, Kratochvil JD,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0842385
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Pred. No. 6.1
D; Mismatches
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                                                                                                                                                                                                                                                  PN, Gordon i
Roberts-Rapp
                                                                         prognosticating,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518;
                                                                                                                                                                                                                                                                          Gordon J;
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sposition of
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RESULT 6
ABG09728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome
                                                                  Claim 20;
                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                           Drmanac RT,
                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of a human prostate-specific PS118 polypeptide, as predicted from a partial consensus cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 42-43; 57pp; English
                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                             2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
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                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 AA;
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                                                                                                                                                                                                                           Liu C,
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                                                             40087; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein #9719.
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Pred. No. 6.1e-35;
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RESULT 7
ABP64835
ID ABP6
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Cc Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at first wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; noctropic; antiallergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                            New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders invaberrant protein expression or biological activity -
                                                                                                               WPI; 2002-590824/63.
N-PSDB; ABQ99421.
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein SEQ ID 495.
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                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                   17-NOV-2000; 2000US-0714936
                                                                                                                                                                                                                                                                                     16-NOV-2001; 2001WO-US42950.
                                                                                                                                                                                                                                                                                                                                                        WO200259260-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                        immunostimulant; cerebroprotective.
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                                                                                                                                                              , Goodrich
Xue AJ, Ya
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                                                                                                                                                              Liu C, Zhou P, Asundi V,
, Wehrman T, Drmanac RT;
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Pred. No. 1.8e-34;
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Claim 20; SEQ ID 495;

394pp; English

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CC The present invention relates to novel human coding sequences
CC (ABQ99268-ABQ99608) and proteins (ABF6482-ABF65022). The sequences are
CC useful in therapeutic, diagnostic and research methods. The
CC polynucleotides may be used in the field of molecular biology as
CC hybridisation probes, primers for PCR, for chromosome and gene mapping,
CC for the recombinant production of protein, or in generation of anti-sense
CC DNA or RNA. The polynucleotides are useful in diagnostics as expressed
CC sequence tags (ESTs) for identifying expressed genes or for physical
CC markers, or as nutritional sources or supplements. The proteins may be used as molecular weight
CC markers, or as nutritional sources or supplements. The proteins may be
CC used to maintain and expand cell population in a totipotential or
CC pluripotential state useful for re-engineering damaged or diseased
CC tissues, transplantation, manufacture of bio-pharmaceuticals or the
CC development of bio-sensors. The polynucleotides and proteins are useful
CC protein expression or biological activity, e.g. haematopoietic disorders,
CC central/peripheral nervous system diseases, mechanical and traumatic
CC disorders, non-healing wounds, immune deficiencies and disorders,
CC disorders, or cancer. The polynucleotide sequences of the invention were
CC assembled from ESTs isolated mainly by sequencing by hybridisation, and
CC in some cases, sequences obtained from one or more public databases.
CC Note: The sequence data for this patent did not form part of the printed
CC security of the printed in electronic format directly from WIPO
Cat fit, wino, int/pub/shelshed not segmences.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG09731 standard; Protein; 1982 AA.
                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG09731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
biodiversity
                                                                                                                                                                                                                                                       Drmanac
                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2001.
                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1505
                                                                                                                                                       2001-639362/73.
DB; AAS73918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
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                                                                                                                                                                                                                                                    RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDDERSTDSSOOCSSEDEDIFEETAQVSPPRGKEKROWRAR 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1839 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                 2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein #9722.
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Pred. No. 1.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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This invention describes novel nucleic acid sequences

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CC Specification, but was obtained in electronic format directly from WIPO at fits, wipo.int/pub/published_pct_sequences.
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Best Local :
                                                        New nucleic acid expressed at encoded polypeptides, useful therapeutic agents -
                                                                                                                                                                                                                                                                                                                     DE19811193-A1
                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tag; EST; prostate tumor; gene therapy; tissue specificity human.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate cancer-associated protein 34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY48248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY48248 standard; Protein; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20;
                          Claim 22; 128; 166pp; German.
                                                                                                                      N-PSDB; AAZ33451.
                                                                                                                                      WPI; 1999-519628/44.
                                                                                                                                                                Specht
                                                                                                                                                                                                                              10-MAR-1998;
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                                                                                                                                                                                                                                                                                        16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                              (META-) METAGEN GES GENOMFORSCHUNG
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                                                                                                                                                                Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1982 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to isolated
                                                                                                                                                                                                                              98DE-1011193
                                                                                                                                                                                                                                                          98DE-1011193
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                                                                                                                                                                Schmitt A,
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                                                                          for
                                                                                        high
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                                                                          treating
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                                                                          in prostatic
g cancer and s
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                                                                        c tumor tis
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                                                                          tissue
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RESULT 10
AAO11359
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Best Local Similarity
Matches 13; Conserv
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides havious cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and
                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 25251; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang
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18-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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DB; AAI91290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192
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2000US-0577409
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100.0%; Pred. No.
tive 0; Mismatc
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8e-06;
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Query Match

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180 AA;

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RESULT 11
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Best Local S
Matches
                                                    expressed at high level in prostatic tumor tissue and encode gene products or their fragments. The products of the invention have antitumor activity. Polypeptides (I) encoded by (A) are used: (i) for identifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. ANY48215-Y48303 represent protein fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                       This invention describes novel nucleic acid sequences (A) that
                                                                                                                                                                                                                                                                  Claim 22; 112-113; 166pp; German.
                                                                                                                                                                                                                                                                                                             New nucleic acid expressed at high level in prostatic tumor tissue encoded polypeptides, useful for treating cancer and screening for
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-519628/44
                                                                                                                                                                                                                                                                                                                                                                                                      Specht T, Hinzmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate cancer-associated protein
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                                      encoded by the expressed sequence
                                                                                                                                                                                                                                                                                                 therapeutic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of cancer,
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Pred. No.
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                                           in the method
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RESULT 12
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AAB93588
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           the treatment of herpes virus infection. The method comprises forming a herpes virus polypeptide/zinc complex; adding a test agent to the polypeptide/zinc complex; and detecting any change in the complex. The invention also relates to the use of known agents, such as 2,2'-dithiobishenzamide (DIBA) and azodicarbonanide (ADA), and unknown agents for the manufacture of a medicament for the treatment of herpes virus infections. The method is useful for detecting agents for use in the treatment of herpes virus infection. The present sequence is Herpes simplex virus type 2 (HSV2) IE63 protein homologue. HSV2 belongs to alphaherpes virus sub-family. IE63 protein is also called ICP27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of detecting an agent for use in the treatment of herpes virus infection. The method comprises forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting an agent useful for treating herpes virus infection comprises determining any change in a polypeptide/zinc complex in the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clements
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-2000; 2000GB-0016890
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    26-JUN-2001
                                            AAB93588;
                                                                                     AAB93588 standard; Protein; 610 AA.
                                                                                                                                                                                                                                                                                                                                                                       Sequence
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RESULT 14
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                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                      AAG41923;
                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                           AAB95893 represent human amino represent oligonucleotides, all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 13012; 2537pp + CD ROM;
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                                                                 AAG41923 standard; Protein; 790
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                                                                                                                                                                                                                                                                                                                                                                                         present invention.
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                                                                                                                                                                                                                                                         Similarity
7; Conserv
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, Sugiyama T,
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                                                                                                                                                                                                                                                                             17.1%;
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Pred. No.
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99US-0139454. 99US-0139454. 99US-0139456. 99US-0139457. 99US-0139457. 99US-0139460. 99US-0139460. 99US-0139461. 99US-0139463. 99US-0139463. 99US-0139463.	000000000000000000000000000000000000000	99US-0131449 99US-0131449 99US-0132484 99US-0132486 99US-0132486 99US-0132486 99US-0132487 99US-0134218 99US-0134218 99US-0134219 99US-0134219 99US-0134219 99US-0134219 99US-0134219 99US-0134219 99US-0134219	2000EP-0301439. 99US-0121825. 99US-0123180. 99US-0125788. 99US-0126785. 99US-0126785. 99US-0127462. 99US-0127462. 99US-0127462. 99US-0128714. 99US-0128714. 99US-0128714. 99US-0128714. 99US-0129845. 99US-0130810.	first entry) aliana protein f. fication; signal assay; genetic m. quence. aliana.
				ragment SEQ ID NO: 52219. transduction pathway; metabolic apping; gene expression control;
				olic pathway; rol; promoter;
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9US-01489 9US-01493 9US-01493 9US-01493 9US-01493 9US-01493 9US-01493 9US-01493 9US-01501 9US-01501	9US-0146: 9US-0147: 9US-0147: 9US-0147: 9US-0147: 9US-0147: 9US-0147: 9US-0147: 9US-0147: 9US-0148: 9US-0148:	2000000000000000000	9US-01422 9US-01422 9US-01422 9US-01432 9US-01432 9US-01443 9US-01444 9US-01444 9US-01444 9US-01444 9US-01444 9US-01444 9US-01444 9US-01444 9US-01444	9US-01399 9US-01399 9US-01400 9US-01400 9US-01400 9US-01400 9US-01400 9US-01400 9US-01401 9US-01401 9US-01401

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RESULT 15
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115-SEP-1999
116-SEP-1999
22-SEP-1999
22-SEP-1999
23-SEP-1999
24-SEP-1999
29-SEP-1999
10-OCT-1999
11-OCT-1999
11-OCT-1999
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22-OCT-1999
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27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
  termination sequence
         Protein identification; signal transduction pathway; metabolic pathway; hybridiaation assay; genetic mapping; gene expression control; promoter;
                                       Arabidopsis thaliana protein fragment SEQ ID NO: 52218.
                                                               18-OCT-2000
                                                                                  AAG41922;
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ALIGNMENTS

US-09-065-383-28 ZIP: 60064-3500 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ FOR WINDOWS Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/065,383 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/842,385 FILING DATE: 23-APR-1997 ATTORNEY/AGENT INFORMATION: NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441 DEFENDANCET NUMBER: 6084,US.P1 Sequence 28, Appli Patent No. 6391543 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 41 amino acid GENERAL INFORMATION: APPLICANT: KLASS, MICHAEL R. APPLICANT: KRATOCHVIL, JON D. APPLICANT: ROBERGS-RAPP, LISA APPLICANT: STROUPE, STEPHEN D. APPLICANT: STROUPE, STEPHEN D. TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE NUMBER OF SEQUENCES: 33 REFERENCE/DOCKET NUMBER: 60 TELECOMMUNICATION INFORMATION: TELEPHONE: 847/935-1729 CORRESPONDENCE ADDRESS: ADDRESSEE: Abbott Laboratories APPLICANT: APPLICANT: APPLICANT: STREET: 100 Abbott CITY: Abbott Park STATE: IL TELEFAX: 847/938-2623 COUNTRY: Application US/09065383 USA GORDON, JUGRANADOS, COHEN, MAURICE COLPITTS, TRACEY L. FRIEDMAN, PAULA N. HODGES, STEVEN C. KLASS, MICHAEL R. BILLING-MEDEL, JULIAN Park Road EDWARD N. 35,441 ER: 60 28: PATRICIA 6084.US.P1

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US-09-065-383-27
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APPLICANT:
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                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/842,385
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.Pl
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065 202
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STROUPE, STEPHEN U.
TITLE OF INVENTION: REACENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPUTER: OPERATING SYSTEM:
                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60064-3500
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Local Similarity 100.0%; Pred. No. 1.4e-35;
Les 41; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                             LENGTH: 518 amino acids
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100 Abbott Park Road
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RUSSELL, JOHN C.
STROUPE, STEPHEN D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRATOCHVIL, JON D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HODGES,
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                                                                               linear
                                                              No. 6391543e
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100.0%;
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                                                                                                                                                               27:
Score 41; DB 4;
Pred. No. 1.2e-34;
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P1
               DB 4; Length 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OSWAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-434
INFORMATION FOR SEQ ID NO: 5:
INFORMATION FOR SEQ ID NO: 5:
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Matches
                                                                                                                                                                      Sequence 5, Application US/09306902A
Patent No. 6277585
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Machine Machi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Patent No. 593927
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APPLICANT: Tessie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
STRANDEDNESS: not releve
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ADDRESSEE: SCIENCE & TECHNOLOGY LAW
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: Netrin Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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TITLE OF INVENTION: Netrin Receptors NUMBER OF SEQUENCES: 9
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Leonardo, E. David
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E: peptide
                                                                    Masu, Masayuki
Kazuko, Keino-Masu
                                                                                                                                      Hink, Lindsay
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ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA

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                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Welser & Associates, P.C.
STREET: 230 S. Fifteenth Street, Suite 500
                   ATTORNEY/AGENT INFORMATION:
NAME: Welser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 37
                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
FELECOMMUNICATION INFORMATION:
                                                                                      APPLICATION NUMBER: US/01
FILING DATE: 18-FEB-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                   ZIP: 19102
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Local Similarity 100.0%; Pred. No. 20;
es 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/306,902A
FILING DATE: 07-May-1999
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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40. 6368790
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TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08801308
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                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scott, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA ENCODING P2P PROTEINS AND USE OF P2P CDNA-DERIVED ANTIBODIES AND ANTISENSE REAGENTS DETERMINING THE PROLIFERATIVE POTENTIAL OF NORMAL, ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS
                                                                                                                                   US/08/801,308
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                                                      Best Local Similarity
Matches 6; Conserv
                                                                                    Query Match
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/912
FILING DATE: July 10, 1992
APPLICATION NUMBER: 07/742
APPLICATION NUMBER: 07/742
FILING DATE: 9-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Ingram
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 07-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ingram, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM-compatible
OPERATING SYSTEM: MS-DOS '
SOFTWARE: WordPerfect 5.1
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                       NAME: Gates, Edward R. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                            ENGTH:
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                            20 IFEETA 25
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                                                                                                                                                                            9 amino acids
                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vernon M., Roder, Hanno M.
No. 5955444el Tau/Neurofilament Protein
                                                                       14.6%;
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                                                                                                                                                                                                                                                                                                  07/742,880
                                                                                                                                                                                                                                                                                                                                07/912,293
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                                                                                                                                                                                                                                       31,616
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                                                        Score 6; DB 2; Pred. No. 2.5
0; Mismatches
                                                                                                                                                                                                                          M0656/7008
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                                                                       DB 2; Length 9;
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RESULT 7
PCT-US92-05825A-9
; Sequence 9, Application PC/TUS9205825A

ENERAL INFORMATION:

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1
                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                       COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              APPLICANT: Tani, Akiyoshi
APPLICANT: IChimori, Yuzo
TITLE OF INVENTION: Method For Assaying MAP Kinase
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/742,880 FILING DATE: 9-AUG-1991 ATTORNEY/AGENT INCRMATION:
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CORRESPONDENCE ADDRESS:
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             CLASSIFICATION: 436
FIGHT APPLICATION DATA:
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                                              APPLICATION NUMBER: FILING DATE: 27-MA
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OPERATING SYSTEM:
                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gates, Edward R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: POFILING DATE: 19920710
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1300 I Street, N.W., Suite 700
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                                               27-MAR-1996
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Novel Tau/Neurofilament
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100.0%; Pred. No.
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JP 320577-1995
                                                             US/08/622,277A
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RESULT 9
US-08-622-277A-5
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Tani, Akiyoshi
APPLICANT: Ichimori, Yuzo
TITLE OF INVENTION: Method For Assaying MAP Kinase
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                                                              PRILING DATE: 08-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 305
FILING DATE: 24-NOV-1995
PRIOR APPLICATION UNMBER: JP 070
APPLICATION NUMBER: JP 070
FILING DATE: 28-MAR-1995
ATTORNEY/AGENT INFORMATION:
AUMED
                                                                                                                                                                                                               CLASSIFICATION: 436
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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APPLICATION NUMBER:
FILING DATE: 28-MAR-
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ELECOMMUNICATION INFORMATION:
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             REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 04221.0039-00000
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0:
FILING DATE: 27-MAR-1996
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TYPE: amino acid
STRANDEDNESS: single
                                  REGISTRATION NUMBER:
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                                                   Toohey, Kimberlin M
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1300 I Street, N.W., Suite 700
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100.0%; Pred. No.
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5. 6.1;
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US-07-893-929A-7
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Best Local Similarity 100.0%; Pred. No. 6.4
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                                                                   Matches
                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                   TELEX: NO. 5336667e
INFORMATION FOR SEQ ID NO. 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 antho acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/893,92
FILING DATE: 19920605
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MOREC DEPIS 1
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                                                                                                                                                                                                                                                         NAME: MONACO, DANIEl A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
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TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
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                                 QQCSSE 16
OQCSSE 80
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                                                                   Conservative
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                                                                14.6%; Score 6; DB 1
100.0%; Pred. No. 41
tive 0; Mismatches
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                                                                                                   DB 1;
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                                                                                                   Length 130;
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                                                                  Indels
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RESULT 11
PCT-US92-10344-7
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                               GENERAL INFORMATION: Edward P.
APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 72
MEDIUM TYPE: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/803,63
APPLICATION UNMBER: 3,1991
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, DANIE! A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEDHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common ADDRESSEE: wealth System of Higher Education
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                   NUMBER OF SEQUENCES:
                                   STREET: 406 University Services CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
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ZIP: 19122
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COUNTRY:
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                  Pennsylvania
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er 3, 1991
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ER: 6056-126
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RESULT 13
PCT-US92-10344-1
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Best Local (
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/80
FILING DATE: December 3,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MODACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 603
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
NAME: MODACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 1215) :
                                                                                                                                          APPLICATION NUMBER: PFILING DATE: 19921201
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Temple University - Of The Common-
ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                         COUNTRY:
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CLASSIFICATION:
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                                                                                     07/803,630
ber 3, 1991
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; Pred. No. 41
0; Mismatches
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Query Match
Best Local Similarity
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                                Matches
                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 5, Application US/07893929A
Patent No. 5336667
                                                                                                                                                                      TELEFAX: (215) 568-5549
TELEX: No. 5336667e
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOXDERFECT 5.1
CURRENT APPLICATION NUMBER: US/07/8
FILING DATE: 19920605
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                NAME: MODACO, DATIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07
FILING DATE: December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                     TELEPHONE: (215) 568-83
TELEFAX: (215) 568-5549
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11 QQCSSE 16
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                             l Similarity
6; Conserv
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AMINO ACID
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    Temple University - Of The Common-
    wealth System of Higher Education
    406 University Services Building

                              Conservative
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Peng, Man-ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alboaggregins: Platelet
Agonists Which Bind To Platelet
Membrane Glycoprotein Ib
                                                                                                                                                                                                                   568-8383
                           14.6%; Score 6; DB:
100.0%; Pred. No. 42
cive 0; Mismatches
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100.0%; Pred. No. 41
Live 0; Mismatches
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                                                                                                                                                                                                                                                    (CIP) 1
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                                                             DB 1;
                                                             Length 132;
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                                Indels
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Search completed: July 24, 2003, 12:28:37 Job time : 5.74231 secs
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PCT-US92-10344-5
                                                                                                                                                                                                                                                                    PCT-US92-10344-5
                                                                                                                                                                                                                                                                                    TELEX: None
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application PC/TUS9210344
GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                                                                                                                       Query Match 14.6%; Score 6; DB: Best Local Similarity 100.0%; Pred. No. 42. Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IN MS/20
COMPUTER: INM MS/20
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERIFICE 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5383
TELEPAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 406 University Services Building CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A. ZIP: 19122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Temple University - Of The Common-ADDRESSEE: wealth System of Higher Education
                                                                                                                               11 QQCSSE 16
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Maximum DB seg length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match
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/ Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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US-10-256-702-5
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Sequence 5, Appli
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Sequence 35, Appl
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Sequence 31, Appl
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Sequence 27, Appl
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ALIGNMENTS

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Sequence 5, Application US/09933261 Publication No. US20030040046A1 GENERAL INFORMATION:
              PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/808,982
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMARE: Batentin Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/933,261
FILING DATE: 20-Aug-2001
CLASSIFICATION: 'Unknown'
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Netrin Receptors NUMBER OF SEQUENCES: 8
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Leonardo, E. David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
TELEFAX: (415) 343-4342
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Query Match 17.1%; Score 7; DB 15; Length 898; Best Local Similarity 100.0%; Pred. No. 53; Matches 7; Conservative 0; Mismatches 0; Indels
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Publication No. US20030059859A1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/933,261
FILING DATE: 20-Aug-2001
APPLICATION NUMBER: 08/808,982
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: No. US20030040046A1 Relevant TOPOLOGY: No. US20030040046A1 Relevant MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                      STRANDEDNESS: No. US20030059859A1 Relevant TOPOLOGY: No. US20030059859A1 Relevant MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/256,702
FILING DATE: 27-Sep-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Netrin Receptors NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tessier-Lavigne, Marc
Leonardo, E. David
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                                                                                                                                                                                           LENGTH: 898 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                           NAME: OSMAN, RICHARD A REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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Hink, Lindsay
Masu, Masayuki
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100.0%; Pred. No.
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LENGTH: 1404
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Applicat Patent No. US2002003 GENERAL INFORMATION:
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CDNA encoding P2P proteins and use of P2P cDNA-
TITLE OF INVENTION: derived antibodies and antisense reagents
TITLE OF INVENTION: in determining the proliferative potential of
TITLE OF INVENTION: normal, abnormal and cancer cells in animals
TITLE OF INVENTION: and humans
FILE REFERENCE: D6386D
CURRENT APPLICATION NUMBER: US/09/811,045A
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 08/801,308
PRIOR FILING DATE: 1997-02-18
PRIOR FILING DATE: 1997-02-18
PRIOR FILING DATE: 1997-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Scott, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
OTHER INFORMATION: P2P polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
APPLICATION NUMBER: 08/480,793
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 07/912,293
FILING DATE: July 10, 1992
APPLICATION NUMBER: 07/742,880
FILING DATE: 9-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          APPLICATION NUMBER: US/09/045,020
FILING DATE: 20-Mar-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    COMPUTER: IBM-compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPorfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ingram, Vernon M., Roder, Hanno M.
TITLE OF INVENTION: No. US20020025942Alel Tau/Neurofilament Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1288 SPPRGKE 1294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Massachusetts Institute of Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.1%; Score 7; DB 9 llarity 100.0%; Pred. No. 78; Conservative 0; Mismatches
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US-09-896-888A-35
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                                                                                                                                                                                                                                                                                             Sequence 35, Application US/09896888A Patent No. US20020116723A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conserv
                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 22
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Best Local Similarity
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                                                                                                                                                                         APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44 CURRENT APPLICATION NUMBER: US/09/896,888A CURRENT FILING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: US/09/048,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LifeSpan Biosciences APPLICANT: Brown, Joseph P.
                                                                                                     PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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100.0%; Pred. No. 15;
tive 0; Mismatches
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100.0%; Pred. No. 4e4
tive 0; Mismatches
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FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 33
LENGTH: 23
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 29
SEQ ID NO 29
LENGTH: 27
Query Match
Best Local Similarity
Thehas 6; Conserve
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Best Local Similarity
Watches 6; Conserv
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                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                      TYPE: PRT
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US-09-896-888A-31
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Best Local Similarity
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Matches 6; Conserv
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SEQ ID NO 31
LENGTH: 28
                                                                                                                                                                                                                                            SEQ ID NO 27
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Patent No. US20020116723A1
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The University of British Columbia TITLE OF INVENTION: INSECT Expression Vectors FILE REFERENCE: 80021-44 CURRENT APPLICATION NUMBER: US/09/896,888A CURRENT FILING DATE: 2001-06-29
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CURRENT APPLICATION NUMBER: US/09/896,888A

CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1997-03-27
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PRIOR FILING DATE: 1998-03-26
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NUMBER OF SEQ ID NOS: 50
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                                                                                                                                                                      LENGTH: 43
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                 14.6%; Score 6; DB 1
100.0%; Pred. No. 37;
Live 0; Mismatches
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RESULT 11

RESULT 13 US-10-034-623-22 ; Sequence 22, Application US/10034623

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RESULT 12
US-10-027-806-22
; Sequence 22, Application US/10027806
; Publication No. US20020160476A1
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Best Local S
Matches 6
                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                    JENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: University of Utah Research Foundation
                                                                                                                                                     TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Conus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT
                                                                                                                                                                                            ENGTH: 199
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                                                                    Local Similarity
87 DEDIFE
                               17 DEDIFE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 RGKEKR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 RGKEKR 32
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McIntosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cartier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watkins, Maren
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                                                                      Conservative
92
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                                                                                    14.6%;
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100.0%; Pred. No.
                                                                                    Score 6; Pred. No.
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Mismatches
                                                                      Mismatches
                                                                                    DB 14; L
. 1.4e+02;
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Sequence 22, Application US/10027801
Publication No. US20030054364A1
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 199
TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
US-10-027-801-22
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
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US-09-738-626-4081
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TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Publication No. US20020198365A1
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCCRP.002A
CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 22
                                                                                                                                                                Sequence 4081, Application US/09738626
Publication No. US20020197605A1
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Best Local (
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100.0%; Pred. No.
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o. 1.4e+02;
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Search completed: July 24, 2003, 12:48:27 Job time: 8.9634 secs

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APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
FILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 4081
LENGTH: 232
TYPE: PRT
TYPE: PRT
COCANISM: COTYNEBACTERIUM Glutamicum
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                                                                                                                             ; ORGANISM: Corynebacterium glutamicum US-09-738-626-4081
                                                               Matches
                                                            Best Local Similarity
Matches 6; Conserv
                                                                                            Query Match
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 27
                    3 DERSTD 8
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OZAKI, AKIO
                                                               Conservative
 32
                                                                                100.0%;
                                                                                            14.6%;
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                                                                               Score 6; I
                                                                 Mismatches
                                                                               DB 10; Length 232;
o. 1.6e+02;
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Result
No.
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Perfect score:
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Maximum DB seq length: 200000000
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                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                   Score
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 100.0
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                  Query
Match Length
                                                                          30222222211111111110987.5.4.3.2.1
30222222221111654432100
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41
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                                                                   Pending_Patents_AA_Main:*
/cgn2_6/ptodata/1/paa/
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/cgn2_6/ptodata/1/paa/US06_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
                    DB
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US-08-842-385-7
US-09-991-681-28
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                 Description
Sequence 7, Appli
Sequence 28, Appl
                                                                                                                             RESULT 1
US-08-842-385-7
; Sequence 7, Application US/08842385
; GENERAL INFORMATION:
                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
CLASSIFICATION: 435
                                                                                     ADDRESSEE:
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100.0
100.0
31.7
31.7
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3 4 100.0 467 12 US-08-942-985-6 Sequence 6, Appli 6 41 100.0 1770 1 PCT-USD-1943-44 Sequence 27, Appli 6 41 100.0 1770 1 PCT-USD-1943-94 Sequence 44, Appl 1 100.0 1700 1 PCT-USD-1943-94 Sequence 44, Appl 1 100.0 1700 1 PCT-USD-1943-94 Sequence 44, Appl 1 100.0 1897 1 PCT-USD-1943-95 Sequence 44, Appl 1 100.0 1893 1 PCT-USD-1943-95 Sequence 45, Appl 1 100.0 1893 1 PCT-USD-1943-95 Sequence 47, Appl 1 PCT-USD-1943-95 Sequence 47, Appl 1 PCT-USD-1943-95 Sequence 47, Appl 1 PCT-USD-1944-95 Sequence 47, A
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PRIOR APPLICATION DATA: APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

6084.US.01

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US-09-991-681-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/09991681 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 41; DB 12; Length 41; Best Local Similarity 100.0%; Pred. No. 4.6e-34; Matches 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: POTEMBERI, PRISCILLA E REGISTRATION NUMBER: 33,207 REFERENCE/DOCKET NUMBER: 6084 TELECOMMUNICATION INFORMATION: TELEPHONB: 847/937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 847/938-2623
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REPERENCE/DOCKET NUMBER: 6084.US.Pl
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 847/935-1729
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-Nov-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                               ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLPITTS, TRACEY L. FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRATOCHVIL, JON D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GORDON, JULIAN
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GENERAL INFORMATION
APPLICANT: RUSSEL
APPLICANT: Colpit
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Best Local Similarity
Matches 41; Conserv
                                                                                                        Query Match
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/842,385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 847/937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6084.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Abbott CITY: Abbott Park
                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                       TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60064-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: None
                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                         Porembski, Priscilla E
                      EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDDERSTDSSOOCSSEDEDIFEETAQVSPPRGKEKROWRAR 41
EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08842385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 41 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colpitts,
                                                                   ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Russell, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 41; DB 25; ilarity 100.0%; Pred. No. 4.6e-34; Conservative 0; Mismatches 0;
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                                                                                                                                                            None
                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REAGENTS AND METHODS USEFUL FOR DETECTING DISEASE OF THE PROSTATE
                                                                                     100.0%; Score 41; DB 12; Length 467; 100.0%; Pred. No. 4.8e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tracey
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                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 41;
                                                                     Indels
                                                                     0;
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                                                                     Gaps
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                                                                                                                                                        PCT-US03-01943-44
                                                                                                                                                                           RESULT 5
                                                                                                              Sequence 44, Application PC/TUS0301943 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
              APPLICANT: ORIGENE TECHNOLOGIES INC
TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 Local
APPLICATION NUMBER: US 10/054,935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 847/935-1729
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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ADDRESSEE: Abbott Laboratories
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                                                                                                                                                                                                                                  184 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 224
                                                                                                                                                                                                                                                          1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                             41; Conservative
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/991,681 FILING DATE: 26-Nov-2001 CLASSIFICATION: <Unknown>
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STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 518 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GORDON, JULIAN GRANADOS, EDWAI
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                                                                                                                                                                                                                                                                                                           Score 41; DB 25;
Pred. No. 5.3e-33;
; Mismatches 0;
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APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: CUstom
; SEQ ID NO 40087
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PCT-US03-01943-44
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GENERAL INFORMATION:
APPLICANT: Origine Technologies Inc
TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION UNMERR: US/10/144,198
CURRENT FILING DATE: 2002-05-14
                                                                                                                                                                                                                                                                                                              Sequence 40087, Application PC/TUS0108631 GENERAL INFORMATION:
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Best Local Similarity
Matches 41; Conserv
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PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/197,824
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/117,229
PRIOR FILING DATE: 2002-04-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/356,130
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100.0%; Pred. No. 1.7e-32;
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Pred. No.
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1505 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 1545

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Sequence 495, Application US/10416993
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: US/10/416,993
CURRENT FILING DATE: 2003-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR PILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
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PCT-US01-42950-495
                                                          Matches
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                                                                         Query Match
Best Local (
                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 495
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Best Local (
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                                                                                                                                  -10-416-993-495
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: PCT/US01/42950
CURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                    LENGTH: 1839
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Helper component proteinase domain identified by PFam, OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX, OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw so
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LOCATION: (941)..(950)
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                                                                           Similarity
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EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
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                                                          Conservative
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Pred. No. 1.8e-32;
Pred. No. 1.8e-32;
Indels
                                                                       Score 41; DB 30;
Pred. No. 1.8e-32;
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Pred. No. 1.8e-32;
                                                          Mismatches
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PCT-US03-04508-32
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CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 93
  · Matches
                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 40090
LENGTH: 1982
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                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: IDEC PHARMACEUTICALS APPLICANT: GATELY, DENNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF IN DESIGN TITLE OF INVENTION: OR THERAPEUTICS
                                                                                              OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX, OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw scor NAME/KEY: DOMAIN
LOCATION: (1065)...(1074)
OTHER INFORMATION: Helper component proteinase domain identified by PFam, OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
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                                                                                                                                                                                                                              NAME/KEY: DOMAIN
LOCATION: (11)..(25)
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Score 41; DB 1;
Pred. No. 1.9e-32;
; Mismatches 0;
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Pred. No. 1.8e-32;
Mismatches 0;
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                                     Length 1982;
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1587 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 1627

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RESULT 14
US-09-623-791-87
; Sequence 87, Application US/09623791
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
                                                                                                                                                                                    문
                                                                                                                                                                                                                                                                                                                                                            ; SOFTWARE: PatentIn version 3.0; SEQ ID NO 30; LENGTH: 2221; TYPE: PRT; ORGANISM: Homo sapiens US-10-144-198-30
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US-10-144-198-30
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-01943-30
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TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 10/054,935
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/356,130
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PRIOR APPLICATION NUMBER: US 10/102,946

PRIOR TILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: US 10/117,229

PRIOR FILING DATE: 2002-04-08

PRIOR PILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

PRIOR PILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: US 10/197,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30, Application US/10144198
GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prostate Cance
FILE REFERENCE: 9U 105 R1
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Tocal Similarity
Tonserv
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Best Local
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LENGTH: 2221
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CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
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Local Similarity 100.0%; Pred. No. 2.1e-32;
les 41; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                   100.0%; Score 41; DB 27; Length 2221; llarity 100.0%; Pred. No. 2.1e-32; Conservative 0; Mismatches 0; Indels 0
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Search completed: July 24, 2003, 12:45:54 Job time : 62.7701 secs
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-791-87
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US-09-623-791A-87
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 87
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SPECHT, THOMAS
APPLICANT: HINZMANN, BERI
APPLICANT: SCHMITT, ARMI
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Best Local Similarity 100.0%;
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Best Local :
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APPLICANT:
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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/DE99/00721
PRIOR FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 201
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ALBRE 11
CURRENT APPLICATION UMBER: US/09/623,791A
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: PCT/DE99/00721
PRIOR FILING DATE: 1999-03-09
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROSENTHAL, ANDRE TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TUMOR TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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SCHMITT, ARMIN
PILARSKY, CHRISTIAN
DAHL, EDGAR
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ROSENTHAL, /
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PILARSKY, CHRI
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Pred. No. 0.0001;
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Perfect score:
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Match Length
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41
1 EDDERSTDSSQQCSSEDEDI......
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140.227 Million cell updates/sec
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// cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

// cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

// cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

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US-10-378-173-130
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PCT-US03-20887-7
US-60-479-962-461
US-10-273-573-8009
US-10-273-573-8011
US-10-273-573-5652
US-09-784-53C-34
US-10-273-573-10391
US-10-294-433-33
US-10-273-573-10371
US-10-273-573-10371
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US-60-479-073-17
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            10391, A
333, App
6201, Ap
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	82, Appl	88, Appl	Appli	18, Appl	10, Appl	2, Appli	6203, Ap	14, Appl	180, App	18, Appl	8942, Ap	420, App	18, Appl	6235, Ap	8649, Ap	9769, Ap	8825, Ap	10372, A	6/4, App

ALIGNMENTS

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RESULT 2
PCT-US02-18638A-127
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TITLE OF INVENTION: OR THERAPEUTICS
FILE REFERENCE: 037003-0301988
CURRENT APPLICATION NUMBER: US/10/367,978
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION UNMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR APPLICATION NUMBER: 60/396,759
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
NUMBER: 60 SEO 11 DNOS: 89
                                                                                                                                                                                                                  Sequence 127, Application PC/TUS0218638A
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc. et al.
APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METH
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035PC
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GENERAL INFORMATION:
APPLICANT: GATELY, DENNIS
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CURRENT APPLICATION NUMBER: PCT/US02/18638A CURRENT FILING DATE: 2002-06-12 PRIOR APPLICATION NUMBER: US 60/298,159 PRIOR FILING DATE: 2001-06-13 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR FILING DATE: 2001-06-13 PRIOR PILING DATE: 2001-06-13 PRIOR APPLICATION NUMBER: US 60/335,936 PRIOR APPLICATION NUMBER: US 60/335,936
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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-60-479-073-17
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18638A-127
Query Match
Best Local Similarity 100
Matches 6; Conservative
                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: CUSCOM
SEQ ID NO 10709
LENGTH: 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10709, Application US/10273573

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILLNG DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
BRIOR ENTINE DATE: 2002-14-18
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 127
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                                                                                                                                                               ORGANISM: Homo sapiens -10-273-573-10709
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APPLICANT: Saunders, Michael John Scott
APPLICANT: Saunders, Michael John Scott
APPLICANT: Logghe, Marc Georges
TITLE OF INVENTION: Amino acid sequences useful for developing compounds for the
TITLE OF INVENTION: prevention and/or treatment of metabolic diseases and nucleotide
TITLE OF INVENTION: sequences encoding such amino acid sequences.
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14.6%; Score 6; DB 6;
100.0%; Pred. No. 49;
ative 0; Mismatches
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100.0%; Pred. No. 37;
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                                                                           Length 1537;
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CURRENT APPLICATION NUMBER: US/10/378,173
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 60/360787
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patentin version 3.2
SEQ ID NO 228
LENGTH: 16
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                                                                                                                                         PEATURE:
OTHER INFORMATION: phosphorylated peptide
PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (7)...(7)
THER INFORMATION: phosphorylation
US-10-378-173-228
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US-10-378-173-228
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PCT-US03-06553-228
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GENERAL INFORMATION:
APPLICANT: Burke et al.
TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO
FILE REFERENCE: MDSP-P01-023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 228, Application PC/TUS0306553
GENERAL INFORMATION:
APPLICANT: MDS PROTEOMICS INC.
TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO
FILE REFERENCE: MDSP-PWO-023
                                                                                       Query Match
Best Local (
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 228
                                                                      Matches
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CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 60/360787
PRIOR FILING DATE: 2002-03-01
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OTHER INFORMATION: phosphorylation
                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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OTHER INFORMATION: phosphorylated peptide
FEATURE:
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ORGANISM: Artificial Sequence
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                                                                                       Local Similarity
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                                                                    12.2%; Score 5; DB 6;
100.0%; Pred. No. 8.8;
tive 0; Mismatches
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Sequence 130, Application PC/TUS0306553

(GENERAL INFORMATION:
APPLICANT: MUS PROTEOMICS INC.
TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO
FILE REFERENCE: MDSP-PWO-023
CURRENT APPLICATION NUMBER: PCT/US03/06553
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 60/360787
PRIOR APPLICATION NUMBER: 60/360787
PRIOR SECOID NOS: 231
NUMBER OF SEG ID NOS: 231
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/360787
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PatentIn version 3.2
SEQ ID NO 130
LENGTH: 19
TYPE: PRT
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Best Local S
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APPLICANT: Burke et al.
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                                                     Query Match
Best Local S
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CURRENT APPLICATION NUMBER: US/10/378,173
CURRENT FILING DATE: 2003-03-03
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                                                                                                                          NAME/KEY: MISC FEATURE
LOCATION: (7)...(7)
OTHER INFORMATION: phosphorylation
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LOCATION: (6). (6)
OTHER INFORMATION: phosphorylation
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OTHER INFORMATION: phosphorylated peptide
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14 SSEDE 18
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                                 12.2%; Score 5; DB (
100.0%; Pred. No. 10, 
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                 APPLICANT: Impact Diagnostics
TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruse:
TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papi
TITLE OF INVENTION: Associated Cancers
TILE REFERENCE: 3352-2-2-1
CURRENT APPLICATION NUMBER: PCT/US03/20887
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 60/394,172
PRIOR APPLICATION NUMBER: US 60/394,172
PRIOR FILING DATE: 2002-07-02
PRIOR FILING DATE: 2003-07-01
NUMBER: US (Not yet assigned)
PRIOR FILING DATE: 2003-07-01
NUMBER: OF SE0 ID NOS: 8
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PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 231
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CURRENT APPLICATION NUMBER: 1
CURRENT FILING DATE: 2003-0
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                                                                                                                                                                             LENGTH: 21
TYPE: PRT
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OTHER INFORMATION: phosphorylation
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OTHER INFORMATION: phosphorylation
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OTHER INFORMATION: phosphorylated peptide
                                                                                                                    OTHER INFORMATION: Derived from the E7 early coding region of
                                                                                                                                         FEATURE:
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                    ilarity 100.0%;
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                  12.2%; Score 5; DB 1
100.0%; Pred. No. 11
ive 0; Mismatches
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100.0%; Pred. No.
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RESULT 11
US-10-378-173-167
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                                                                                                ; TYPE: PRT; CRGANISM: Zea mays
US-60-479-962-461
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SOFTWARE: PatentIn ver
SEQ ID NO 461
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 167
                               Matches
                             Best Local Similarity 100 Matches 5; Conservative
                                                               Query Match
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APPLICANT: LeDeaux, John R
APPLICANT: Fabbri, Brandon J
APPLICANT: Fabbri, Brandon J
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Protein in Plants
FILE REFERENCE: 38-21 (53372)A
CURRENT EPPLICATION NUMBER: US/60/479,962
CURRENT FILING DATE: 2003-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Burke et al.
TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO FILE REFERENCE: MDSP-P01-023
CURRENT APPLICATION NUMBER: US/10/378,173
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 60/360787
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Monsanto Technology, LLC
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LOCATION: (8) . (8)
OTHER INFORMATION: phosphorylation
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: phosphorylation
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100.0%;
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                               Mismatches
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEV: misc_feature
LOCATION: (1) ... (85)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-273-573-8009
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US-10-273-573-8011
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Best Local Similarity
Matches 5; Conserve
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US-10-273-573-8009
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Sequence 8009, Application.
Sequence 8009, Application.
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
APPLICANT: INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: US/10/273,573
                                                                 Query Match
Best Local S
Matches 5
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SOFTWARE: Custom
SEQ ID NO 8009
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SEQ ID NO 8011
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/770,160 PRIOR FILING DATE: 2001-01-26
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                                                                                                                                                                                                                                            LENGTH: 90
TYPE: PRT
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 10994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc
                                                                                                                                                     FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(90)

OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd
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RESULT 2 S44954 Limbo protein - Strep C,Species: Streptom C,Date: 13-Jan-1995 C,Date: 13-Jan-1995 C,Date: 13-Jan-1995 C,Peschee, U, Schm. Mol. Microbiol 16, A,Fittle: Molecular A,Reference number: A,Accession: S69816 A,Status: prelliminaa A,Molecule type: DNI A,Residues: 1-266 A,Fote: the nucleot: C,Genetics: C,Genetics:	Query Match Best Local Matches Qy 29 Db 4	RESULT 1 E86425 C;Species: Arabidogo C;Date: 02-Mar-2001 C;Accession: E86425 R;Theologis, A.; Ec) Chin, C.W.; Hughes, Nature 408, 816-820, A;Authors: Hunter, C.A.; Li, J.H.; Li, Rizzo, M.; Rooney, 1 A;Authors: Salzberg, ker, M. Wu, D.; Yu, A;Title: Sequence and A;Reference number: A;Accession: E86425 A;Status: preliminal A;Residues: 1-221 A;Cross-references: C;Genetics: C;Genetics: C;Senetics: C;Genetics: C;Genetic		4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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yces lincolni lincolnensi quence_revis /4954 H.; Zhang, 7-1156, 1995 7-1156, 1995 acterization 805; MUID:96 nucleic acid h.:X79146; NI	17.1%; 100.0%; ive 0	[7.6 - Arabi haliana (mo puence_revis J.R.; Palm, L.; Conn, L.; Conn, L.; Conn, L.; Conn, L.; Contagn, L.; Schemat, Z.; Sc		271 2 AB 277 1 00 279 2 172 288 2 17 300 2 16 300 2 16 300 2 17 301 2 17 301 2 17 302 7 2 13 327 2 13 327 2 13 327 2 13 327 2 13 327 2 13 327 2 13 327 2 13 327 2 13
-1995 #text ersberg, W. ncomycin-pr ID:8577249 not shown; pIDN:CAA55	core 7; DB 2; Leng Pred. No. 6.6; Mismatches 0;	RESULT 1 E86425 hypothetical protein T2H7.6 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change C;Accession: E86425 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J. C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arab A;Accession: E86425 A;Accession: B86425 A;Residues: 1-221 <sto> A;Cross-refterences: G8:AE005172; NID:g11094784; PIDN:AAG29716.1; C;Genetics: A;Map position: 1</sto>	ALIGNMENTS	AB0754 QQBEC2 T25579 T15735 T15735 T157321 T17321 P85068 P85068 T36087 T36087 T36087 T36087 T36087 T36087 T36087
change 22-Oct-1999 coduction gene cluster of translation not shown 753.1; PID:g487697 L Data Library, May 1994	th 221; Indels 0; Gaps 0;	31-Dec-2001 11, S.; White, O.; Creasy, T.H.; De S.; Khaykin, E.; I.S.; Maiti, R.; M i. A.M.; Sun, H.; ibidopsis.		conserved hypothet HKRFX protein - hu hypothetical prote hypothetical prote DNA processing Smf probable SKP1-like hypothetical protein [i protein F20N2.8 [i protein F20N2.8 [i probable binding p FIP1 protein - yea hypothetical prote ABC transporter in TATA-binding prote hypothetical prote
Strepton		.; Alonso, Dewar, K.; .; Kim, C., Marziali, ; Tallon, I		

A; Gene: 1mbG

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m N,Alternate} names: hypothetical protein L0919
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                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F22G12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T21278
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A;Cross-references: EMBL:Z92831; PIDN:CAB07366.1; GSPDB:GN00019; CESP:F22G12.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Purnelle, B.; Goffeau, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: Streptomyces lincolnensis lmbG protein
                                                                                                                                                                                                                                                        A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
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A; Residues: 1-318 < PUR>
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                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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A;Experimental source: strain 972h-; cosmid c16C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: T41105
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100.0%; Pred. No
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)%; Pred. No. 11;
0; Mismatches
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proliferation potential-related protein - mouse C;Species: Mus musculus (house mouse) C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 C;Accession: T42727
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A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83889
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A;Cross-references: EMBL:U83913; NID:g3858884;
A;Cross-references: strain Balb/C
                                                                         R; Takami, H.; Nakasone, Nucleic Acids Res. 28,
                                                                                                                hypothetical protein BH1916 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: D83889
                                                                                                                                                                                                         D83889
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A; Accession: T42727
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A;Map position: 12L
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A; Accession: S64785
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C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2
C;Accession: S64785
R;Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Function:
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7; Conserv
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                                                                                             K., Takaki,
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k; Pred. No. 22;
0; Mismatches
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                                                                                        Y.; Maeno,
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                                                                                             R.; Masui, N.; Fuji,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN: AAC72432
                                                       Bacillus halodurans
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C;Accession: B44890
R;Tawheed, A.R.; Beaudenon, S.; Favre, M.; Orth, G.
J. Clin. Microbiol. 29, 2656-2660, 1991
A;Title: Characterization of human papillomavirus type 66
A;Reference number: A44890; MUID:92129556; PMID:1663515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DN/
A; Residues: 1-51 < ST
A; Cross-references:
RESULT 10
$36528
$7 protein - human papillomavirus type 53
$1 proteis: human papillomavirus type 53
$2;Species: human papillomavirus type 53
$2;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                             R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus
A;Reference number: S36469
                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X74483; NID:g397053; PIDN:CAA52597.1; PID:g397055
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                E7 protein - human papillomavirus type 56 C;Species: human papillomavirus type 56 C;Date: 20-Feb-1995 #sequence_revision 20-C;Accession: S36580
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C;Species: human papillomavirus type 66
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-May-1998
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A; Residues: 1-105 < DEL>
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C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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A; Residues: 1-105 < TAW>
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100.0%; Pr/
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100.0%; Pred. No
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100.0%; Pred. No.
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A;Molecule type: DNA
A;Residues: 1-113 <OST>
A;Crose-references: EMBL:M37717
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E7 protein - rhesus papillomavirus (''''''''.)
C;Species: rhesus papillomavirus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <STO>
A;Cross-references: GB:AE005174; NID:g12518469; PIDN:AAG58842.1; GSPDB:GN00145; UWGP:Z51:
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                         R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Filler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou Nature 409, 529-533, 2001
A;Tille: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F86047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 181, 424-429, 1991
A;Tille: Characterization of the complete RhPV 1 genomic
A;Reference number: A38503; MUID:91135018; PMID:1847267
A;Accession: B38503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, August 1993 A;Description: Primer-directed sequencing of human
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R;Delius, H.; Hofmar
                                                                                                                                                                                                                                                                                                                               hypothetical protein Z5129 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli (c;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: F86047
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A; Residues: 1-105 < DEL>
                                                                            A;Gene:
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SEDEDI 20

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A;Molecule type: DNA
A;Residues: 1-148 <FUL>
A;Cross_references: EMBL:U10398; NID:g551328; PIDN:AAB68421.1; PID:g551329; MIPS:YHR136d
                                                                          submitted to the EMBL Data Library, June 1994
A;Description: The sequence of S. cerevisiae cosmid 9315.
A;Reference number: S48967
A;Accession: S48980
                                                                                                                                                                                                         hypothetical protein YHR136c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 23-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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(;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                      S48980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:BA000007; PIDN:BAB38001.1; PID:g13364053; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ECs4578 (imported) - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
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Biophnys. Res. Commun. 263, 723-727, 1999
Biochem. Biophnys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin,
A;Reference number: PC7027; MUID:99443731; PMID:10512747
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;Accession: B91201
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N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
8, 11-22, 2001
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C;Genetics:
A;Gene: SGD:SDL2
A;Gene: SGD:SD001178; MIPS:YHR136c
A;Map position: 8R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YHR136c
Query Match
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 17 DEDIFE 22
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Db 135 DEDIFE 140
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Search completed: July 24, Job time: 10.9224 secs

2003, 12:27:17

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Title:
Perfect score:
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41
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  GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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CAKE COTJA
YL34 YEAST
VE7 HPV53
VE7 HPV56
VE7 HPV66
VE7 RT RIAB
ABAI TRIAB
ABA2 TRIAB
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ABA2 TRIAB
ABA YHT6 YEAST
YE54 SCHPO
OMTB2 BACAM
YL13 YEAST
YE54 SCHPO
OMTB2 BACAM
YL14 YEAST
YE54 SCHPO
OMTB2 BACSU
MF0F SALTYV
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YADA STAHA
YADA TARATT
DAA BOVIN
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P09711 human cyto-
p54694 staphylocc
Q09265 caenorhabd
P39813 bacillus gal
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P39813 bacillus gal
Q013371 homo sapie
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Q013376 gallus gal
P45976 saccharomy
Q9wtq6 rattus nor
Q9sta homo sapie
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P46196 bos taurus
P26696 xenopus la
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Human papillomavirus ty
Viruses; dsDNA viruses,
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Hypothetical protein; ATP-binding; Repeat.

NP_BIND 246 253 ATP (POTENTIAL).

NP_BIND 574 581 ATP (POTENTIAL).
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InterPro; IPR003959; AAA_ATPase_centr.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft
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InterPro; IPR000148;
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Early protein; Trans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Viruses; dsDNA viruses, no RNA
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E7; 1. Transcription regulation; Oncogene;

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28-FEB-2003
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E7 protein.
E7.
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Viruses; dsDNA
Papillomavirus
                            Rhesus papillomavirus type 1 (Rhpv 1).
Viruses; dsDNA viruses, no RNA stage;
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o. 18;
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RESULT 7
ABA1_TRI/
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Best Local S
Matches 6
                                                              -!- SUBCELLULAR LOCATION: Secre
-!- SIMILARITY: Contains 1 C-ty
HSSP; P23806; 1IXX.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
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P81111;
                   SMART; SM
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M60184; AAA79312.1; -. PIR; B38503; W7WLR1. InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alboaggregin A subunit 1.
Trimeresurus albolabris (White-lipped pit viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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MEDLINE=91135018; PubMed=1847267;
MEDLINE=91135018; PubMed=1847267;
Ostrow R.S., Labresh K.V., Faras A.J.;
"Characterization of the complete RhPV 1 g
"Characterization locus from a metastatic tumor.
                                                                                                                                                                                                                                                                                                                                                                    Kowalska M.A., Tan L., Holt J.C., Calvete J.J., Niewiarowski S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology 181:424-429(1991).
-!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
                                                                                                                                                                                                         -!- SUBUNIT: Heterotetramer of the subunits
disulfide-linked.
                                                                                                                                                                                                                                                                          Thromb. Haemost. 79:
                                                                                                                                                                                                                                                                                                                        platelets."
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98189535; PubMed=9531050;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viperidae; Crotalinae; Trimeresurus.
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Early protein; Transcription regulation; Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                              "Alboaggregins A and B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lepidosauria; Squamata; Scleroglossa;
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                                                                                                                                                                                                                                                       agglutination.
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6; Conserv
                   PS00615; C_TYPE_LECTIN_1; 1. PS50041; C_TYPE_LECTIN_2; 1.
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106
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nds to platelet G
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                                                                                                                                                             c-type
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b; Pred. No. 19;
0; Mismatches
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C-XX-C MOTIF-2.
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                                                                                                                                                               lectin
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0. 19;
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P81112;
15-JUL-1998
15-JUL-1998
28-FEB-2003
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Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                         MEDLINE=98189535; PubMed=9531050; Kowalska M.A., Tan L., Holt J.C., Calvete J.J., Niewiarowski S.;
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Lepidosauria; Squamata; Scleroglossa; Serpentes;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                 P81115;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin B alpha subunit.
Trimeresurus albolabris (White-lipped pit viper).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABBA
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TISSUE=Venom;
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nes 6; Conserv
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SIMILARITY: Contains 1 C-type lectin family doma
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131 AA;
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. 36, Created)
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nds to platelet G
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127
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sequence update) annotation updat
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                                                                                                              Score 6; DB 1
Pred. No. 22;
0; Mismatches
                                                                                                                                                                                 C-TYPE LECTIN
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6;
Pred. No
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BY SIMILARITY.
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BY SIMILARITY.
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22;
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YHT6_YEAST
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01-FEB-1995 (Rel. 3
01-NOV-1997 (Rel. 3
Hypothetical 17.0 k
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SEQUENCE
                                                                                              MEDLINE=94378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Du Z., Favello A., Fulton L., Johnston L., Langston Y.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Macri C., Mardis E., Menezes S., Mouser L.
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001304; Lectin C.
InterPro; IPR0013990; Pancreatis ac.
Pfam; PF00059; lectin c: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alboaggregin A subunit 2.
Trimeresurus albolabris (White-lipped pit viper).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; I
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lectin.
                                     "Complete nucleotide VIII.";
                                                                                                                                                                                                                                                  STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical YHR136C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YHT6_YEAST
P38839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kowalska M.A., Tan L., Holt J. Calvete J.J., Niewiarowski S.;
               Science 265:2077-2082(1994).
                                                                               Vaudin M.;
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P23806; 1IXX.
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01-FEB-1995 (Rel. 31, 0

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Probable protein-tyros:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD; S0001178; SPL2.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0009266; P:response to temperature; IGI.
Hypothetical protein.
SEQUENCE 148 AA; 17036 MW; 67C02AA833FB42E9
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SGD;
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                                                                                                                                                                                                                                                                                        EMBL; X72385; CAA51078.1; -. PIR; S32124; S32124.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Apiales; Apiaceae; Daucus.
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InterPro; IPRO00387; TYR phosphatase.
Pfam; pF00782; DSPc; 1.
SMART; SM00195; DSPc; 1.
PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50054; TYR PHOSPHATASE DUAL; 1.
PYPOTHETICAL PROSPHATASE DUAL; 1.
PYPOTHETICAL PROSPHATASE DUAL; 1.
                                                                                                                                                                                                                                                                                                                    15-JUL-1998
30-MAY-2000
28-FEB-2003
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-i- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

-i- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
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SCHPO
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GO; GO:0005634; C:nucleus; IDA.
GO; GO:0017017; F:MAP kinase phosphatase activity; IDA.
GO; GO:000196; P:MAPKKK cascade (cell wall biogenesis)
InterPro; IPR000340; DS phosphatase.
InterPro; IPR000387; TYR phosphatase.
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PIR; S48459; S48459.
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                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                014171;
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                                                                                                                                                                                                                                                                Hypothetical protein C4D7.04c SPAC4D7.04C.
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MEDLINE=21848401;    PubMed=11859360;
                                 STRAIN=972
                                                                                                                                               Schizosaccharomycetales;
Schizosaccharomyces.
                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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4.
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Pred. No
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                                                                                                                                                                                                                                                                                            in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                678371462A890A69 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 264
                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
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MTB2_BACAM
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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brows S., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Simmonds M., Squares S., Kodonald S., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Wueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti E., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RT Mature 415:871-880 (2002)

D. Barrell B.G., Nurse P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990
01-NOV-1990
SEQUENCE FROM N.A.
STRAIN=H;
MEDLINE=90326538; PubMed=2374727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPTo; IPR001441; UPP_Synth.

Pfam; PF01255; UPP synthetase; 1.

ProDom; PD003461; UPP synth; 1.

TIGR00055; UPP; 1.

PROSITE; PS01066; UPP SYNTHETASE; 1.

Hypothetical protein; Transferase.
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                                                                                                                                                                   Bacillus amyloliquefaciens
Bacteria; Firmicutes; Baci
                                                                                                                                                                                                                                                                             specific
                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Modification methylase BamHII (EC 2.1.1.113)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
SEQUENCE 2
                                                                                                                                 NCBI_TaxID=1390;
                                                                                                                                                                                                                                              BAMHIIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE UPP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Z98602; CAB112
T38795; T38795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACAM
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                                                                                                                                                                                                                                                                      methyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                       Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rajandream M.A., Lyne M., Lyne
                                                                                                                                                                                                                                                                      BamHII)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 6;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7DCC6094B114D29D CRC64;
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                                                                                                                                                                                                                                                                      (M.BamHII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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InterPro; IPR002941; N6/N4 mtase.
InterPro; IPR000941; SAM bind.
Pfam; PF01555; N6 N4 mtase; 1.
PRINTS; PR00506; D21N6MTFRASE.
PRINTS; PR00506; D21NMTFRASE.
PRINTS; PR00508; S214MTFRASE; 1.
PROSITE; PS00093; N4 MTASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                      YDDK_BACSU
P96648;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                      BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                     Kasahara Y., Nakai S., Lee "A 148 kbp sequence of the Bacillus subtilis genome."; Submitted (MAR-1997) to the
                                                                                                                                                                                                                                                                              Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X53032; CAA37205.1;
PIR; S10316; S10316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Connaughton J.F., Kaloss W.D., Vanek P.G., Nardone G. Chirikjian J.G.;
                                                                                          MEDLINE=98044033; PubMed=9384377;
                                                                                                            STRAIN=168
                                                                                                                                                                                                                     STRAIN=168;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                           28-FEB-2003
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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REBASE; 186; M.BamHII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adenosyl-L-homocysteine + DNA N(4)-methylcytosine.
-!- MISCELLANEOUS: THIS METHYLASE IS ENCODED ON THE PROVIRAL PHAGE H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete sequence BamHI methylase gene.";
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001091; CN4_Metransf.
InterPro; IPR002295; D21N6_mtfrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leic Acids Res. 18:4002-4002(1990)
FUNCTION: THIS PRECIFIC METHYLASE RECORDIZES THE DOUBLE-STRANDED SEQUENCY
GGATCC, CAUSES SPECIFIC METHYLATION ON C-5 ON BOTH STRANDS, AND
PROTECTS THE DNA FROM CLEAVAGE BY THE BAMHI ENDONUCLEASE.
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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3 (Rel. 41, Last seque
3 (Rel. 41, Last annotation and protein yddK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methyltransferase; Restriction system. 65 AA; 30981 MW; 895A51217A814820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.6%;
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                                                                                                                                                                                  S., Sadaie Y., region between
                                                                                                                                                                                                                                                                                                                                           annotation
                                                                                                                                                                                                                                                                                                                                                         sequence update)
                                                                                                                                                         EMBL/GenBank/DDBJ databases
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Pred. No.
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35 and 47
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RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Sooffone F.,
RA Scrökin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                        EMBL; AB001488; BAA19337.1; -.
EMBL; Z99106; CAB12307.1; -.
PIR; D69776; D69776;
SubtiList; BG12118; YddK.
InterPro; IPR000157; TIR_domain.
SMART; SM00255; TIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 266 AA; 31288 MW; E65A1ECE3D2CE8CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghimm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.
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Hilbert H., Holsappel S., Hosono
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158 DEDIFE 163
                                              17 DEDIFE 22
                                                                                               Conservative
                                                                                            14.6%; Score 6; DB:
100.0%; Pred. No. 42.
Live 0; Mismatches
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Haga K., Haieth J., Harwood C.R., Honaut A.
S., Hosono S., Hullo M.F., Itaya M., Jones L.
Kasahara Y., Klaerr-Blanchard M., Klein C.,
                                                                                                                    DB 1;
lo. 42;
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Search completed: July 24, 2003, 12:22:06 Job time: 4.70132 secs 밁 ફ Query Match
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DB seq length: 2000000000
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Match
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
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41
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sp_virus:*
sp_vertebrate:*
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Q96ch9 homo sapien
Q8xm35 clostridium
O93393 gallus gall
Q9c6z5 arabidopsis
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Q54360 s
Q8x0j7 n
Q9y7p4 s
Q8ixq4 h
Q8bny8 mus musculu
Q940b8 arabidopsis
Q9lus1 arabidopsis
Q08721 rattus norv
                                       Q8ixq4 homo sapien
Q9c0f9 homo sapien
Q45396 caenorhabdi
                                                                                                                                                    Q9ulh6 homo sapien
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                                                                     neurospora
schizosacch
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165	163	159	158	155	154	154	153	148	136	135	135	133	126	124	123	123	120	117	111	96	89	69	83	65	57	51	1591	1524
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P72251	Q9ARN1	Q8CHY9	Q9EYD0	032248	Q9YGN5	Q8WW89	085178	P87290	Q91841	Q8IQR5	Q93P25	Q15908	Q8N8D9	Q65327	085638	052132	Q8NWH0	Q9LGA2	Q8PAC7	036208	Q9B049	QBPUC7	Q922X7	Q8ZV17	Q9UNX2	Q9KBL0	P97868	Q8RYN2
rhodosj	Q9arn1 oryza sativ	mus m		O32248 bacillus su	Q9ygn5 agkistrodon	Q8wmw9 bos taurus		Ð		Q8iqr5 drosophila		homo	-37	Q65327 orgyia pseu	O85638 escherichia	O52132 escherichia	staph	Q9lga2 oryza sativ	Q8pac7 xanthomonas	O36208 human immun	Q9b049 mycobacteri		Q922x7 mus musculu	Q8zv17 pyrobaculum	Q9unx2 homo sapien	bac		Q8ryn2 oryza sativ

ALIGNMENTS

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RESULT 2
Q8N4Y4
ID Q8N4
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Q9ULH6
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Best Local S
Matches 41
Q8N4Y4 .. I
Q8N4Y4;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                             "KIĀA1244 as a novel distantly related member (BIG3) of the BIG1/Sec7p subfamily of ARF GEFs.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413080; AAL04174.1; -.
InterPro; IPR000904; Sec7.
SMART; SM00222; Sec7; 1.
                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 1770 AA; 195845 MW;
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ULH6; Q96P46;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 Hong W.;
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                                                                                                                                                               ch 100.0%; Score 41; DB 4; 1
1 Similarity 100.0%; Pred. No. 3.9e-36;
41; Conservative 0; Mismatches 0;
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(TrEMBLrel. 22, (TrEMBLrel. 22,
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Matches 33
                                                                                                                                                                                                                                                                                                                   Q8XM35;
01-MAR-2002
01-MAR-2002
01-MAR-2003
                           SEQUENCE FROM N.A. STRAIN=13 / Type A; PubMed=11792842;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
   Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similar to KIAA1244
                                                                                                                                                                         Clostridium perfringens.
Bacteria; Firmicutes; Clostridia;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8XM35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; BC014227; AAH14227.1; -.
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Mammalia; Eutheria;
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Ohtani K.,
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Primates;
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   Hirakawa
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Last annotation updat
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F4A1E807B0DF47B5 CRC64;
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H., Ohshima K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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8.5e-28;
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8.5e-28;
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   Yamashita
                                                                                                                                                                                                    Clostridiaceae;
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RESULT 5
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Best Local (
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O93393;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative calcium-activated potassium channel regulatory
(Calcium-activated potassium channel beta subunit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003251; Rubrerythrin.
InterPro; IPR006895; zf.Sec23 Sec24.
Pfam; PF09915; Rubrerythrin; 1.
Pfam; PF04810; zf.Sec23 Sec24; 1.
ProDom; PD006198; Rubrerythrin; 1.
                                                                                                                                                                                                                                                                                         Balt S.L., Hudspeth A.J.;
Submitted (SEP-2001) to the
EMBL; AF077369; AAC27490.1;
EMBL; AF420468; AAL16898.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Oberst C., Bister K.; "Chicken homolog of a quail gene (CO6) encoding a membrane related to mammalian potassium channel regulatory subunits. Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Oberst C., Bister
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97224079; PubMed=9070660;
Oberst C., Weiskirchen R., Hartl M.,
"Suppression in transformed avian fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Archosauria; Aves; N
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                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                  InterPro; IPR003930;
Pfam; PF03185; CaKB;
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subunits.";
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73
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                                                                                        Similarity 7; Conserv
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7; Conserve
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SEDEDIF
                                             SEDEDIF 21
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                                                                                                                                                                                              200 AA;
                                                                                           Conservative
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  79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani
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                                                                                                                                                                                              22663 MW;
                                                                                                                    17.1%;
100.0%;
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Pred. No.
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                                                                                                                    DB 13;
o. 9.3;
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RESULT Q9C6Z5

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White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheu R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Peldblyum T.V., Peng J.-D., Fong B., Fujii C.Y.,

A Chung M.K., Conn L., Conway A.B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Ngyyen M., Nierman M.C., Osborne B.I.,

A Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Militscher J., Tambunga G., Toriumi M.J., Town C.D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Mu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 7
 Query Match
                                                                                                                                                                                                                                                                                                                                                                              Q54360;
Q54360;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                       LMBG
                                       SEQUENCE
                                                     Peschke U., Schmidt H., Zhang H.Z., Piepersberg W.; "Molecular characterization of the lincomycin-production of Streptomyces lincolnensis 78-11."; Mol. Microbiol. 16:1137-1156(1995).
EMBL; X79146; CAA55753.1; -.
                                                                                                                                                                     STRAIN=78-11
                                                                                                                                                                                                                      Streptomycineae; Streptomycetaceae; Streptomyces
NCBI_TaxID=1915;
                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                 Streptomyces lincolnensis.
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
SEQUENCE 22
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EMBL; AC074176; AAG50860.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21016719; PubMed=11130712;
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01-JUN-2001
                                                                                                                                                 MEDLINE=96020646;
                                                                                                                                                                                       SEQUENCE FROM N.A.
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STRAIN=cv. Columbia;
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                     29268 MW;
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17.18;
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Last sequence update)
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Last annotation updat
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                                     F21C81B6207DFB24 CRC64;
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 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                   266 AA
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 BB
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edons; core eudicots; Rosidae;
2;
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Length 266;
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.F., Chin C.W.,
Creasy T.H., Dewar K.
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                                                                                                            gene cluster
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Q8X0J7
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Q9Y7P4
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Y7P4;
 SEQUENCE
                     Ribosomal
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Best Local Similarity Matches 7; Conserv
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01-MAR-2003 (TrEMBLrel.
Mitochondrial ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German Neurospora genome proje
Submitted (JAN-2002) to the EM
EMBL; AL670005; CAD21276.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Cr
01-MAR-2002 (TrEMBLrel. 20, La
01-OCT-2002 (TrEMBLrel. 22, La
Hypothetical 30.7 kDa protein.
                         Pfam; PF00181; Ribosomal L2; 1.
Pfam; PF03947; Ribosomal L2_C; 1.
TIGRFAMs; TIGRR1171; rplB bact; 1.
PROSITE; PS00467; RIBOSOMAL L2; 1.
                                                                                                                                      Submitted (SEP-1998) to the EMBL; AL031535; CAB38631.1; HSSP; P04257; IRL2.
                                                                                                                                                                                 SEQUENCE:
STRAIN=972h-;
STRAIN=972h-;
GOFfeau
                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 280 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheise
Nyakatura G., Mewes H.W., Ma
Submitted (JAN-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.
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                                                                                                                                                                                                                                                                        Schizosaccharomyces.
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                                                                                       GeneDB_SPombe; SPCC16C4.15; -...
InterPro; IPR005880; L2_bact_org.
InterPro; IPR002171; Ribosomal_L2
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=4896;
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7; Conserv
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protein.
318 AA;
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
al ribosomal protein L2.
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 35211 MW;
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                                                                                                                                                                                           Wood V.,
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ne EMBL/GenBank/DDBJ
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Last
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 4CBC78529658F93E CRC64;
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annotation updat
                                                                                                                                                                                           Rajandream M.A.,
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RESULT
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Best Local S
Matches 7
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Best Local S
Matches 7
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Best Local Similarity
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein KIAA1704 (Fragment).
KIAA1704.
                                                                                                                                                                                                                                                                      EDUENCE FROM N.A.

MEDLINE=21082932; PubMed=11214970;

MEDLINE=21082932; PubMed=11214970;

Mikuno R., Hattori A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9C0F9;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Similar to RIKEN CDNA 1200011I18 gene.
                                                                                                                                                                                                                                     Nagase T., Kikuno R., Hattori A., Kongo "Prediction of the coding sequences of The complete sequences of 100 new cDNA
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (NOV-2002) to the
EMBL; BC039586; AAH39586.1;
SEQUENCE 340 AA; 38141 M
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                                                                                                                                                           Hypothetical protein.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ovary;
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                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                              Res.
                                                                                                                                                                                            large proteins in vitro.";
Res. 7:347-355(2000).
.; AB051491; BAB21795.1; -.
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                                                                    7; Conserv
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                                    SSEDEDI 20
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                                                                                                                                         351 AA;
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                                                                      Conservative
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Primates;
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Primates;
                                                                                                                                         39406 MW;
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100.0%;
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                                                                                                       17.1%;
                                                                                        100.0%;
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Pred. No.
                                                                                      Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F752A6A2917132E6
                                                                                                                                         6F5252CB5A6FE2F2 CRC64;
                                                                      Mismatches
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                                                                                                                                                                                                                                             Kondo Y., Okumura K., Ohara O.; es of unidentified human genes. cDNA clones from brain which co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351
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                                                                                      DB 4
). 15;
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DT 01-JU
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GN Caeno
OC Eukar
OC Rhabd
OX NCB1
RN [1]
RP SEQUE
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Retinoblastoma binding protein 6 (Fragment).
Mus musculus (Mouse)
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01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                        The FANTOM Consortium,
the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based o
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. investigating biology."; Science 282:2012-2018 (1998). EMBL, 292831, CAB07366.1; -. WormPep; F22G12.2; CE15889. InterPro; IPR001584; Rve.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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SEOUENCE 402 AA; 44
                                                                                               SEQUENCE
                                                                                                               EMBL; AK079129; BAC37553.1; -.
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01-MAR-2003
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Submitted (MAR-1997)
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                                                                                               48396 MW; A0D10DD8BCCAFCD4 CRC64;
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tive 0; Mismatches
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; AV056129; AAL07208.1; -
R Interpro; IPR001752; kinesin motor.
Pfam; PF00225; kinesin; 1.
R Pfam; PF00225; kinesin; 1.
R PRINTS; PR00380; KINESINHEAVY.
R SMART; SM00129; KISC; 1.
R PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
R PROSITE; PS00411; KINESIN_MOTOR_DOMAIN2; 1.
R PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
SEQUENCE 794 AA; 89081 MW; 13CBD4DDBEE2454B CRC64;
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Q940B8;
01-DEC-2001
01-DEC-2001
01-MAR-2003
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Q9LUS1;
Q1-CT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similarity to kinesin protein.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Ekkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                            "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC clones.";
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                          STRAIN=Columbia;
MEDLINE=20277480; PubMed=10819329;
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STRAIN=Columbia;
Sato S., Nakamura
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100.0%; Pred. No.
tive 0; Mismatc
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o the EMBL/GenBank/DDBJ databases.
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PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Microfubules; Motor protein.
ATP-binding; Coiled coil; Motor D700B00DB33A6647 CRC64;
SEQUENCE 799 AA; 89720 MW; D700B00DB33A6647 CRC64;
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HSSP; P17119; 31
                                                      Local Similarity nes 7; Conserv
648 VSPPRGK 654
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                                                           Conservative
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11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
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216
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

100.0 31.9	100.0	2 216 100.0 41 3 216 100.0 518 4 216 100.0 518		Result Query No. Score Match Length DB
22	978	8 8 1	41 23) 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
2 ABG09731 0 AAY48248			- ;	ID
Novel human diagno Human prostate can	PS118 prostate mar Novel human diagno Human protein SEQ	PS118 prostate mar PS118 protein enco Human prostate-spe	Human prostate-spe	Description

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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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AAU99324	52	ABP62812	w	AAG67399	AAU07894		w	AAW72152	AAW73139	AAR47811	AAW81867	ABG35521	AAM01498	AAM26151	AAM13753	AAM65886	AAM53508	ABB18177	ABB32686	ABB27527	ABG47541	ABB60513	ABG93257	AAB48964	AAW84052	AAR79912	AAB92836	J	79	8	ũ	5	В	607	AAE19559
Human CD63 antigen	Human nucleic acid	Human polypeptide	Human prostate can	acid s	ra .	human diagn	Candida albicans e	2 strain SBS	SBS	N	tumour supp	ptid	#180	#188	Peptide #187 encod	ne m	Human brain expres.	Protein #176 encod	Peptide #192 encod	ptide	Human liver peptid	Drosophila melanog	C. albicans BAX-as	lir		nucle		Human DITHP organe	ida alb:	l human	1 human	l human c	1 human	human c	Herpes simplex vir

ALIGNMENTS

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RRESULT 1
AAO19166
ID AAO1916
AC AAO1
XX AAO19
DT 27-N
DT 27-N
DT Huma
XX Huma
XX Homo
XX Homo
XX EST;
XX OS Homo
XX 26-N
PN US20
XX 26-N
XX 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate; prostate-specific sequence; prostate cancer; PS118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate-specific PS118 protein fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-2002 (first entry)
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                                                                                                                    (BILL/)
(COHE/)
(COLP/)
(FRIE/)
(GORD/)
                                                                                                                                                                                                                                                                                                                                                                           23-APR-1998;
23-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-2001; 2001US-0991681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST; expressed sequence tag; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002086316-A1.
                                                                                  (GRAN/)
                                  COHEN M.
COLPITTS T L.
FRIEDMAN P N.
GORDAN J.
GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                                                         BILLINGEL P A.
        KLASS M R.
                                                                                                                                                                                                                                                                                                                                                                           98US-0065383.
97US-0842385.
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RESULT 2
AAM50810
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
Billing-Medel
Granados EN,
                                                                                                                                                                         23-APR-1998;
                                                                                                                                                                                                                  US2001055758-A1
                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                     PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                               PS118 prostate marker immunogenic polypeptide.
                                                                                                                                                                                                                                                                                                                      01-MAY-2002
                                                                                                                                                                                                                                                                                                                                            AAM50810;
                                                                                                                                                                                                                                                                                                                                                                AAM50810 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-665429/71.
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Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Billingel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ROBE/)
(RUSS/)
(STRO/)
                                                                  (FRIE/)
(GORD/)
(GRAN/)
(HODG/)
                                                                                                                                                     23-APR-1997;
                                                                                                           (COPL/)
                                                                                                                                 (AILL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRAT/)
                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   -
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) ROBERTS-RAPP
) RUSSELL J C.
) STROUPE S D.
                                  KLASS M R.
KRATOCHVIL J D.
ROBERTS-RAPP L.
                                                                                                                                BILLING-MEDEL P
                                                                GRANADOS E N.
HODGES S C.
                                                                                       FRIEDMAN P N. GORDON J.
                                                                                                             COPLPITTS T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                       COHEN M
                                                                                                                                                                                                                                                                                                                                                                                                                              EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                   EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Cohen
, Hodges
Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                     (first entry)
    PA, Cohen
Hodges SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,
                                                                                                                                                     97US-0842385
                                                                                                                                                                         98US-0065383
                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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    M, Coplpitts TL, Friedman Klass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klass MR,
                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 216; DB 2
Pred. No. 1e-21;
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R, Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
   PN, Gordon J
Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordan J;
Roberts-Rapp L;
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RESULT 3
AAW85472
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Comprising amino acids 184-224 of human prostate-specific PS118
Comprising amino acids 184-224 of human prostate-specific PS118
Comprising amino acids 184-224 of human prostate-specific PS118
Comprising amino acids 184-284 of human prostate in prostate than
Comprising and at least 12 times more often in prostate than
Comprising amino acids prostate polymerleotides,
Comprising the prostation of an individual to, diseases and conditions of the
Comprising comprising prostatic hyperplasia, prostations of the
Comprising comprising prostatic hyperplasia, prostations and
Comprising comprising prostations of the
Comprising prostations conner, tumours and
Comprising prostates and prostations of the
Comprising prostates and prostations of the
Comprising prostates and provides and prostations and
Comprising prostate and may also provide new markers which can differentiate
Comprising prostate cancers which can differentiate
Comprising prostate and may also provide new markers which can differentiate
Comprising prostate cancers which can differentiate concers the comprision of the contraction of the cont
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Best Local S
Matches 41
WPI; 1998-610000/51
N-PSDB; AAV82812.
                                                             Billing-medel PA,
Granados EN, Hod
Russell JC, Stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate disease -
                                                                                                                                                                                                                                              23-APR-1998;
                                                                                                                                                                                                                                                                                         29-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    EST clone; PS118; prostate tumour tissue; prostatic disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS118 protein encoded by consensus sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW85472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 without the use of surgery.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 43; 57pp; English
                                                                                                                                                                                                   23-APR-1997;
                                                                                                                                                                                                                                                                                                                                WO9848054-A1
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                                                                                                                                                        (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; silarity 100.0%; sometive 0;
                                                                 Hodges
Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first_entry)
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                                                                                                                                                                                                   97US-0842385
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                                                               Cohen M, Colpitts TL, les SC, Klass MR, Kratupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 216; DB 23; Pred. No. 1e-21; Mismatches 0;
                                                                                        g TL, Friedman
Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23;
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                                                                 PN, Gorus.
Robertsrapp L;
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acid

and proteins

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RESULT 4
AAO19165
ID AAO1
XX AAO1
XX AAO1
XX Huma
XX Huma
XX Huma
XX Homc
XX (S1)
PA (COI
PA (
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Best Local
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                                                         Billingel
Granados E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
EST; ex
                                                                                                                                                                                                                                                                                                                                                                                        23-APR-1998;
23-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate-specific PS118 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                           (BILL/)
(COHE/)
(COLP/)
(FRIE/)
(GORD/)
(GRAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening
                                                                                                                                          (KRAT/)
(ROBE/)
(RUSS/)
                                                                                                                                                                                                     (HODG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed
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                                                                                                                                                                                                                                              FRIEDMAN P N.
) GORDAN J.
GRANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate;
                         PA,
EN,
JC,
                                                                                                                  HODGES S C.
KLASS M R.
KRATOCHVIL J I
ROBERTS-RAPP I
RUSSELL J C.
STROUPE S D.
                                                                                                                                                                                                                                                                                                       COLPITTS
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sequence tag; cytostatic; gene therapy.
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97US-0842385.
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                                                         Colpitts TL,
Klass MR, 1
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Pred. No. 1.9e-20;
; Mismatches 0;
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                                                         Friedman
Kratochvil
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                                                     Gordan J;
Roberts-Rapp
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RRESULT 5
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AAMSOS 1
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AX COHOMO 27-D
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PD 27-D
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XX COHOMO 2
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                          Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS118; prostate; man
benign prostatic hyp
prostatitis; human;
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                                                                                                                                                                                                                                      Granados
                                                                                                                                                                                                                                                       Billing-Medel PA,
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(GORD/)
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DB; ABA91651.
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GORDON J.
GRANADOS E N.
HODGES S C.
KLASS M R.
KRATOCHVIL J I
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nilarity 100.
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les SC,
pe SD;
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Klass MR, Kratochvil JD, Roberts-Rapp
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No. 1.9e-20;
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                                                                    prognosticating,
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Consensus sequence is found at least 12 times more often in
prostate than in non-prostate tissue. PS118 polypeptides,
including derivatives of the present sequence, polynucleotides,
contribodies, agonists and inhibitors are useful for detecting,
contribodies, staging, monitoring, prognosticating, preventing and
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contribution of the prostate cancer, tumours and
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contribution of the prostate can be produced by expression
contribution of the invention may provide an early means of
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Best Local !
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome
                                                                                                  Claim 20; SEQ ID No 40087; 103pp; English.
                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                              Drmanac RT,
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23-AUG-2000; 2000US-0649167.
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/peptide, as predicted from a partial consensus cDNA sequence
                                                                                                                                                                                                                                                                        2001-639362/73.
DB; AAS73915.
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Pred. No. 1.9e-20;
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CC Onte: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coaquilation disorder; nootropic; antiallergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide; immunostimulant; cerebroprotective.
                                                                                           aberrant
                                                                                                                         New isolated polynucleotide, useful in research, diagnostic therapeutic methods, e.g. preventing or treating disorders i
                                                                                                                                                                                                                    WPI; 2002-590824/63.
N-PSDB; ABQ99421.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000; 2000US-0714936
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                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                Xue AJ,
                                                                              rıc methods, e.g. preventing
protein expression or biolog
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                                                                                                                                                                                                                                                                                                             Goodrich RW,
ue AJ, Yang
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                                                                                                                                                                                                                                                                                                                Liu C, Zhou P, Asundi V,
, Wehrman T, Drmanac RT;
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                                                                                        or biological
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Pred. No. 8e-20;
Mismatches
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Claim

20; SEQ

ID 495;

394pp; English

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RESULT 8
ABG09731
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CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO or this patent did not format directly from WIPO
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Best Local S
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                            WPI; 2001-639362/73.
N-PSDB; AAS73918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                   RT,
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                                                                                                                                                                                                                                                                           Liu C,
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Pred. No. 8.2e-20;
); Mismatches 0;
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밁 δ

This invention describes novel nucleic acid sequences

(A) that are

Claim 22; 128; 166pp; German.

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RESULT 9
AAY4A
AC AAY4
AC AAY4
AC AAY4
AC BAY4
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CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO
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Best Local Similarity
                                                                                                                    New nucleic acid expressed at high level in prostatic encoded polypeptides, useful for treating cancer and therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1999
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                                                                                                                                                                                                                                                                                                                                Specht T, Hinzmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tag; EST; prostate tumor; antitumor; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate cancer-associated protein 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY48248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        98DE-1011193
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                                                                                                                                                                                                                                                                                                                                      Schmitt A,
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Pred. No. 8.9e-20;
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                                                                                                                                                                                                                                                                                                                                   Pilarsky C,
                                                                                                                                                                                                                                                                                                                                   Dahl E,
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                                                                                                                                                      screening
                                                                                                                                                      tumor tissue screening for
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                                                                                                                                                                                                                                                                                                                                      Rosenthal A;
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RESULT 10
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Best Local :
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                                                                                                                                              The invention relates to a method of detecting an agent for use in the treatment of herpes virus infection. The method comprises formin a herpes virus polypeptide/zinc complex; adding a test agent to the polypeptide/zinc complex, and detecting any change in the complex. The invention also relates to the use of known agents, such as 2,2'-dithiobisbenzamide (DIBA) and azodicarbonanide (ADA), and unknown agents for the manufacture of a medicament for the treatment of
                                                    herpes virus infections. The method is useful for detecting agents for use in the treatment of herpes virus infection. The present sequence is Herpes simplex virus type 2 (HSV2) IE63 protein homologue
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Fig 1; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the test agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting an agent useful for treating herpes virus infection comprises determining any change in a polypeptide/zinc complex in the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-226983/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clements JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2001; 2001WO-GB03114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpes simplex virus type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes virus infection; detection; therapy; IE63 protein; antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpes simplex virus type 2 (HSV-2) IE63 protein homologue.
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belongs to alphaherpes virus sub-family. IE63 protein is also
ed ICP27.
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Pred. No.
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Sequence

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RESULT 11
ABG06075
The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, and in recombinant production of (II). The collectides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for testore normal activity of (II) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. CC The polypeptide and polypurelectide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and no acid sequences. ABG00010-ABG30377 represent novel human continued and acid sequences of the invention.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                             Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
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2000US-0649167.
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Pred. No. 3
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Query Match

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Matches
                                                                                                                                                                                                                                                    polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PR) primers oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and the protone and polynucleotide sequences have applications.
                                                       and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from WI at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 41174; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Sequence
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23-AUG-2000; 2000US-0649167.
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DB; AAS75002.
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17; Conser
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ilarity 35.4%;
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6; Mismatches
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Query Match

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RESULT 13
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                                        CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polypeptide (II) sequences, (II) is useful as hybridisation probes, CC polypucleotides are also used in diagnostics as expressed equence tags (II). The CC polypucleotides are also used in diagnostics as expressed sequence tags (II). (II) is useful in gene therapy techniques (II) cristore normal activity of (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or comparitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating comparing of sites expressing (II). (I) and (II) are useful for treating comparing of sites expressing (II). (I) and (II) are useful for treating comparing of sites expression or biological activity. The polypeptide and polymucleotide sequences have applications in comparing and to produce other types of data and products dependent on DNA and comparing and to produce other types of data and products dependent on DNA and comparation acid sequences. ABG00010-ABG30377 represent novel human comparation, but was obtained in electronic format directly from WIPO are contacted in the printed experification, but was obtained in electronic format directly from WIPO are contacted in the printed expression in the printed experification, but was obtained in electronic format directly from WIPO are contacted the contact and contacted in the printed experification in the printed experification.
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23-AUG-2000; 2000US-0649167.
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food supplement; medical imaging; diagnostic; genetic disorder.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 36977; 103pp; English
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CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC (III). (II) a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC diagnostics mains acid sequences of the invention.
CC diagnostic amino acid sequences of the invention.
CC diagnostic amino acid sequences of the invention.
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                                                                                                                  Sequence
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23-AUG-2000; 2000US-0649167.
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CC diagnostics, forensics, gene mapping, identification of mutations (II) and to produce other types of data and products dependent on DNA and and act as a second of the invention.

CC and to produce other types of data and products dependent on DNA and (II) are useful and sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC second action, but was obtained in electronic format directly from WIPO (II) are treating the product of the invention.
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags
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imaging; diagnostic; genetic disorder.
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-25-243-41
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US-09-303-064-55
US-08-132-649-6
US-08-677-579-6
US-08-615-170-16
US-08-615-170-16
US-08-630-915A-196
US-08-630-915A-196
US-08-931-080-26
US-08-931-080-26
US-08-931-284-28
US-08-938-534-28
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	•	18,	18,		Sequence 15, Appl	'n			e 2,	Sequence 4238, Ap	۳	Sequence 3237, Ap	Sequence 2, Appli	Sequence 47, Appl	-	Sequence 2, Appli	Sequence 5, Appli

ALIGNMENTS

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Sequence 28, Applicat Patent No. 6391543 GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 41 amino acids
                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/842,38
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                 ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: REAGENTS AND TITLE OF INVENTION: FOR DETECTING NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDORESS: ADDORESSEE; ADDORT LABORATORIES
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/065,383 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 Abbott Park Road CITY: Abbott Park
                                                                               TELEFAX: 847/938-2623
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ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
STEPHEN D.
NVENTION: REAGENTS AN
    41 amino acids
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
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amino acid

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; MOLECULE TYPE: No. 6391543e US-09-065-383-28
                                                 ; MOLECULE TYPE: US-09-065-383-27
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Query Match
Best Local Similarity
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                                                                                                                                                                                               NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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APPLICANT: KLASS, MI
APPLICANT: KLASS, MI
APPLICANT: KRATOCHYI
APPLICANT: ROBERTS-F
APPLICANT: RUSSELL,
APPLICANT: STROUPE,
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
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ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
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                                                                                 STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                TYPE: amino acids
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mes 41; Conservative
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TOPOLOGY: lin
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CLASSIFICATION:
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ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
VENTION: REAGENTS AND METHODS USEFUL
VENTION: FOR DETECTING DISEASES OF THE PROSTATE
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
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                                                                  No. 6391543e
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Pred. No. 6.7e-22;
 Score 216; DB 4;
Pred. No. 1.2e-20;
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               Length 518;
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US-09-241-333-3
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Sequence 3, Application US/09241333 Patent No. 6313266
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Best Local Similarity
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APPLICANT: Bandman
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SEQUENCE CHARACTERISTICS:
LENGTH: 714 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                   MEDIAL
LIBRARY: Gen-
TONE: 128842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: Herew: CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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                                                                                             248 EDEDEEEDEEEEEEEEEEEEEPVKPAPGKRKKE 284
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                 650-845-4166
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Shah, Purvi
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Pred. No. 2.8;
8; Mismatches 1
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GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Yue, Henry Corley, Neil C.

Bandman, Olga

APPLICANT: Shah, Purvi

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RESULT 5
US-09-252-991A-28964
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                                       US-09-252-991A-28964
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                                                                                                                                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                              PRIOR FILING DATE: 1:
NUMBER OF SEQ ID NOS:
SEQ ID NO 28964
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.2%;
Best Local Similarity 32.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                           Sequence 28964, Application US/09252991A
Patent No. 6551795
 Query Match
                                                                                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                     ORGANISM: Pseudomonas aeruginosa
                                                                          LENGTH: 923
TYPE: PRT
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APPLICATION NUMBER:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
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CITY: Palo Alto
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CLONE: 128842
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 27.3%; Score 59;
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 DB 4;
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Length 923;
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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Patent No. 647882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C13
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-04-28
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PRIOR APPLICATION NUMBER: 60/066770
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PRIOR FILING DATE: 1998-02-25
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                                                                         APPLICATION NUMBER: 60/087827
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Godowski, Paul J.
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Gerritsen, Mary E.
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Williams, P. Mickey
Wood, William I.
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60/088025
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R FILING DATE:
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APPLICATION NUMBER:
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                                                                                                                                                 FILING DATE: 1998-07 APPLICATION NUMBER:
                                                                                                                                                                        APPLICATION NUMBER: 60/091633
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                                             Conservative
                                                                                                      : 1998-07-07
NUMBER: 60/
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29.8%;
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                                             13;
                                            Score 58.5; DE Pred. No. 8.5; 13; Mismatches
                                                                    BB
                                             9
                                                                  Length 566;
                                             Indels
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PRIOR PRIOR

PRIOR

FILING DATE:

1998-06-1

APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514

FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089440

APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-12

FILING DATE: 1998-06-1 APPLICATION NUMBER: 60/088876

APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 PRIOR PRIOR PRIOR

FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826

APPLICATION NUMBER: 60/088824 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10

FILING DATE:

1998-06-10 1998-06-10 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088734 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-05

FILING DATE: 1998-06-10

FILING DATE: 1998-06 APPLICATION NUMBER:

APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05

1998-06-05

60/088217

FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202

APPLICATION NUMBER: 60/088167

APPLICATION NUMBER: 60/088033

FILING DATE:

FILING DATE:

FILING DATE:

APPLICATION NUMBER: 60/088030

PRIOR PRIOR PRIOR

FILING DATE:

APPLICATION NUMBER: 60/088326

1998-06-04 1998-06-04 1998-06-04 1998-06-04

FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029

FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04

NUMBER: 60/088026

FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028

PRIOR

FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 FILING DATE: 1998-06-16

APPLICATION NUMBER: 60/089598

1998-06-17

60/089599

PRIOR

FILING DATE: 1998-06 APPLICATION NUMBER:

FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653

PRIOR PRIOR PRIOR PRIOR

FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907

R APPLICATION NUMBER: (
R FILING DATE: 1998-06R APPLICATION NUMBER: (
R FILING DATE: 1998-06-

NUMBER: 60/089952

1998-06-19

60/089948

FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19

FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908

Gaps

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                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 55; LENGTH: 667; TYPE: PRT; ORGANISM: Toxoplasma gondii US-09-086-503-55
                                                                                                                                                                                                                                                                    APPLICANT: MAINE, Gregory T.
APPLICANT: HUNT, Jeffery C.
APPLICANT: HONDANAC, Susan
APPLICANT: JYH-TSING SHEU, Michael
APPLICANT: CHOVAN, Linda E.
APPLICANT: TYBER, Joan D.
APPLICANT: HOWARD, Lawrence V.
TITLE OF INVENTION: ANTIGEN COCKTAILS AND USES THE TEBERENCE: 6361, US.01
CURRENT APPLICATION NUMBER: US/09/086,503A
CURRENT PLING DATE: 1998-05-28
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US-09-303-064-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ANTIGEN COCKTAILS, P35 AND USES THEREOF FILE REFERENCE: 6361.US.P1
CURRENT APPLICATION NUMBER: US/09/303,064
CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 09/086,503
EARLIER FILING DATE: 1998-05-28
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 55
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APPLICANT: PARMLEY, Stephen F.
APPLICANT: REMINGTON, Jack S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHOVAN, Linua APPLICANT: CHOVAN, Linua D. TYNER, Joan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JYH-TSING SHEU, Michael APPLICANT: CHOVAN, Linda E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MAINE, Gregory T
APPLICANT: HUNT, Jeffery C.
APPLICANT: BROJANAC, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 667
TYPE: PRT
ORGANISM: Toxoplasma gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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265 ÉGEGTSTTESASENSEDDDTFHDALQELPEDGLEVR 300
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Similarity 38.9%;
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SUZUKI, Yashuhiro
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                                                                        Conservative
                                                                                       26.4%;
38.9%;
                                                                      ; Score 57; DB;
; Pred. No. 16;
4; Mismatches
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Pred: No. 16;
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                                                                                                         DB 4; Length 667;
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US-08-767-579-6
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Patent No. 5585462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,649
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
                                                                                                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                     APPLICANT: Kimmel, Älan R.
APPLICANT: Egan, John J.
TITLE OF INVENTION: CLONING OF PERILIPIN PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CLONING OF PERILIPIN PROTEINS NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                      ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                         ZIP: 94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 37,330
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                                                                                                                                                                                                                                                                                                                                                                                                                                          298 EDHEDQTDTEGEDTEEEEELETEENKFSEVAALPGPRG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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Greenberg, Andrew S.
Kimmel, Alan R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Egan, John
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Greenberg, Andrew S
Kimmel, Alan R.
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34.2%;
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                                                                                                                                                                                                                                                                                                            US-09-232-160-23
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Best Local Similarity
                                                                                           Patent No.
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                           GENERAL INFORMATION:
APPLICANT: ORDAHL
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PERL Program
EQ ID NO 23
LENGTH: 522
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/232,160
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Steve Daniel
APPLICANT: James Gilmore
APPLICANT: Susan G. Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELLITTLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Laura Stuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 3688209
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                              APPLICANT:
                                            APPLICANT:
                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Garrett-Wackowski, Eu
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15
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10 6368794
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                                                                                                                                                                                                                                            13;
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                                                                                       5, Application US/08615170
5776776
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FARRANCE, Iain K.G.
HALL, Deborah E.
                                         ORDAHL, Charles
AZAKIE, Anthony
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                            Janet H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543-5043
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34.2%;
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34.2%;
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Pred. No. 13;
7; Mismatches
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Pred. No.
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RESULT 13
US-08-630-915A-196
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Best Local
                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 326-24 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US95/01526
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                       CORRESPONDENCE ADDRESS:
                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Heslin, James M. REGISTRATION NUMBER: 29,541 REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 06-FEB-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                           STREET:
                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                    E OF INVENTION:
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                           1155 Avenue
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                                                                                                                                McCONNELL,
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                        SPARKS, Andrew B.
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                                           .Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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31.8%;
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Pred. No. 1:
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e Market Plaza
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                                                                                                     METHODS OF IDENTIFYING AND
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US-08-741-134-6
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sequence 6, Apr-

No. 5861498
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERISTICS:
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NAME: MISTOCK, S. Leslie
REGISTRATION UNMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,163
FILING DATE: 01-NOV-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
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MOLECULE TYPE:
                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.11
SOFTWARE: WordDerfect for Windows 6.1
CURRENT APPLICATION DATA:
                                    ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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FILING DATE: 03-APR-1996
CLASSIFICATION: 536
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJ
                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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mino acid
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Alnemri, Emad S.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                Matches
                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 226 amino acids
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                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: ARC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08
FILING DATE: October 20,
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TELEFAX: 79-0924
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                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/431,080 FILING DATE: Concurrently Herewith
                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                            NAME: Parker, David L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Houston
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146 DDDGSDSDSDSETSSDDENIDFVKLTAQ-----RKKRAMKA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQ 37
                            1 EDDERSTDSSQQCSSEDE--DIFEETAQVSPPRGKEKRQWRA 40
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                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
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                                                                                                                                              linear
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                                                                                                                                                          single
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29.7%;
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                                                                              25.0%;
35.7%;
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                                                                                                                                                                                                                                                                                                              ARCD:155/PAR
                                                                              Score 54; DB 1;
Pred. No. 12;
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Pred. No. 17;
                                                              Mismatches
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Search completed: July 24, 2003, 12:16:22 Job time : 5.66179 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB seq length: 0
DB seq length: 2000000000
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  62
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| Cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_RUW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_RUW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_RUW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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US-09-989-722-41
US-09-989-723-41
US-09-989-727-41
US-09-989-727-41
US-09-989-731-41
US-09-989-73-41
US-09-989-73-41
US-09-991-073-41
US-09-991-073-41
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US-09-864-761-33475
US-10-151-736-4
US-10-121-988-156
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1026.746 Million cell updates/sec
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           Sequence 3, Appli
Sequence 9888, Ap
Sequence 33475, Ap
Sequence 4, Appli
Sequence 156, App
Sequence 80, Appl
Sequence 41, Appl
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Sequence
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-09-990-443-4	-09-997-601-	-09-997-559-	-09-990-726-4	9-991-172-	-09-997-573-4	97-514-4	-09-991-157-4	-09-990-437-	98-156-	9-989-7	-09-990-711-	-09-990-5	90-438-4	-09-997-666-	-09-997-42	67-4	-09-997-	-09-989-	-09-993-6	-09-990-	-09-989-730-	91-181-4	-09-990-	-09-989-73	89-29	9-992-598-4	-09-989-7	-09-990-456-4	93-6
Sequence 41, Appl	equence 41, App	equence 41, App	e 41, App	e 41,	e 41,	e 41,	e 41,	equence 41,	e 41,	equence 41,	equence 41,	equence 41,	e 41,	e 41,	e 41,	e 41,	e 41,	equence 41,	Sequence 41, Appl	e 41,	equence 41,	e 41,	e 41,	e 41,	e 41,	equence 41,	e 41,	equence 41,	•

ALIGNMENTS

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Sequence 3, Application US/0978242
Patent No. US2002009566A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Yue, Henry
Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: 31940
COUNTRY: USA
ZII: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/978,242
FILING DATE: 15-Oct-2001
CLASSIFICATION NUMBER: US/09/978,242
FILING DATE: CUNKnown>
APPLICATION NUMBER: 09/241,333
FILING DATE: CUNKnown>
APPLICATION NUMBER: 08/990,114
FILING DATE: CUNKnown>
APPLICATION NUMBER: 08/990,114
FILING DATE: CUNKnown>
AFICHARGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0451 US
TELEPHONE: 650-855-0555
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RESULT 3
US-09-864-761-33475
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-9888
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                                                       APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENC
TITLE OF INVENTION: GENE EXPR
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                                                                                                                                                                                  Sequence 33475, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                       Matches
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LENGTH: 376
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Best Local
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Best Local Similarity
                                                                                                                                                                   GENERAL INFORMATION:
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
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CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: GenBank
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                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: 128842
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SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                       HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                        28.9%;
36.7%;
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Pred. No. 9.
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Pred. No.
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US-10-151-736-4
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Sequence 4, Application US/10151736
Publication No. US20020192160A1
GENERAL INFORMATION:
APPLICANT: Callaghan, Michelle J.
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US-09-864-761-33475
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SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 33475
LENGTH: 268
                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/774,203
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PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                 OTHER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2
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                                                                                                                                                                 INFORMATION:
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   17
                               10 SQQCSSED--EDIFEETAQVSPPRGKEKRQWR 39
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SQRAKSEDHVRNIFKETEEMSKTEGKLENCWR
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                                                                          Conservative
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EST_HUMAN
SWISSPROT
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                                                                                                                                                                                                                                                                     EXPRESSED
EXPRESSED
EXPRESSED
                                                                                                                                                                                                                                                                                                                                           MAP TO AF118808.1
EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
EXPRESSED IN LUNG, SIGNAL = 0.87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-01-30
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EXPRESSED
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                                                                                       28.7%;
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                                                                                                                                                                                                                                   D IN LUNG, SIGNAL = 0.87
D IN PLACENTA, SIGNAL = 1.1
D IN HEART, SIGNAL = 1.2
D IN BRAIN, SIGNAL = 1.2
D IN ADULT LIVER, SIGNAL = 0.94
D IN HELA, SIGNAL = 6.93
D IN HELA, SIGNAL = 6.3
                                                                                                                                                             HIT: BE295973.1, EVALUE 5.006
HIT: P49910, EVALUE 7.00e-38
                                                                                                                                                                                IN BT474, SIGNAL = 4.1
HIT: BE295973.1, EVALUE 5.00e-83
                                                                                                                                                                                                                     IN BONE MARROW, SIGNAL = 0.74
                                                                      Score 62; DB 9; Pred. No. 7.8; 6; Mismatches 1
                                                                          10;
                                                                                                             Length 268;
                                                                          2
                                                                        Gaps
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; LENGTH: 512
; TYPE: PRT
; ORGANISM: HSV2
US-10-121-988-156
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US-09-801-574-80
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US-10-121-988-156
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; LENGTH: 2799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-736-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 183
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 156
                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                   Sequence 80, Application US/09801574 Patent No. US20020081592A1
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity 34.1%;
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                 APPLICANT: Wang, Peijing Jeremy
APPLICANT: Page, David C.
TITLE OP INVENTION: Reproduction-Specific Genes
FILE REFERENCE: 0399.2007-002
CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT FILING DATE: 2001-03-07
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APPLICANT:
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CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 09/403,402
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICATION NUMBER: PCT/AU98/00280
PRIOR FILING DATE: 1998-04-20
NUMBER OF SEQ ID NOS: 17
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APPLICANT: Watts, Colin K.
TITLE OF INVENTION: No. US20020192160Alel Human Tumour Suppressor Gene
FILE REFERENCE: RICE-010CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Swanson, Ryan M.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERDES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.538C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE:
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CURRENT APPLICATION NUMBER: US/10/121,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hosken, Nancy Ann
APPLICANT: McGowan, Patrick
RIOR APPLICATION NUMBER: 60/187,518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EDDERSTDS---SOQCSSEDEDIFEETAQVSPP------RGKEKROWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McGowan, Patrick
Sleath, Paul R.
Mossman, Sally P.
Evans, Lawrence S.
                                                                                                                                                                                                                                                                                                   DDPESDSSGECSSSDEDMEDPCGDGGAEAIDAAIPKGPPAR 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 62; DB; Pred. No. 90; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Score 60.5;
Pred. No. 23;
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US-09-989-722-41
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-574-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 41, Application US/09989722 Patent No. US20020072067A1
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Best Local Similarity 31.6%;
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CURRENT FILING DATE: 2001-11-19
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/065186 PRIOR FILING DATE: 1997-11-12 PRIOR APPLICATION NUMBER: 60/065311
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                            PRIOR APPLICATION NUMBER: 60/078910 PRIOR FILING DATE: 1998-03-20
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                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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                                                                                                                                                   APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
                                                      APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
                                   APPLICATION NUMBER: 60/084600
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Roy, Margaret Ann
Stewart, Timothy
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Godowski, Paul J.
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                     1998-05-07
60/087106
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NUMBER: 60/091360 : 1998-07-01 NUMBER: 60/091478 : 1998-07-02 NUMBER: 60/091544 : 1998-07-01 : 1998-07-02 NUMBER: 60/091519 : NUMBER: 60/091626 : 1998-07-02 NUMBER: 60/091633 : 1998-07-02 NUMBER: 60/091978 : 1998-07-02 NUMBER: 60/091978	NUMBER: 60/090540 NUMBER: 60/090542 1998-06-24 NUMBER: 60/09057 1998-06-25 NUMBER: 60/090676 1998-06-25 NUMBER: 60/090690 1998-06-25 NUMBER: 60/090691 1998-06-25 NUMBER: 60/090691 1998-06-25 NUMBER: 60/090695 1998-06-25 NUMBER: 60/090695 1998-06-25 NUMBER: 60/090695 1998-06-25 NUMBER: 60/090695 1998-06-26 NUMBER: 60/090696	

OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087759
OR APPLICATION NUMBER: 60/087759
OR APPLICATION NUMBER: 60/087827
OR APPLICATION NUMBER: 60/08021
OR APPLICATION NUMBER: 60/08022
OR APPLICATION NUMBER: 60/08022
OR APPLICATION NUMBER: 60/08022
OR APPLICATION NUMBER: 60/08026
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08030
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08031
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08032
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08032
OR APPLICATION NUMBER: 60/08032
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/08021
OR APPLICATION NUMBER: 60/080810
OR APPLICATION NUMBER: 60/080820
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RESULT 8
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PRIOR PAPPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
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APPLICANT: Baker, Kevin P.
APPLICANT: Bestein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferzara, Angoleone
APPLICANT: Fong, Sherman
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C62
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APPLICATION NUMBER: 60/092182
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                                                                    APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/087609
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Gerritsen, Mary E
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FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1997-11-24
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FILING DATE: 1998-06-04
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Wood, William I.
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Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Goddard, Audrey
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Stewart, Timothy A.
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmeml
TITLE OF INVENTION: Acids Encoding the S:
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
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OR FILING DATE: 1998-06-17
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OR FILING DATE: 1998-06-17
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OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089600
OR FILING DATE: 1998-06-17
OR FILING DATE: 1998-06-17

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FILING DATE: 1998-01 APPLICATION NUMBER:

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OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088876
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OR APPLICATION NUMBER: 60/089512

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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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Williams, P. Mickey
Wood, William I.
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Botstein, David
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/088826
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FILING DATE: 1998-06-APPLICATION NUMBER:

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APPLICATION NUMBER:

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FILING DATE: 1998-06-APPLICATION NUMBER: 6 FILING DATE: 1998-06-APPLICATION NUMBER: 6

1998-06-24

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RESULT 11
US-09-989-731-41
: Sequence 41, Application US/09989731
: Patent No. US20020103125A1
: GENERAL INFORMATION:
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OR APPLICATION NUMBER: 60/090557
OR FILING DATE: 1998-06-24
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OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090678
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APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/090542
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-06-16
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Grimaldi, J. Christopher
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David

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Sequence 41, Application US/09
Patent No. US/0020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Goddard, Audrey
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Ferrara, Napoleone
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APPLICATION NUMBER: 60/091519
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Botstein, David
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                                                                                       Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                    Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Ferrara, Napoleone
                        Napier, Mary A.
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Paoni,Nicholas
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13; Mismatches
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TITLE OF INVENTION: Acids Encoding the S.
FILE REFERENCE: PE7300F1C15
CURRENT APPLICATION NUMBER: US/09/991,073
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Stewart, Timothy A.
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US-09-990-442-41
; Sequence 41, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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OR APPLICATION NUMBER: 60/091360
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OR APPLICATION NUMBER: 60/09154
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Williams, P. M
Wood, William
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Stewart, Timothy
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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Paoni, Nicholas F.
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DR APPLICATION NUMBER: 60/090445

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OR APPLICATION NUMBER: 60/090252
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090254
OR APPLICATION NUMBER: 60/090349
OR FILING DATE: 1998-06-22
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-06-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-06-
                                                                                                                                                                                                                                                                                               FILING DATE:
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Best Local S
Matches 14
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-66-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
       139
                                                                                                                               1 EDDERS-----TDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                      l Similarity
14; Conserv
= | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --
                                                                                                                                                                                                                                                               27.1%;
nilarity 29.8%;
Conservative 1:
                                                                                                                                                                                                                                                               ; Score 58.5; I; Pred. No. 45; 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
       -RRRORREWEAR
                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 566;
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Search completed: July 24, 2003, 12:18:16 Job time : 6.94231 secs

11;

Gaps

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
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                                                                                                        Ö
                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 2000000000
      216
216
   100.0
                                                                                              Query
Match Length
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216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
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(cgn2_6/ptodata/1/paa/US084_COMB.pep:*
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(cgn2_6/ptodata/1/paa/US099_COMB.pep:*
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(cgn2_6/ptodata/1/paa/US09_COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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   US-08-842-385-7
US-09-991-681-28
                                                                                                                                                                                               SUMMARIES
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Sequence 28, Appl
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Sequence 22, App1 Sequence 27328, A Sequence 22, App1	e 11767, 19, Apr	957, <i>‡</i> 7546,	Sequence 11383, A Sequence 2651, Ap	6595,	7631,	Seguence 155/5, A Seguence 5024, Ap	e 7631, A	15575,	34360,	Sequence 40014, A	36977,	41174	36434,	equence 9466	equence 946	e 528,	e 769, F	equence 2147,	e 214	e 771,	42, A	equence 770,	e 87,	equence 87	e 87	e 30.	30. Apr	400	32, 1	e 49!	495,	40087	e 44,	quence 44,	equence 27,	Sequence 6, Appli

ALIGNMENTS

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US-08-842-385-7
US-08-842-385-7
Sequence 7, Application US/08842385
GENERAL INFORMATION:
APPLICANT: RUSSell, John
APPLICANT: COlpitts, Tracey
ITILE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASE OF THE PROSTATE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 110 Abbott Park
STREET: 110 Abbott Park
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER FEADABLE FORM:
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
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GENERAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -08-842-385-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 41 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                              APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-Nov-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 100.0%; Score 216; DB 12; Similarity 100.0%; Pred. No. 2.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                             CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09991681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRANADOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COHEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRATOCHVIL, JON D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDWARD N.
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                                                           6084.US.P1
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Sequence 6, Application US
GENERAL INFORMATION:
APPLICANT: Russell, Jo
APPLICANT: Colpitts, T
TITLE OF INVENTION: RE
TITLE OF INVENTION: FC
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                                                                                                                                           US-08-842-385-6
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US-08-842-385-6
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Matches 41; Conserva
                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 41; Conservative 0
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                                                                                                                                                                                                                                                                                                                 NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 606
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                          STRANDEDNESS: 811
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                   TELEFAX: 847/938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
133 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 173
                                                                                                                                                                                                             amino acid
                    EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
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                                                                   Score 216; DB 12;
Pred. No. 4.8e-18;
D; Mismatches 0;
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                                                                                                      DB 12;
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RESULT 5
PCT-US03-01943-44
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                   Sequence 44, Application PC/TUS0301943
GENERAL INFORMATION:
APPLICANT: ORIGENE TECHNOLOGIES INC
TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01943
CURRENT FILING DATE: 2002-01-25
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Sequence 27, Application US/09991681
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acids
RIOR APPLICATION NUMBER: US 10/054,935
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: line MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 847/935-1729
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ADDRESSEE: Abbott Laboratories
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TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 27:
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                                                                                                                                                                                                                                               184 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 224
                                                                                                                                                                                                                                                                               1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-Nov-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                           Score 216; DB 25;
Pred. No. 5.5e-18;
; Mismatches 0;
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; TYPE: PRT; ORGANISM: Homo sapiens US-10-144-198-44
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PCT-US03-01943-44
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                                                          NUMBER OF SEQ ID NOS:
SOFTWARE: Custom
SEQ ID NO 40087
                                                                                                                                                                                                                                                                                                           Sequence 40087, Application PC/TUS0108631 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0 SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1 SEQ ID NO 44
                                                                                               APPLICANTION INVESTIGNATION AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
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Best Local Similarity
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TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 TA
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
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PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR FILING DATE: 2002-05-14
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PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-03-22
ORGANISM: Homo sapiens
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                                         ENGTH: 1807
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100.0%; Pred. No. 2.6e-17;
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Pred. No. 2.6e-17;
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                                                                                                                               ; LENGTH: 1839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-416-993-495
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                                                           Matches
                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 495
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                                                                                           Query Match
                                                                                                                                                                                                                                               APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: US/10/416,993
CURRENT FILING DATE: 2003-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: PCT/US01/42950
CURRENT FILING DATE: 2001-11-16
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PRIOR FILING DATE: 2000-11-17
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NUMBER OF SEQ ID NOS: 682
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX, OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw score of 11.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Helper component proteinase domain identified by PFam, OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
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EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
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                                                           Conservative
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Pred. No. 2.6e-17;
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Pred. No. 2.7e-17;
                                                         Mismatches
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RESULT 10
PCT-US03-04508-32
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CURRENT APPLICATION NUMBER: PCT/US03/0.
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
                                                                                  Query Match
Best Local
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Best Local
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                                                               Matches
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CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/540,217 PRIOR FILING DATE: 2000-03-31
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                                                                                                                                                NAME/KEY: DOMAIN
LOCATION: (1065)..(1074)
COTHER INFORMATION: Helper component proteinase domain identified by PFam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
                                                                                                                                                                                                                                            NAME/KEY: DOMAIN
LOCATION: (11)..(25)
OTHER INFORMATION: Busion glycoprotein F0 domain identified by eMATRIX,
OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw so
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TYPE: PRT
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1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
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                                                                                  Similarity
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                                                                 Conservative
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                                                                                  Score 216; DB 1
Pred. No. 3e-17;
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Pred. No. 2.8e-17;
                                                                 Mismatches
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1587 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 1627

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RESULT 14
US-09-623-791-87
; Sequence 87, Application US/09623791
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
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                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 2221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-198-30
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US-10-144-198-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Application US/10144198
GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION UNMEBR: US/10/144,198
CURRENT FILING DATE: 2002-05-14
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local S
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LENGTH: 2221
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PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 10/144,198
PRIOR PILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/197,824
PRIOR PILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 102
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PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR FILING DATE: 2002-03-22
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CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 10/054,935
PRIOR FILING DATE: 2002-01-25
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FILE REFERENCE: 3U 9U 901 PCT
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Search completed: July 24, 2003, 12:15:12 Job time : 62.7701 secs
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US-09-623-791A-87
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-791-87
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 201
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 87
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Best Local
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Best Local Similarity 100.0%;
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CURRENT APPLICATION NUMBER: US/09/623,791A
CURRENT FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DAHL, EDGAR
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TUMOR TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SPECHT,
APPLICANT: HINZMI
APPLICANT: SCHMIT
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CURRENT APPLICATION NUMBER: US/09/623,791
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/DE99/00721
PRIOR FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 201
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/DE99/00721 PRIOR FILING DATE: 1999-03-09
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SCHMITT, ARMIN
PILARSKY, CHRISTIAN
DAHL, EDGAR
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2: /cgn2_6/ptodata/2/paa/USO6_NEW COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO9_NEW COMB.pep:*

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US-09-820-843B-58
PCT-US02-41612A-576
US-10-275-595A-17
PCT-US02-41612A-574
US-10-274-433-270
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428, App	5843, Ap	5845, Ap	5844, Ap	7, Appli	10655, A	10656, A	9690, Ap	1, Appli	172, App	174, App	176, App	335, App	3320, Ap	36, Appl	319, App	42, Appl	3236, Ap	2, Appli

ALIGNMENTS

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Sequence 156, Application PC/TUS0311231

Sequence 156, Application

APPLICANT: Corixa Corporation

APPLICANT: Day, Craig H.

APPLICANT: Hosken, Nancy A.

APPLICANT: Parsons, Joseph M.

APPLICANT: Parsons, Joseph M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION FILE REFERENCE: 210121.5380.PC

CURRENT APPLICATION NUMBER: PCT/US03/11231

CURRENT FILING DATE: 2003-04-09

NUMBER OF SEQ ID NOS: 267

SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 1872
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-978-32
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US-10-367-978-32
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PCT-US03-11231-156
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TITLE OF INVENTION: OR THERAPEUTICS
FILE REFERENCE: 03700-0301988
CURRENT APPLICATION NUMBER: US/10/367,978
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
PRIOR FILING DATE: 2002-06-10
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APPLICANT: GATELY, DENNIS
APPLICANT: WITHOUT PROST!
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; Sequence 243, Application PC/TUS0311231
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SEQ ID NO 243
LENGTH: 512
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                    PRIOR APPLICATION NUMBER: PCT/US01/50256
PRIOR FILING DATE: 2001-12-19
                                                          CURRENT APPLICATION NUMBER: US/10/451,901
CURRENT FILING DATE: 2003-06-23
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                                                                                              FILE REFERENCE: PF-0869 USN
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                                                                                                                PPLICANT: JACKSON, Alan A.
THE OF INVENTION: NUCLEIC ACID-ASSOCIATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDPESDSSGECSSSDEDMEDPCGDGGAEAIDAAIPKGPPAR 74
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                                                                                                                                                                                                                                                                                                                                                                                RAMKUMAR, Jayalaxmi; YAO, Monique G.; POLICKY, Jennifer L.; WALIA, Narinder K.; TRIBOULEY; Catherine M.; YUE, Henry;
                                                                                                                                                                                                          MASON, Patricia M.; BURFORD, Neil; HAFALIA, April J.A.; LEE, Ernestin YANG, Junming; GORVAD, Ann E.;
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                                                                                                                                                                                                                                                                                                                                                                    BATRA
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                                                                                                                                      LING, Brooke M.; MARQUIS, Joseph P.;
Soo Yeun; SWARKAKAR, Anita;
Y, Roopa M.; JIANG, Xin;
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                                                                                                                                                                                                                                                                                                                                              A, Sajeev; DING, Li;
Preeti G.; BOROWSKY, Mark L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jоверh M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.0%;
                                                      2003-06-23
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US 60/257,714
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60.5; DB 1; Length 512; Pred. No. 0.4;
                                                                                                                                                                                                                                LEE, Ernestine A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                  PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND
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; TYPE: PRT ; ORGANISM: Homo sapiens US-10-294-433-359
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US-10-294-433-359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; NAME/KBY: misc feature
; OTHER INFORMATION: Incyte ID No: 3187174CD1
US-10-451-901-16
                Best
                                                                                                                                  SOFTWARE: Custom
SEQ ID NO 359
LENGTH: 767
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 359, Applic GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.1%;
Best Local Similarity 34.8%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PERL Program SEQ ID NO 16
                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/294,433
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/US01/14826
PRIOR FILING DATE: 2001-05-16
                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/263,823
PRIOR FILING DATE: 2001-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/260,081 PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/577,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/989,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/266,088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                          RIOR FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 10/115,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIOR FILING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 517
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/262,302
                                                                                                                                                                                                                                                                                                                                                 RIOR APPLICATION NUMBER: 10/150,802
                  Local Similarity
                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/775,330
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-02-02
APPLICATION NUMBER: US 60/348,442
                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 10/167,379
                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               FILING DATE: 2002-05-15
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/695,781
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                            CATION NUMBER: 09/677,298
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  Conservative
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                  27.1%;
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9;
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                Score 58.5; DF
Pred. No. 1.2;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                      DB 6;
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15;
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                                    Length 767;
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  Indels
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  Gaps
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APPLICANT: Roemer, Terry
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF ASPERGILLUS FUMIGATUS AND I
TITLE OF INVENTION: USE
FILE REFERENCE: 10182-026-888
CURRENT APPLICATION NUMBER: US/60/478,196
CURRENT FILING DATE: 2003-06-13
NUMBER OF SQ ID NOS: 4000
SOFTWARE: PAtentin version 3.1
SEQ ID NO 3253
LENGTH: 538
TYPE: PAT
ORGANISM: Aspergillus fumigatus
US-60-478-196-3253
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US-10-294-433-316
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US-60-478-196-3253
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Query Match
Best Local Similarity
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APPLICANT:
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CURRENT FILING DATE: 2002-11-13
                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/775,330 PRIOR FILING DATE: 2001-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-05-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq, II
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jiang, Bo
                                                                LENGTH: 413
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                  SOFTWARE: Custom
                                                                                                                                                                      NUMBER OF SEQ ID NOS: 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/577,408 FILING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/989,600 FILING DATE: 2001-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 10/115,831
                                                                                                                                                                                                                             FILING DATE: 2002-06-10
                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 10/150,802 FILING DATE: 2002-05-15
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Similarity 30.6%;
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Hu, Wengi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                              2000-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
24.1%;
                                                                                                                                                                                                                                             10/167,379
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Score 52;
Pred. No.
 DB 6;
4.5;
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                   Length 413;
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FILE REFERENCE: 800.032US1
CURRENT APPLICATION NUMBER: US/10/353,856
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US 60/353,972
PRIOR FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   문
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PCT-US03-11231-161
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; TYPE: PRT
; ORGANIZM: Reston Ebola virus
US-10-353-856-1
                                                                                                                                           ; TYPE: PRT
; ORGANISM: HSV2
PCT-US03-11231-161
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                                                             Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 161, Application PC/TUS0311231 GENERAL INFORMATION:
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 161
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                                                                                                                                                                                                                                                                   APPLICANT: Hosken, Nancy A.
APPLICANT: Parsons, Joseph M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.53801PC
CURRENT APPLICATION NUMBER: PCT/US03/11231
CURRENT FILING DATE: 203-04-09
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Corixa Corporation APPLICANT: Day, Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kawaoka, Yoshihiro APPLICANT: Jasenosky, Luke D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Filovirus Vectors and Noninfectious Filovirus-Based Particles
                                                                                                                                                                                                  LENGTH: 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 KDDNRASDNNQQ-SADSE---EQEGQYNRHRGPER 555
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                                2 DDERSTDSSQQCSSEDEDIFEE---TAQVSPPRGKEKRQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEK 35
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DDDLHRDSTSEAGSTDTEMFEAGLMDAATPPARPPAERQ
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Neumann, Gabriele
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                                                                      Conservative
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                                                                                     23.8%;
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                                                                                     Score 51.5; 1
Pred. No. 12;
                                                                      Mismatches
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                                                                                                       DB 1;
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                                                                    17;
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95
                                                                                                       Length 825;
                                                                    Indels
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PCT-US0311-47
FCT-US0311-47
; Sequence 47, Application PC/TUS0311231
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation

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CURRENT FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 267
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 826
TYPE: PRT
ORGANISM: HSV-2
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                              Sequence 3182,
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10381, Application US/10273573 GENERAL INFORMATION:
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Best Local
FILE REFERENCE: 10182-026-888
CURRENT APPLICATION NUMBER: US/60/478,196
CURRENT FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 4000
                                                                      APPLICANT: Roemer, Terry
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF ASPERGILLUS FUMIGATUS AND
TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PARSONS, JOSEPH M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.53801PC
                                                                                                                                                                      APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(352)
OTHER INFORMATION: Xaa = X or * as defined in Table
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                             143 EDEKETD-----EDDEAFGEALQ-SPASGKQ 167
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                                                                                                                                                                                                                                                                                                                                                    2 DDERSTDSSQQCSSEDEDIFEETAQVSPPRGKE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DDERSTDSSQQCSSEDEDIFEE---TAQVSPPRGKEKRQ 37
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                                                                                                                             Lemieux, Sebastien
Hu, Wengi
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                                                                                                                                                                                                                Application US/60478196
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Pred. No. 5.2;
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Pred. No. 1;
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US-10-273-573-8148
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                                                                                                                                       SOFTWARE: Custom
SEQ ID NO 8148
                                                                                                                                                                                                                                                                                                                                                         Sequence 8148, Application US/10273573
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
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SEQ ID NO 3182
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                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-08 NUMBER OF SEQ ID NOS: 23
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CURRENT APPLICATION NUMBER: US/09/200,650E
CURRENT FILING DATE: 1998-11-25
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 10994
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/770,160 PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/066,815 PRIOR FILING DATE: 1997-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Eidhinn, Deirdre Ni
APPLICANT: Perkins, Samuel L.
TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
FILE REFERENCE: P06283US2/BAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Patti, Joseph M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Staphylococcus aureus
LOCATION: (1)...(45)
OTHER INFORMATION: Xaa = X or *
              NAME/KEY: misc_feature
LOCATION: (1)...(45)
                                                                          ORGANISM: Homo sapiens
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                                                                                                                      ENGTH:
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  as defined in Table 2
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; NUMBER OF SEQ ID NOS: 864
; SOFTWARE: Custom
; SEQ ID NO 308
; SEQ ID NO 308
; LENGTH: 375
; TYDE: PRT
; ORGANISM: Homo sapiens
US-10-294-433-308
Search completed: July 24, 2003, 12:16:47 Job time: 1.40059 secs
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US-10-294-433-308
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                                                                                                                                                                                           Query Match 22.9%; Score 49.5; DB 6; Length 375; Best Local Similarity 33.3%; Pred. No. 8.9; Matches 13; Conservative 10; Mismatches 9; Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERNCE: 792CIP4
CURRENT APPLICATION NUMBER: US/10/294,433
CURRENT FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 10/167,379
PRIOR FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/775,330
PRIOR FILING DATE: 2001-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/US01/14826
PRIOR FILING DATE: 2001-05-16
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APPLICATION NUMBER: 10/150,802
FILING DATE: 2002-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/577,408 FILING DATE: 2000-05-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/715,869
                                                                                                  228 DESSSDEDEKKNKEESSDDED---KESEEEPPKKTAKRE 263
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                                                                                                                                             3 DERSTD----SSQQCSSEDEDIFEETAQVSPPRGKEKRQ 37
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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2: pir2:*
3: pir3:*
4: pir4:*
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JH0148
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S70004
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S44649	C40646	B84545	T01225	F84886	S43445	T31069	S49634	A42136	JU0466	S50617	E96558	T08855	T05676	S48647
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ALIGNMENTS

RESULT A35804

	A35804
	N;Alternate names; phosphoprotein pp100; protein B50; protein C23
	C; Species: Homo sapiens (man)
	ר;ושמרפ: גז-טכר-באיט #Bequence ופיוברסה גז-טכר-באיט #רפאר_כותחופ בז-טנו-באיט C;Accession: A3504; S04631; A48138; A55996
	R;Srivastava, M.; McBride, O.W.; Fleming, P.J.; Pollard, H.B.; Burns, A.L. J. Biol. Chem. 265, 14922-14931, 1990
	A;Title: Genomic organization and chromosomal localization of the human nucleolin gene.
	A; Accession: A35004 A; Accession: A35004
	A; Molecule type: DNA
have a	A;xesiques: 1-70/ <5K1> A;xesiques: 1-70/ <5K1> A;xesiques: 1-70/ <5K1>
ng printed,	R/Srivastava, M.; Fleming, P.J.; Pollard, H.B.; Burns, A.L.
,	FEBS Lett. 250, 99-105, 1989
	A; Title: Cloning and sequencing of the human nucleolin cDNA.
	A;Reterence number: S04631; MUID:89290043; PMID:2737305
,	A/Status: not compared with conceptual translation
iption	A, Molecule type: mRNA
olin - human	R; Ishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R.
olin - rat	Mol. Cell. Biol. 13, 4301-4310, 1993
olin - Chines wn protein Fl	A;Title: Nuclear proteins that bind the pre-mRNA 3' splice site sequence r(UUAG/G) and to a .Reference number a Magias MITH-93300464 b MBTH-8331737
protein - hum	A;Accession: A48138
protein - yea	A; Molecule type: protein
hetical prote	A; KeSiqueS: 458-474 <1584
	A; Note: sequence extracted from NCBI backbone (NCBIP:134645)
olin - mouse	R;Jordan, P.; Heid, H.; Kinzel, V.; Kuebler, D.
protein - hum	A; Title: Major cell surface-located protein substraces of an ecco-protein kindse are nome
protein - Eme	A; Accession: A55996
rved hypothet	A; Molecule type: protein
hetical prote	A; Represental source: surface-labelled HeLa cells
ble protein w	C;Genetics:
hetical prote	A;Cross references: GDB:125908; OMIM:164035
hetical prote	A; Map position: 2q12-2qter
mine transpor hetical prote	C; Supersamity: nucleolin; rioonucleoprocein repeat nomology C: Keywords: DNA binding nucleolis; nucleos bobseboorotein: RNA binding
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in binding pr	F;573-634/Domain: ribonucleoprotein repeat homology <rrm4></rrm4>
nt-specific s	Ouery Match 29.6%: Score 64: DB 2: Length 707:
100000000000000000000000000000000000000	

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N;Alternate names: nonchromosomal protein C23; nucleolar protein C23 C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 19-Nov-1988 #sequence revision 19-Nov-1988 #text_change 23-Jul-1999
C;Accession: A27441; A24808; Ā24070
R;Lapeyre, B.; Bourbon, H.; Amalric, F.
Proc. Natl. Acad. Sci. U.S.A. 84, 1472-1476, 1987
A;Title: Nucleolin, the major nucleolar protein of growing eukaryotic cells: A;Reference number: A27441; MUID:87175501; PMID:3470736
A;Recession: A27441
A;Molecule type: mRNA
A;Residues: 1-713 <LAP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Sequence and structure of the nucleolin promoter in A;Reference number: 148118; MUID:89121496; PMID:2906027 A;Accession: 163130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: the authors translated the initiation codon GTG for residue 1 as Val R;Lischwe, M.A.; Cook, R.G.; Ahn, Y.S.; Yeoman, L.C.; Busch, H. Biochemistry 24, 6025-6028, 1985
A;Title: Clustering of glycine and Ng,Ng-dimethylarginine in nucleolar protein A;Reference number: A24088; MUID:86104094; PMID:4084504
A;Accession: A24088
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C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change
C;Accession: JH0148, 244088; I63130
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C;Keywords: DNA binding; nucleus
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A;Introns: 5/3; 44/3; 211/1; 274/1; 303/1; 350/2; 392/1; 433/2; 485/1; 526/2; 571/1; 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M22090; NID:g205793; PIDN:AAA41733.1; PID:g205794 C;Comment: This protein is the major nucleolar-specific protein in eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 'MV', 2-44 < RES>
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A; Residues: 1-712 <BOU>
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UL54 proteis: human herpesvirus 2
C;Species: human herpesvirus 2
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revis
C;Accession: J01498
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; I Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
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A; Residues: 522-541, '(7,543-544, 'R',546-713 <LA2>
A; Cross-references: GB:M13757; NID:g191004; PIDN:AAA36961.1;
R; Lapeyre, B.; Caizergues-Ferrer, M.; Bouche, G.; Amalric, F.
Nucleic Acids Res. 13, 5805-5816, 1985
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                                                                                                                                                                                                                                                                   A; Cross-references:
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A; Residues: 1-2599 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown protein F16M22.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Residues: 179-238 <LA3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A24808
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                                                                                            l Similarity
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                                                                                                                   28.2%;
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                                                                                                                   Score 61;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB 2; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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t homology <RRM3>

t homology <RRM4>
                                                                                                                        49;
                                                                                                                                          DB
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                                                                                                                                          Length 2599;
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H.; Tallon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E.; Kim,
                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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#sequence_revision

31-Dec-1992

#text_change

N

(strain HG52)

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hypothetical protein 206 - radish mitochondrion C;Species: mitochondrion Raphanus sativus (radish) C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: JQ1494; MUID:92113549; PMID:1662697 A;Accession: JQ1498
                     A;Genome: mitochondrion C;Keywords: mitochondrion
                                                             A;Cross-references: GB:U43507
A;Note: the authors translated
C;Genetics:
                                                                                                                                                                       Curr. Genet. 29, 564-571, 1996
A;Title: Characterization of the radish mitochondrial nad3/rps12 locus: analysis A;Reference number: S70000; MUID:96269916; PMID:8662196
A;Accession: S70004
                                                                                                                                                                                                                                                R; Rankin, C.T.; Cutright, M.T.; Makaroff, C.A.
                                                                                                                                                                                                                                                                                                                                                   S70004
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C; Keywords: transcription
                                                                                                                  A; Molecule type: DNA
A; Residues: 1-206 < RAN>
                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-395 <BOH>
A;Cross-references: EMBL:Z74965; NID:g1420194; PID:e251976; PID:g1420195; GSPDB:GN00015;
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the Protein S
A;Reference number: S66929
A;Accession: S66940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Alternate names: protein 02805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: UL54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-512 < MCG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;McGeoch, D.J.; Cunningham, C.; McIntyre, G.; Dolan, A.
J. Gen. Virol. 72, 3057-3075, 1991
                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 15R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Bohn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:D10471; DDBJ:D01128; NID:g221784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Gene: SGD:SGT1; GSS1; MIPS:YOR057w
;Cross-references: SGD:S0005583; MIPS:YOR057w
                                                                                                                                                                                                                                                                      Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Description: suppressor of G2 allele of SKP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                            371
                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 SSEDEDIFEETAQVSPPRGKEKRQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                        S70004
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                                                                                                                                                                                                                                                                                                                                                                                                                            STDWEDVSKGTVKTSPPEGMEPKHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDPESDSSGECSSSDEDMEDPCGDGGAEAIDAAIPKGPPAR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DERSTDSSQQCSSEDEDIFE----ETAQVSPPRGKEKR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.8%;
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                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Daignan-Fornier, B.; Dang, D.V.; Valens, M. Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein YOR057w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 60.5;
Pred. No. 10;
                                                                            codon GAT for residue 147 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            395
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                                                                                                                                                                                                                                                                                      #text_change 25-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:BAA01269.1; PID:g221788
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                                                                            Asn
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                                                                                                                                                                                                             of reco
R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; .; Lory, S.; Olson, M.V.
                                                                     hypothetical protein PA3074 (imported) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision
                                                       C; Accession:
                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                              8
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                                                                                                                                    C83262
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A;Molecule type: DNA
A;Residues: 1-767 cPAN>
A;Residues: 1-767 cPAN>
A;Cross-references: EMBL:Z71500; NID:g1302244; PID:e239703; PID:g1302245; MIPS:YNL224c
A;Experimental source: strain S288C
A;Experimental source: strain S288C
R;Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:271500; NID:g1302244; PID:e239703; A;Experimental source: strain S288C R;Pandolfo, D.; De Antoni, A.; Lanfranchi, G.; Valle, G. submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S63182; S63190; S67374; S72092
R;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl,
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62944
                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: SGD:S0005168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z69381; NID:g1183970; A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown; translation not A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast 12, 1071-1076, 1396
A;Title: The DNA sequence of cosmid 14-5 from chromosome
A;Reference number: S72073; MUID:97051596; PMID:8896273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-767 <PAW>
A;Residues: 1-767 <PAM>
A;Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: DNA sequence of A;Reference number: S67355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S63190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S63188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein YNL224c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S63182
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;Residues: 1-767 <DUE>
                                                                                                                                                                                                                                                                                                                                ;Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Residues: 1-767 <PAF>
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics
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                                                                                                                                                                                                      Query Match
Best Local Similarity
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Best Local
181 EDDDSQNSPSTDHSLSSNESKVEDGDLFFVDEEAQQSPDLTKIKR 225
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                                                                                                                                                                20;
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                                                                           EDDER----STD---SSQQCSSEDEDIF--EETAQVSPPRGKEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESSFHCGEEDPFELDVLEESFSDSPPAGSPRRK 170
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                      27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cosmid 14-5 from chromosome
                                                                                                                                                                4.
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                                                                                                                                                                                                      Score 59.5; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59.5;
Pred. No. 5
                                                                                                                                                                Mismatches
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to the EMBL Data Library, Febr
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                                                                                                                                                                                                                                            Length 767;
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Coulter, S.N.; Folger, K.R.; Kas,

P.; Hickey, A.; Larbig,

Bri

15-Sep-2000

#text_change 31-Dec-2000

Pseudomonas aeruginosa

(strain PAO1

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F;311-316/Region: F
F;349-356/Region: F
F;396-458/Domain: F;397-402/Region: F
                                                                                                                                                                                                                                                                                                                                                                                              Gene 68, 73-84, 1988
A;Title: Sequence and structure of the nucleolin promoter A;Reference number: I48118; MUID:89121496; PMID:2906027
A;Accession: I84688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         u. mol. Biol. 200, 627-638, 1988
A;Title: Structure of the mouse nucleolin gene. The complete sequence reveals that each A;Reference number: A29958; MUID:88316930; PMID:3137346
A;Accession: A29958
                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M22089; NID:g200111; PIDN:AAA39841.1; PID:g554246 C;Comment: This housekeeping protein is involved in the synthesis, packaging,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 2-20,'X',22-24 < PAS>
R; Residues: 1-20,'X',22-24 < PAS>
R; Residues: 1-20,'X',22-24 < PAS>
R; Yang, T. H.; Tsai, W.H.; Lee, Y.M.; Lei, H.Y.; Lai, M.Y.; Chen, D.S.; Yeh, N.H.;
Mol. Cell. Biol. 14, 6068-6074, 1994
Mol. Cell. Biol. 14, 6068-6074, 1994
A; Title: Purification and characterization of nucleolin and its identification as A; Reference number: A56240; MUID:94344117; PMID:8065340
A; Accession: A56240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:X07699; NID:g53453; PIDN:CAA30538.1; PID:g53454 R;Pasternack, M.S.; Bleier, K.J.; McInerney, T.N. J. Biol. Chem. 266, 14703-14708, 1991 A;Tille: Granzyme A binding to target cell proteins. Granzyme A binds A;Reference number: A40769; MUID:91317840; PMID:1860869 A;Accession: A40769
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A;Residues: 1-586 <STO>
A;Cross-references: GB:AE004731; GB:AE004091; NID:g9949171; PIDN:AAG06462.1; GSPDB:GN001
A;Experimental source: strain PAO1
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A;Accession: C83262
                                             F;489-494/Region:
                                                                      F;488-551/Domain:
                                                                                     F;431-438/Region:
                                                                                                                                                                                                                                                               A; Introns: 6/3; 45/3; 211/1; 273/1; 302/1; 349/2; 391/1; 432/3; 484/1; 525/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: PA3074
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                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-44 < RES>
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                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;Molecule type: protein
4;Residues: 2-19;558-567 <YAN>
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                                                                                                                                                                                              Superfamily: nucleolin; ribonucleoprotein repeat homology ;Keywords: DNA binding; duplication; nucleus; phosphoprotein; ;310-375/Domain: ribonucleoprotein repeat homology <RRM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999; Accession: A29958; A40769; A56240; I84688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bourbon, H.
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                  ribonucleoprotein repeat homology <RRM2>
RNA-binding RNP2 motif
RNA-binding RNP1 motif
ribonucleoprotein repeat homology <RRM3>
RNA-binding RNP2 motif
RNA-binding RNP1 motif
                                                                                                                                                   RNA-binding RNP2 motif
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50; MUID:20437337; PMID:10984043
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    repeat
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  homology <RRM4>
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C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_1
C;Accession: I30089
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                                                             UL54 protein -
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                                                                                                            RESULT 13
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                                                             human herpesvirus 1 (strain 17)
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A;Gene: UL54
C;Superfamily: varicella-zoster virus gene 4 protein C;Keywords: transcription regulation
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UL54 protein - human herpesvirus 1 (strain HFEM)
C;Species: human herpesvirus 1
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Feb-1997
C;Accession: A48560
C;Accession: A48560
                                                                                                                                                                                                                                          A; Note: sequence extracted from NCBI backbone (NCBIN:117573, NCBIP:117574)
                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-511 < ROS>
                                                                                                                                                                                                                                                                                                     A; Accession: A48560
                                                                                                                                                                                                                                                                                                                    RiRosen-Wolff, A., Frank, S., Raab, K., Moyal, M., Becker, Y., Darai, G. Virus Res. 25, 189-199, 1992
A,Title: Determination of the coding capacity of the BamHI DNA fragment BA,Reference number: A48560; MUID:93070559; PMID:1332274
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A; Residues: 1-182 < AAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Date: 04-Feb-2000
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                                                                                                  Similarity
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                                     DERSTDSSQQCSSEDEDIFEETAQVSP 29
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RNA-binding RNP1 motif
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                                                                                                26.9%;
40.7%;
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                                                                                              Pred.
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Pred. No. 6.1;
8; Mismatches
                                                                               9
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Pred. No. 22;
                                                                                                Score 58; DB
Pred. No. 21;
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#sequence_revision

31-Dec-1989

#text_change

16-Jun-2000

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A; Molecule type: DNA
A; Residues: 1-1738 «VOL»
A; Cross references: EMBL.X61368; NID:g11550; PID:g11551
A; Cross references: EMBL.X61368; NID:g11550; PID:g11551
A; Wolfe, K.H.; Morden, C.W.; Ems, S.C.; Palmer, J.D.
J. Mol. Evol. 35, 304-317, 1992
A; Title: Rapid evolution of the plastid translational a A; Reference number: S78378; MUID:93021155; PMID:1404416
A; Accession: S78401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: UL54
C;Superfamily: varicella-zoster virus gene 4 protein
C;Keywords: transcription remulariam
                                                                                                                                                                                                                                                              R;Wolfe, K.H.; Morden, C.W.; Palmer, J.D.

J. Mol. Biol. 223, 95-104, 1992

A;Title: Small single-copy region of plastid DNA in the non-photosynthetic angiosperm on at a non-bioenergetic locus.
                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein 1738 - beechdrops plastid C;Species: plastid Epifagus virginiana (beechdrops) C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 05-Jun-1998 C;Accession: S20614; S78401; S16720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Mirabito, P.M.; Adams, T.H.; Timberlake, W.E.
Cell 57, 859-868, 1989
A;Title: Interactions of three sequentially expressed genes
A;Reference number: A32434; MUID:89249350; PMID:2655931
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A;Title: The complete DNA sequence of the long unique region in the genome of herpes sim A;Reference number: A30083; MUID:88274327; PMID:2839594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abaA protein - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #
                                                                                                                                                                                                                                                   A; Reference number: S20614; MUID: 92114084; PMID: 1731088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-796 < MIR>
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A;Accession: A32434
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Best Local Similarity
Matches 12; Conserv
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40.7%;
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                                    the plastid translational apparatus in MUID:93021155; PMID:1404416
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6; Mismatches
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nucleic acid sequence not shown; translation not shown

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A;Residues: 1-1738 <WOW>
A;Cross-references: EMBL:M81884; NID:g336917; PID:g336940
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
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                                                                                                              A;Genome: plastid C;Keywords: plasti
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A; Residues: 1-173
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Best Local
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245 TLKKEQQKVEDEDI -- ETVNQMPPLGLEKRE
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                                                                    Score 58; DB Pred. No. 75;
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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YCF1 EPIVI
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RGP1 XENLA
ANR6 HUMAN
PLIN HUMAN
PLIN HUMAN
CHD1 MOUSE
CTO6 HUMAN
DPOA MOUSE
CTO6 HUMAN
DPOA MOUSE
DPO3 HUMAN
PKB3 YEAST1
SSF1 MOUSE
NPH1 HOUSE

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CC45_HUMAN
MNT_HUMAN
PESC_BRARE
IE63_HSV1E
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P13383 rattus norv
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9 homo sapien
1 brachydanio
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5 herpes simp
8 herpes simp
9 emericella
1 canine oral
6 canopus lae
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"Sequence and structure of the nucleolin promoter in rodents:
"Sequence and structure of the nucleolin promoter in rodents:
"Sequence and structure of the nucleolin promoter in rodents:
                                                                                                                                                                       SEQUENCE OF 1-44 FROM N.A. MEDLINE=89121496; PubMed=2906027;
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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28-FEB-2003 (Rel. 41, Last annotation update)
Nucleolin (Protein C23).
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                                          Lapeyre B., Bourbon H., Amalric "Nucleolin, the major nucleolar an unusual protein structure reverse. Natl. Acad. Sci. U.S.A. 84
                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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MEDLINE=88312631; PubMed=3409881; Erard M.S., Belenguer P., Caizerg Amalric F.;
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15-SEP-2003
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                                                                                                      NCBI_TaxID=10036;
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    84:1472-1476(1987).
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Sciurognathi; Muridae;
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MBL outstation -
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RESULT 4

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Dec R.C., Somenberg N., Burley S.K.;

"X-ray structure of the human hyperplastic discs protein: an ortholog of the C-terminal domain of poly(A)-binding protein.";

Proc. Natl. Acad. Sci. U.S. A. 98:4414-4419(2001).

-!- FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates (By similarity). This protein may be involved in maturation and/or post-transcriptional regulation of mRNA. May play a role in control of cell cycle progression. May have tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O95071; O94970; Q9NPL3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ubiquitin--protein ligase EDD (EC 6.3.2.-) (Hyperplastic protein homolog) (hHYD) (Progestin-induced protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human if the complete sequences of 100 new cDNA clones from brain wifor large proteins in vitro.";
DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Heart, and Placenta;
MEDLINE=99153743; PubMed=10030672;
Callaghan M.J., Russell A.J., Woollatt E., Sutherland G.R.,
Sutherland R.L., Watts C.K.W.;
"Identification of a human HECT family protein with homology to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Construction of expression-ready cDNA curation of Expression-ready cDNA curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Honda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cooperation of HECT-domain ubiquitin ligase hHYD and DNA topoisomerase II-binding protein for DNA damage response. J. Biol. Chem. 277:3599-3605(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saya H., Nakao M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Fetal brain;
MEDLINE=21671350; PubMed=11714696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila tumor suppressor gene hyperplastic discs."; Oncogene 17:3479-3491(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21192643; PubMed=11287654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
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function. Regulates DNA topoisomerase II binding protein (TopE for the DNA damage response.
SUBCELLULAR IOCATION: Nuclear.
TISSUE SPECIFICITY: Widely expressed. Most abundant in testis expressed at high levels in brain, pituitary and kidney.
MISCELLANEOUS: A cysteine residue is required for ubiquitinthiolester formation.
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or KIAA
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genes: manual
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ID IE63_HSV2H
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Best Local
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GO; GO:0004840; F:ubiquitin conjugati
GO; GO:0004842; F:ubiquitin-protein I
GO; GO:0004842; F:ubiquitin-protein I
GO; GO:0008283; P:cell proliferation;
InterPro; IPR000569; HECT domain.
InterPro; IPR002004; PABP/HECT.
InterPro; IPR003126; Znf_Nrecognin.
InterPro; IPR003126; Znf_Nrecognin.
Pfam; PF00632; HECT; 1.
Pfam; PF00632; HECT; 1.
Pfam; PF00657; UBA; 1.
Pfam; PF00627; Jf-UBR1; 1.
SMART; SM00519; HECTc; 1.
SMART; SM00519; HECTc; 1.
SMART; SM00396; Znf_UBR1; 1.
PROSITE; PS50237; HECT; 1.
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EMBL; U95000; AAF88143.1; -.
EMBL; AB020703; BAA74919.2; -.
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                                                                                                                                                                                                        CONFLICT
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AIN 2393 2449 PABP-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005625; C:soluble fraction; TAS.
GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
GO:0004842; F:ubiquitin-protein ligase activity; TAS.
GO:0008283; P:cell proliferation; TAS.
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                                                                                                           l Similarity
17; Conserv
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                                                                                    EDDERSTDS--SQQCSSEDEDIFEETAQVSPP------RGKEKRQWRAR 41
                                                             EDDSQSNDSSDSDSSSSQSDDIEQETFMLDEPLERTTNSSHANGAAQAPRSMQWAVR 1719
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AUITIN (BY SIMILARITY).

A. LOSS OF UBIQUITIN BINDING.

5 -> P (IN REF. 2).

5 -> Y (IN REF. 2).

1G -> M (IN REF. 2).

1G -> M (IN REF. 2).

2 -> P (IN REF. 2).

5 -> P (IN REF. 2).

6 -> M (IN REF. 2).

7 -> H (IN REF. 2).

8 -> P (IN REF. 2).

9 -> G (IN REF. 2).

10 -> G (IN REF. 2).

11 -> H (IN REF. 2).

12 -> P (IN REF. 2).

13 -> P (IN REF. 2).

14 -> H (IN REF. 2).

15 -> P (IN REF. 2).

16 -> R (IN REF. 2).

17 -> H (IN REF. 2).

18 -> P (IN REF. 2).

19 -> P (IN REF. 2).
                                                                                                                                                          MW; 871300DB404FF561 CRC64;
                                                                                                           6,
                                                                                                                        Score 62;
Pred. No.
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ARG/ASP-RICH
ASP/GLU-RICH
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    512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P28276;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Transcriptional regulator IE63 (VMW63) (ICP
                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes simplex virus (type 2 / strain HG52).
Viruses; dsDNA viruses, no RNA stage; Herpes
SEQUENCE FROM N.A.
MEDLINE=97279235; PubMed=9133743;
VALENS M., Bohn C., Daignan-Fornier
"The sequence of a 54.7 kb fragment
                                                                             Submitted
                                                                                           SEQUENCE FROM N.A. Kitagawa K., Conne
                                                                                                                                                                                                  SGT1 protein.
SGT1 OR YOR057W OR YOR29-08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D10471; BAA01269.1; -.
EMBL; Z86099; CAB06702.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INVOLVED IN THE DOWN-REGULATION OF VIRAL IMMEDIATE-EARLY
GENES AND ACTS IN COMBINATION WITH ICPO AND ICP4 AS AN ACTIVATOR
OF LATE GENES (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Transcription r
NCE 512 AA; 54958 MW;
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l Similarity 34.1%;
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annotation update)
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 B., Dang
of yeast
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               Bolotin-Fukuhara
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REMBL; Z70678; CAA94542.1; -.

REMBL; Z74965; CAA99250.1; -.

REMBL; Z74965; CSHAP9250.1; -.

REMBL; Z44965; CSHAP92500.1; -.

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"The DNA sequence of cosmid 14-5 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97051596; PubMed=8896273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
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Saccharomycetales; Saccharomycetaceae; Saccharomyces
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                                                                                                                                                                                                                      SEQUENCE OF 1-298
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                                                                                               2., Hampsey M.;
nitred (MAR-1996) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: Contains 1 G-patch domain.
CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN FROW
257 ONWARD DUE TO A FRAMESHIFT.
ween the Small structe. The European Bloinformatics Institutions as long by non-profit institutions as long that and this statement is not removed.
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Pred. No. 5.4;
6; Mismatches
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MEDLINE=91317840, PubMed=1860869;

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MEDLINE=91317840, PubMed=1860869;

MEDLINE=91317840, PubMed=1860869;

MEDLINE=91317840, PubMed=1860869;

MEDLINE=91317840, McInerney T.N.;

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Best Local
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P09405; Q61991;
01-MAR-1989 (Re
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01-MAR-1989 (Rel. 10, Last
28-FEB-2003 (Rel. 41, Last
                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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DOMAIN 720 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000467; G patch.
Pfam; PF01585; G-patch; 1.
SMART; SM00443; G_patch; 1.
PROSITE; PS50174; G_PATCH; 1.
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EMBL; Z71500; CAA96127.1;
EMBL; U20390; AAA86499.1;
PIR; S63182; S63182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bourbon H.M., Prudhomme M., Amalric F.;
"Sequence and structure of the nucleolin promoter in rodents:
characterization of a strikingly conserved CpG island.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 68:73-84(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89121496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bourbon
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ucture of the mouse nucleolin gene.
each RNA binding domain is encoded
ol. Biol. 200:627-638(1988).
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767 AA;
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; CE5650B8679BF8C0 CRC64;
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Pred. No. 1
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not removed.
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two independent exons.";
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RESULT 9
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Matches 11
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O75419; O60856;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
7-7-7-7-1-1-1-1 (PORC-PI-1)
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EMBL; M22089;
PIR; A29958; D
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MEDLINE=99160479; PubMed=10051334; Shaikh T.H., Gottlieb S., Sellinge Emanuel B.S., Budarf M.L.;
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                                                               MEDLINE=99325026; PubMed=9660782;
Saha P., Thome K.C., Yamaguchi R., H
"The human homolog of Saccharomyces
J. Biol. Chem. 273:18205-18209(1998)
                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                    HUMAN
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PROSITE; PS00030; RRM RNP 1; 3.
Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:97286; Ncl.
InterPro; IPR000504; RNA_rec_mot
Pfam; PF00076; rrm; 4.
SMART; SM00360; RRM; 4.
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                                 TISSUE=Brain;
                                            SEQUENCE FROM N.A.
                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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706 AA;
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134
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Primates;
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32.4%;
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7; Mismatches
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Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Homo sapiens (Human).

protein (Rel. (Rel. (Rel.

. 37, Created) . 37, Last sequ . 40, Last anno

t sequence up t annotation ROX protein)

update) (MYC antagonist

MNT)

update)

STANDARD;

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Tonlorenzi Brent R., E

zi R., Lo Nigro (
, Ballabio A., C

Alcalay M., Borsani G., o C., Messali S., Zollo Carrozzo R.;

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Tanigami

Α.,

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Ledbetter D.

Meroni G.,

TISSUE=Fetal brain; MEDLINE=97327566; PubMed=9184233;

SEQUENCE FROM NCBI_TaxID=9606;

N.A.

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MNT HUMAN
ID MNT HUMAN
ID MNT HUMAN
AC Q99583;
DT 15-DEC-1998
DT 15-DEC-1998
DT 16-OCT-2001
DE MAX binding I
GN MNT OR ROX.
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Matches 14
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Mamm. Genor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA replication; Cell cycle; Nuclear CONFLICT 115 115 I -> V (SEQUENCE 566 AA; 65568 MW; AE1BEZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED, HIGHEST LEVELS ARE !
ADULT TESTIS AND TYHNUS AND IN FETAL LIVER.
-!- DEVELOPMENTAL STAGE: TRANSCRIPT PEAKS AT G1-S TRANSITION,
TOTAL PROTEIN REMAINS CONSTANT THROUGHOUT THE CELL CYCLE.
EXPRESSED IN MULTIPLE TISSUES DURING EMBRYOGENESIS, INCLUING NEURAL CREST-DERIVED STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GK; 075419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: REQUIRED FOR INITIATION OF CHROMOSOMAL DNA REPLICATION -!- SUBUNIT: ASSOCIATED WITH ORC2L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 8:834-841(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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expressed during murine and human development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CDC45 FAMILY.
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10:322-326(1999).
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R.B., Sutherland H.F., Taylo
of conserved cDNAs from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDC45L.
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29.8%;
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Pred. No. 12;
13; Mismatches
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initiation;
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EMBL; Y13440; CAA73851.1; J
EMBL; Y13441; CAA73851.1; J
EMBL; Y13442; CAA73851.1; J
EMBL; Y13443; CAA73851.1; J
EMBL; Y13443; CAA73851.1; J
EMBL; Y13444; CAA73851.1; J
C_BRARE S
PESC_BRARE S
P79741; Q91906;
28-FEB-2003 (Rel
28-FEB-2003 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                         Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ballabio A., Carrozzo R.; "The human ROX Gene: genomic structure
                                                                                                                                                                                                                                                                                                                                PROSITE; PS00038; HLH_1; FALSE_NEG. PROSITE; PS50888; HLH_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Rox, a novel bHLHZip protein expressed in quiescent cells that heterodimerizes with Max, binds a non-canonical E box and acts as
                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P25912; 1HLO.
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                                                                                                                                                                                                                                                                                                                                                                                    GO:0003713; F:transcription co-activator activity; TAS. GO:0003714; F:transcription co-repressor activity; TAS. GO:0003709; F:transcription factor activity; TAS. GO:0003705; F:development; TAS. GO:0007275; P:development; TAS. GO:0008285; P:negative regulation of cell proliferation; GO:0000074; P:regulation of cell cycle; TAS. GO:0000074; P:regulation of cell cycle; TAS. GO:0000366; P:transcription from Pol II promoter; TAS. GO:00006366; P:transcription from Pol II promoter; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE 5'-CACGGG-3' AND, WITH HIGHER AFFINIAL, BOX SEQUENCE SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
                                                                                                                                                                                       l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumors."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:7188; MNT.
                                                                                                                                                                                                                                                  iption regulation; Repressor;
D 222 233 BASIC DC
D 234 270 HELIX-LO
271 299 LEUCINE-
E 582 AA; 62299 MW; 06AC32
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ilarity 34.2%;
Conservative
 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0677; PubMed=9598315;
Venesio T., Reymond A., Meroni G., All
Enrico F., Stack M., Ledbetter D.H.,
Carrozzo R.;
                                                STANDARD;
 Last sequence update)
                 Created)
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JOINED.
JOINED.
                                                                                                                                                                                      Score 58.5; D
Pred. No. 12;
9; Mismatches
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                                                                                                                                                                                                                                             BASIC DOMAIN.

BASIC DOMAIN.

HELIX-LOOP-HELIX MOTIF (POTENTIAL)

LEUCINE-ZIPPER.

1 06AC320D79BF18A0 CRC64;
                                                PRT;
                                                582
                                                                                                                                                                                                                                                                                                              Nuclear protein; DNA-binding
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                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                   Length 582;
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Liscia D.S.
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RESULT 12
IB63_HSV1E
ID __IE63_H:
ID __IE63_H:
AC __P36295
DT __01-JUN
DT __01-JUN
DT __01-JUN
DT __28-FEB
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                                                                                                                                                                             Matches
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 P36295;
01-JUN-1994
01-JUN-1994
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawakami K., Grosshans H., Hopkins N.;
"The genomic sequence of the zebrafish pescadillo gene.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: May have an essential role for embryonic devel
-i- SUBCELLULAR LOCATION: Nuclear; nucleolar.
-i- DEVELOPMENTAL STAGE: Widely and highly expressed during
                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                           PROSITE;
Nuclear p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EWBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB046108; BAB01764.1; JOINED EFIN; ZDB-GENE-990415-206; pes.
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U77627; AAB61138.1;
EMBL; AB046115; BAB01764.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-180 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Insertional mutagenesis in zebrafish identifies pescadillo and dead eye, essential for embryonic Genes Dev. 10:3141-3155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allende M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97138157; PubMed=8985183; Allende M.L., Amsterdam A., Becker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00533; BRCT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                  [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      first 3 days of embryogenesis. Prominent sites of expression the eyes and optic tectum on day 1, the fin buds, liver primordium, and gut on day 2, and the branchial arches on day MISCELLANEOUS: PES mutant embryos exhibit smaller eyes, a red brain and visceral skeleton, shortened fins and a lack of expansion of liver and gut, and die on day 6 of development. SIMILARITY: Contains 1 BRCT domain.
                                                      HSV1E
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                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                       SM00292; BRCT;
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29, Created)
29, Last sequence up
41, Last annotation
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a; Chordata;
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416
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BRCT.
COILED COIL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNI
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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zenafish pescadillo
'Canmank/DDBJ data
                                                                                                                                                                                         Score 58.5;
Pred. No. 1:
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Best Local
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IE63_HSV11
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01-MAR-1989 (Rel. 10,
28-FEB-2003 (Rel. 41,
the
1.";
J. G
                                                                                                                                                                                              MEDLINE=88274327; PubMed=2839594;
McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A.,
McNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region i
herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                    "The
                                                                                                       MEDLINE=89036163; Pu
Perry L.J., McGeoch
                                                                                                                                                                                                                                                                                                                                                                                            Alphaherpesvirinae; Simplexvirus. NCBI_TaxID=10299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P10238;
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SEQUENCE 511 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Early protein; Transcription regulation; Activator; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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NCBI_TaxID=10303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses;
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                   Gen.
                                                         long unique
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SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
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                                                                                    y L.J., McGeoch D.J.;
DNA sequences of the
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                Virol.
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                                                                                                                                                     N.A.
                69:2831-2846(1988)
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                                                            region
                                                                                                                                  PubMed=2846760;
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40.7%;
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                                                         in the genome of herpes simplex virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                   ype 1 / strain
no RNA stage;
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                                                                                 long repeat region and adjoining parts of
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5; Mismatches
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Pred. No.
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S AN ACTIVATOR
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RESULT 14

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Best Local
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01-FEB-1996 (Rel. 33, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
                                                                               between
                                                                                                                                                            -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Contains 1 TEA DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buerglin T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mirabito P.M., Adams T.H., Timberlake W.E.; 
"Interactions of three sequentially expressed genes control temporal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P20945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Early protein; Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X14112; CAA32290.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91300541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89249350; PubMed=2655931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                        1 66:11-12(1991).
FUNCTION: CONTROLS TEMPORAL AND SPATIAL SPECIFICITY DEVELOPMENT. EXPRESSION OF ABAA LEADS TO ACTIVATION WETA, CESSATION OF VEGETATIVE GROWTH, AND ACCENTUATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENES AND ACTS IN COMBINATION WITH ICPO AND ICP4 AS AN ACTIVATO OF LATE GENES.

PTM: PHOSPHORYLATED.

SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54, HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
                           European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                        FUNCTION: BRLA, ABAA & WETA ARE PIVOTAL REGULATORS OF CONIDIOPHORE DEVELOPMENT AND CONIDIUM MATURATION. THEY ACT INDIVIDUALLY AND TOGETHER TO REGULATE THEIR OWN EXPRESSION AND THAT OF NUMEROUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: INVOLVED IN THE DOWN-REGULATION OF VIRAL IMMEDIATE-EARLY GENES AND ACTS IN COMBINATION WITH ICPO AND ICP4 AS AN ACTIVATOR
                                                                                                                                                                                                             DEVELOPMENT AND CONIDIUM MATURATION. THEY TOGETHER TO REGULATE THEIR OWN EXPRESSION OTHER SPORULATION-SPECIFIC GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spatial specificity in 57:859-868(1989).
                                                                                                                                                                                                                                                                                                                        VACUOLIZATION.
                                                                         SWISS-PROT entry is copyright. It is produced througen the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I30089; WMBEY4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEA domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \mathfrak{a}^{\mathfrak{a}}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      a novel, highly conserved DNA-binding motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=2070413;
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40.7%;
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Pred. No.
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        removed.
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     Usage .
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BRLA AND
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Best Local Similarity
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Q00383;
                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                            MEDIINE=93066301; PubMed=1332054; Wolfe K.H., Morden C.W., Palmer J.D.; Function and evolution of a minimal plastid genome nonphotosynthetic parasitic plant."; Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolfe K.H., Morden C.W., Palmer J.D.;
"Small single-copy region of plastid DNA in the non-photosynthetic angiosperm Epifagus virginiana contains only two genes. Differences among dicots, monocots and bryophytes in gene organization at a non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Lamiales; Orobanchaceae; Orobancheae; Epifagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T01085; -.
InterPro; IPR000818; TEA/ATTSdom.
Pfam; PF01285; TEA; 1.
       SEQUENCE
                         Chloroplast;
                                             EMBL; X61368; CAA43644.1; -. EMBL; M81884; AAA65870.1; -. PIR; S20614; S20614.
                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 among dicots, monocot
bioenergetic locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=92114084; PubMed=1731088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epifagus virginiana (Beechdrops).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical YCF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activator; DNA-binding; Nuclear protein.
DNA_BIND 135 200 TEA-DOMAIN.
DOMAIN 341 362 LEUCINE-ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00554; TEA DOMAIN; 1. Developmental protein; Conidiati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PROODES; TEADOM SMART; SMOO426; TEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J04850; AAA33286.1; -.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4177;
                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE YCF1 FAMILY.
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     1738 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 41, Last annotation update)
1 208 kDa protein ycfl (ORF 1738).
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Hypothetical protein.
738 AA; 208318 MW; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223:95-104(1992).
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35.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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Pred. No.
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  65C63F63BDC8364B CRC64;
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                                      Conservative
                                                 48.48;
                                                         26.9%;
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                                                Score 58; DB
Pred. No. 48;
                                       Mismatches
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                                                         1:
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                                                         Length 1738;
                                       Indels
                                       <u>۵</u>
                                       Gaps
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۲.

Search Job tim

rch completed: July 24, 2003, 11:54:21 time : 5.86091 secs

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB
                                                                                                                                      216
195.5
195.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                              SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_vertebrate:
13: sp_vertebrate:
14: sp_unclassific
15: sp_hacteriap:*
17: sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 2000000000
  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    July 24, 2003, 11:47:53 ; Search time 9.12445 Seconds (without alignments) 1159.539 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                              sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                      sp_organelle:*
sp_phage:*
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sp_mammal:*
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  589
592
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090146
080474
096CH9
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090578
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Compugen Ltd
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                                                                           Q9n4y4 homo sapien
Q96ch9 homo sapien
Q96ch9 mus musculu
Q8n5y2 homo sapien
Q9y5z8 homo sapien
Q9y5z8 homo sapien
Q9ned2 leishmania
Q9ned2 leishmania
Q9v7n4 drosophila
Q8t092 drosophila
Q8t092 drosophila
Q8wun3 homo sapien
Q38969 arabidopsis
Q9c727 arabidopsis
Q9c727 rattus norv
                                                                                                                                   Q9ulh6 homo sapien
Q8n4y4 homo sapien
Q96ch9 homo sapien
Q9cr92 mus musculu
                                                                                                                                                                                            Description
           9 arabidopsis
5 arabidopsis
7 arabidopsis
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57	57.5 26.	57.5 26.	58 26.	,	58 26.	58 26.	58 26. 58 26.	58 26. 58 26. 58 26.	5 8 8 26. 5 8 26.	58 26. 58 26. 58 26.	58.5 27. 58 26. 58 26. 58 26. 58 26.	58.5 27. 58.5 27. 58.26. 58.26. 58.26. 58.26.	58.5 27.58.5 27.58.5 26.58 26.50 26.58 26.58 26.58 26.58 26.58 26.58 26.58 26.58 26.58 26.58 26.	58.5 58.5 58.5 58.5 27. 58.5 27. 58.26. 58.26. 58.26.	58.5 27.58.5 27.58.5 27.58.5 27.58.5 26.5 26.5 26.5 26.5 26.5 26.5 26.5 26	59 27 58.5 27 58.5 27 58.5 27 58.5 27 58.5 27 58 26 58 26 58 26	59 27. 58.5 27. 58.5 27. 58.5 27. 58.5 27. 58.5 27. 58.6 26.	59 27. 58.5 27. 58.5 27. 58.5 27. 58.5 27. 58.6 26. 58.6 26.	59 27. 58.5 27. 58.5 27. 58.5 27. 58.5 27. 58.5 27. 58.6 26. 58.26.26.26.26.26.26.26.26.26.26.26.26.26.	59 27 59 27 59 27 59 27 58 59 27 58 5 27 58 5 27 58 26 58 26	59.5 59.5 59.27 59.27 59.27 58.5 58.5 58.5 27 58.5 27 58.5 27 58.26 28.6 28.6 28.6 28.6 28.6 28.6 28.6	59.5 59.5 59.5 27. 59.27. 59.27. 58.5 58.5 58.5 58.5 58.5 58.5 58.5 58	59.5 59.5 59.5 59.5 59.5 27.7 58.5	59.5 59.5 59.5 59.5 27.5 58.5	59.5 27.50.5 27.50.5 2	59.5 27.5 8.5 27.5 27.5 8.5 27	59.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27	59.5 27.50.5 27.50.5 2
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Q8AVR0	Q8CAP0	Q931C4	Q9P4Z1	Q8IJG6	Q9UKW2	Q8WYB5	Q9UKW3	Q8WML3	Q9UKX0	Q9UP68	Q96JI8	Q96LT9	Q9NSU7	Q8ND97	Q9BXT9	Q8CE30	Q9HZD4	Q8BQD8	Q8MTN8	Q81520	Q95XD2	Q96AJ1	Q9LVH1	Q8W0X4	Q8IWB6	Q9NJH7	Q9CS98	Q8MYL8
Q8avr0 xenopus	Q8cap0 mus musculu	4 rhi	Ħ	plasi	homo	Q8wyb5 homo sapien	homo	Q8wml3 macaca fasc	homo	homo	homo	powo		homo	Q9bxt9 homo sapien		pseu			Q8i520 plasmodium			larab			Q9njh7 drosophila	œ	Q8myl8 caenorhabdi

ALIGNMENTS

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RESULT 1

QUILA

QUILA

AC QUIL

AC QUIL

DT 01-0

DT 01-0

DT 01-0

DT 01-0

CU BIG3

OS Homo

OC Euka

OC NCBI

RN (1)

RP SEQU

RA HONG

RT "KIA

RT "KIA

RT Subff

  RESULT 2
Q8N4Y4
ID Q8N4
AC Q8N4
DT 01-0
DT 01-0
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Best Local (
Q8N4Y4
Q8N4Y4;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "KIĀA1244 as a novel distantly related member (BIG3) of the BIG1/Sec7p subfamily of ARF GEFs.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413080; AAL04174.1; -.
InterPro; IPR000904; Sec7.
SMART; SM00222; Sec7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 1770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
[1]
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ULH6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 100.0%; Score 216; DB 4; Similarity 100.0%; Pred. No. 4.5e-20; 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                        EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 1476
                                                                                                                                                                                                                                                                                                                                                       EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
(TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
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                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195845 MW;
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RESULT 4
99CR92
ID 99CR
AC Q9CR
DT 01.-J
DT 01.-J
DT 01.-M
DE 4921
DE 4921
DE 4921
OS Mus
OC Enka
OC Enka
OC Mamm
OX NCBI
RN [1]
RN [1]
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Q96CH9
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Best Local S
Matches 39
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Best Local S
Matches 39
                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4921513E08Rik protein (Hypothetical aspartic acid-rich acid-rich region containing protein).
                                                                                                                                                                                                                                                                                                 Q9CR92
Q9CR92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Homo sapiens (Human).
Eukaryota, Merarr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC014227; AAH14227.1; -.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
NON TER 1
SEQUENCE 592 AA; 6
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SEOITEWAY: 1 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similar to KIAA1244
                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                         4921513E08RIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                   musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66400 MW;
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97.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 195.5;
Pred. No. 7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 195.5;
Pred. No. 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                       Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F4A1E807B0DF47B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8041EEA348DE65F7 CRC64;
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                                                                                                                                                                                                                                                                                                                       584
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                                                                                                       Vertebrata; Euteleostomi;
chi; Muridae; Murinae; Mus
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RESULT 5
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Battalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuc Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuc Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuc Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
     Matches
                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8N5Y2;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
Male-specific lethal 3-like
                                                                                                                                                                    Submitted (JUN-2002) to the I EMBL; BC031210; AAH31210.1; Genew; HGNC:7370; MSL3L1. InterPro; IPR00953; Chromo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8N5Y2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK015646; BAB299914.1; -.
EMBL; AK014878; BAB29599.1; -.
EMBL; AK03023; BAC26742.1; -.
MGD; MGI:1913967; 4921513E08Rik.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                   ISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                 SM00298; CHI
DE 521 AA;
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     Conservative
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                                                                                                                 CHROMO; 1.
AA; 59823 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
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                             30.3%;
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Last annotation update)
1 (Drosophila)
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Pred. No. 1.9;
7; Mismatches
Score 65.5; DI
Pred. No. 2;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; V
Catarrhini;
                                                                                                                 6DFFB9E183D0CFB9 CRC64;
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i; Hominidae;
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                                                        Length 521;
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     Indels
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; Homo.
  7;
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EDDERSTDSSQQCS----SEDEDIFEETAQVSPPRGKEKRQWRAR 41

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Q9Y5ZB
ID Q9Y5
AC Q9Y5
DT 01-N
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  Query Match
Best Local
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Q9Y5Z8;
01-NOV-1999
                                                                                                                                                                                                                      Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuu K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., "NEDO human cDNA sequencing project.", Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8NB06;
01-OCT-2002
                                                                                                    Pfam; PF00076; rrm; 4.
SMART; SM00360; RRM; 4.
PROSITE; PSS0102; RRM; 4.
PROSITE; PSS0030; RRM RNP 1;
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01-OCT-2002 (TrEMBLrel. 22, Last
01-MAR-2003 (TrEMBLrel. 23, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF117065; AAD38499.1; -. InterPro; IPR000953; Chromo. SMART; SM00298; CHROMO; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Male-specific lethal-3 homolog 1.
                                                                  Hypothetical SEQUENCE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein FLJ34423.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8NB06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of a novel chromo domain gene in Xp22.3 with homology to Drosophila msl-3."; Genomics 59:77-84(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prakash S.K.,
Zoghbi H.Y.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                 InterPro; IPR000504; RNA_rec_mot
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Similarity
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687 AA; 7
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den Veyver I.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
                                                                  74324 MW;
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29.6%;
35.3%;
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Score
Pred.
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Pred. No. 2;
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Catarrhini; Hominidae;
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4.2;
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                     4
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                     Length 687;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Homo.
                                                                                                                                                                                                                                                                                                                   B., Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ballabio
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RESULT 9
Q99K50
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Best Local
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01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ol-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 119.2 kDa protein.
pil05.11.
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q99K50
Q99K50;
PROSITE; PS50102; RRM; 4.
PROSITE; PS00030; RRM RNP 1; 3.
SEQUENCE 707 AA; 76779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A physical map of the Leishman Genome Res. 8:135-145(1998).
EMBL; AL139794; CAB75569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ivens A.C., Lewis S.M., Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ivens A.C., Murphy L., Quail M., Harris D., Ol Rajandream M.A., Barrell B.G.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                            Strausberg R.;
Submitted (MAR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 1114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NED2
                                                                                      InterPro; IPR000504; R
Pfam; PF00076; rrm; 4.
                                                                                                                                                                            EMBL; BC005460; AAH05460.1;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  Nucleolin.
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STRAIN=Friedlin;
                                                                                                                                 MGD; MGI:97286; Ncl.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98146435; PubMed=9477341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164
                                                                                                                                                     P09651; 1HA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                    SM00360; RRM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the Leishmania
                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
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                                                                                                        RNA_rec_mot
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                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63.5;
Pred. No. 8
                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
    44B42C6E146E5D50 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                  RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Cherry J.M., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Bvangelista C.C., Ferrae C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kunp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Renington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Renington K.A., Sunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Gibbs R.A., Phong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Shong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E. W., Rubin G.M., Venter E., Wang A.H., Wang Y.,
RA Gibbs R.A., Myers E. W., Rubin G.M., Venter J., Shoo Q. A.,
RA Gibbs R.A., Shooley R., Shoo Q., Shooley R., Shoo Q., Shooley R., Shoo Q., Shooley
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Best Local S
Matches 11
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Q9V7N4;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE=201790000; runnier S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Miklos
                                                                                                                                                                                                                                                                            Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster.";
SMART; SM00384; AT hook; 1.
SMART; SM00355; ZnF_C2H2; 9.
PRÖSITE; PS00028; ZINC_FINGER_C2H2_1;
                                                                                             InterPro; IPR000637; AT hook
InterPro; IPR007087; Znf C2H;
Pfam; PF00096; zf-C2H2; 9.
                                                                                                                                                                                                                        Science 287:2185-2195(2000).
EMBL; AE003807; AAF58014.1; -.
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Bukaryota; Metazoa; Arthropoda; Hasabyoda; Inse
Neoptera; Endopterygora; Diptera; Brachycera;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                           lyBase; FBgn0034114; CG4282.
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| :: | :: | :: |24
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23,
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Last annotation update)
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Pred. No. 5.9;
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226
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RESULT 11
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Best Local S
Matches 15
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0034114; CG4282.
InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; 10.
SMART; SM00355; ZnF C2H2; 10.
PROSITE; PS00028; ZINC FINGER C2H2 1; 8
PROSITE; PS50157; ZINC_FINGER_C2H2 1; 8
PROSITE; PS50157; ZINC_FINGER_C2H2 1; 7
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 652 AA; 75232 MW; C8724857;
                                                                                                                                                                             Q8WUN3
                                                                          NCBI
                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50157; ZINC_FINGER_C2H2_2;
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 642 AA; 74195 MW; P3B91A
                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Numoo J., Pacleb J., Paragas V., Park S., Phouanenavong Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY069474; AAL39619.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Haranda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG4282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LD21421p.
                                                                          _TaxID=9606;
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                                                                                                                                                                                                                                                         KAEDGSSVDKDKDEDGVEETAEPAPPK---KRRGRPR
                                                                                                                                                                                                                                                                                RSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR
                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                     Zinc; Zinc-ting
AA; 75232 MW;
                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                     28.9%;
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21,
23,
                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                         Score 62.5; DB Pred. No. 6.3; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62.5; I
Pred. No. 6.2;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                 Length 652;
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                                                                                                                                                                                                                                                                                                         Indels
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Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
--- GURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

SEQUENCE

FROM N.A

TISSUE=Cervix;

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SOUR BEAR AND DESCRIPTION OF THE PROPERTY OF T
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Q38969
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Matches 12
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Best Local Similarity
Matches 14; Conser
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PRINTS; PR00048; ZINCFINGER.
ProDom; PD000003; Znf C2H2; 1.

SMART; SM00355; ZnF C2H2; 8.

SMO3TE; PS00011; GTU CARBOXYLATION; 1.

PROSITE; PS0002B; ZINC FINGER C2H2 1; 7.

PROSITE; PS0002B; ZINC FINGER C2H2 2; 9.

Hypothetical protein; Metal-binding; Nuclear pr Zinc-finger.

NON TER 1.

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                                                                                                                                                                                                                                          Genes Dev. 9:330-340(1995).

EMBL; U19134; AAC49734.1; JOINED.

EMBL; U19122; AAC49734.1; JOINED.

EMBL; U19123; AAC49734.1; JOINED.

EMBL; U19124; AAC49734.1; JOINED.

EMBL; U19125; AAC49734.1; JOINED.

EMBL; U19126; AAC49734.1; JOINED.

EMBL; U19127; AAC49734.1; JOINED.

EMBL; U19128; AAC49734.1; JOINED.

EMBL; U19129; AAC49734.1; JOINED.

EMBL; U19129; AAC49734.1; JOINED.

EMBL; U19130; AAC49734.1; JOINED.

EMBL; U19131; AAC49734.1; JOINED.

EMBL; U19131; AAC49734.1; JOINED.

EMBL; U19131; AAC49734.1; JOINED.

EMBL; U19133; AAC49734.1; JOINED.
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Q38969;
01-NOV-1996
                                                                                                                                                                                                    Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The SABRE gene is Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=WS ecotype;
MEDLINE=95172383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical SABRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel 01, Created)
01-NOV-1996 (TrEMBLrel 01, Last sequence update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
Hypothetical 153.9 kDa protein.
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InterPro; IPR000294; VitK_dep_GLA.
InterPro; IPR007087; Znf_C2H2.
InterPro; IPR007086; Znf_C2H2_sub.
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                                                                                                                          Similarity
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SSLQCPTEDEDVEEEADEVVP
                                             SSQQCSSEDEDIFEETAQVSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 AA;
                                                                                                                                                                                                    l protein.
1347 AA;
                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=7867930;
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                                                                                                                          28.2%;
                                                                                                                                                                                                    153905 MW;
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                                                                                                                          Score 61;
Pred. No.
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                                                                                               Mismatches
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xpansion in
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                                                                                                                                                  Length 1347;
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RX MEDLINE=21016719; PubMed=11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Dunn F., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Prong B., Fujii C.Y.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Willescher J., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9C727
Q9C727;
01-JUN-2001
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01-JUN-2001 (TrEMBLrel. 17, Last seq.
01-JUN-2001 (TrEMBLrel. 17, Last annowance)
Typothetical 210.0 kDa protein (Fragm T18124.18.
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Q9C6Q6;
01-JUN-2001
01-JUN-2001
STRAIN=cv. Columbia;
MEDLINE=21016719; Pubmed=11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dev
                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eypermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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PADunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Lin X., Liu S.Y., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sukano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana ";
RI Nature 408:816-820(2000).
RE EMBL; AC073943; AAG50951.1; -.
RW Hypothetical protein.
SQ SEQUENCE 2599 AA; 292445 MW; 6FAF3CCA592F4A3C CRC64;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Search completed: July 24, 2003, 11:56:59

Job time: 12.1245 secs
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Result
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Maximum DB seq length: 200000000
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Perfect score:
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Match
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Gapop 60.0 , Gapext 60.0
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1 RIRAMAQQVFMLDT
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   AAW85472
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                                                                                                                                                                                         Description
                                                          Novel
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PS118
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8 protein enco prostate-spe prostate mar 1 human diagno protein SEQ 1 human diagno prostate can prostate can prostate can prostate-spe
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Peptide from human	AAW86052	20	13	1.4	7	
10	AAW86046	20	13	1.4	7	
from	AAW86072		13	1.4	7	
from	AAW86066	20	13	1.4	7	
from	AAW86065	20	13	1.4	7	
Peptide from human	AAW86038	20	13	1.4	7	
=	AAG96976	22	10		7	
coccus f	AAU35339	22	1031		8	
Alpha subunit of A	AAR10098	12	578		œ	
monocyto	ABB47760	23	483		œ	
	AAR43999	15	477	1.5	89	
thal	AAG20815	21	448		8	
	œ	21	427		89	
cycle	ū	23	351	1.5	8	
c	8	21	343		89	
ä	w	22	121		89	
peptide	N	23	32	1.5	89	
e #2512	AAM03830	22	32	•	80	
e #2631	AAM28594	22	32		8	
e #25	AAM16103	22	32		89	
bone m	AAM68280	22	32	٠	8	
	AAM55910	22	32		8	
n #2506	ABB20507	22	32	1.5	89	
e #2	ABB35089	22	32	1.5	80	
Peptide #2562 enco	ABB29911	22	32	1.5	8	
live	ABG49938	22	32		89	
eumon	ABU01364	24	216	1.7	9	
tococcus [ABP81377		216		9	
PS118 prostate mar	AAM50811		35		35	
n prostate-	AA019167		35	6.8	35	
prostate	081		40	7.7	40	
Human prostate-spe	AA019168		40	7.7	40	
prostate	81				41	
7	AA019166	23	. 41	7.9	41	
vel human diagn	972		50	8	43	
PS118 prostate mar	AAM50813		49	9.5	49	

ALIGNMENTS

25-MAR-2003 25-FEB-1999 AAW85472;

(updated)
(first entry)

PS118 protein encoded by consensus sequence.

AAW85472 standard; Protein; 518 AA

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Granados EN, Hode
Russell JC, Stro
                                             WPI; 1998-610000/51.
N-PSDB; AAV82812.
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                                                                                                                                                                           Cohen M, Colpitts TL, Friedman es SC, Klass MR, Kratochvil JD, pe SD;
                                                                                                                                                                                                           PN, Gordon J
Robertsrapp
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ertsrapp L;
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Human;
                          Human prostate-specific PS118
                                                     27-NOV-2002
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 prostate-specific
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Granados EN,
Russell JC, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
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(COHE/)
(COLP/)
(FRIE/)
(GORD/)
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23-APR-1997;
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RUSSELL J C.
STROUPE S D.
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HODGES S C.
KLASS M R.
KRATOCHVIL J I
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Granados EN, Hod
Russell JC, Stro
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benign prostatic
The present sequence is that of a human prostate-specific PS118 polypeptide, as predicted from a partial consensus cDNA sequence (see ABA91651), and lacking the N-terminal region. The PS118 consensus sequence is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, including derivatives of the present sequence, polymucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and
                                                                                                                               Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostit preventing or treating or determining predisposition to prostate disease -
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(HODG/)
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HODGES S C.
KLASS M R.
KRATOCHVIL J D.
ROBERTS-RAPP L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marker; prostate cancer; tumour; metastasis; hyperplasia; prostatic intraepithelial neopl
                                                                                                                                                                                                                            Cohen M, Coplpitts TL, Friedmanes SC, Klass MR, Kratochvil JD, pe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                            mapping; gene mapping; gene
medical imaging; diagnostic;
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                                                                                                                                                                            therapy; forensic genetic disorder.
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CC Note: The sequence data for this patent did not appear in the printed consecrification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
                                                            TPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD
                                                                                      TPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD
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cc hybridisation probes, primers for PCR, for chromosome and gene mapping, cc for the recombinant production of protein, or in generation of anti-sense CR NA or RNA. The polynucleotides are useful in diagnostics as expressed CR sequence tags (ESTs) for identifying expressed genes or for physical CR mapping of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or CR pluripotential state useful for re-engineering damaged or diseased CR tissues, transplantation, manufacture of bio-pharmaceuticals or the CR tissues, transplantation, manufacture of bio-pharmaceuticals or the CR protein expression or biological activity, e.g. haematopoietic disorders, CR protein expression or biological activity, e.g. haematopoietic disorders, CR disorders, non-healing wounds, immune deficiencies and disorders, infectious diseases caused by viral, bacterial or fungal infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haematopoletic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; antiallergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel human coding sequences (ABQ99268-ABQ99608) and proteins (ABQ4862-ABB65022). The sequence useful in therapeutic, diagnostic and research methods. The polynucleotides may be used in the field of molecular biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID 495; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLLLDSYRTAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQET
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                                                                                                                                         KIYTMAADKTISKLMTSYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLM 412
                                                                                                                                                                                                                    TGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGN
                                                                                                                                                                                                                                                                                              VSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPS
  DQTFTALQPAVFPCISQLTCHVTDIRVRQAV
                                        DQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILP
                                                             DQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILP
                                                                                                                    KIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLM
                                                                                                                                                                                                TGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGN
                                                                                                                                                                                                                                                                           VSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPS
                                                                                                                                                                                                                                                                                                                                                     I TAEQVKKVLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLLDSYRTAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1982 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 100.0%; I Conservative 0;
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Length 1982; Indels

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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CPCR polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations (CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Control of the printed of the polynucle data for this patent did not appear in the printed cartification, but was obtained in electronic format directly from WIPO cart from wipo in/nub/liched not sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 40090; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutations
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                                                                                                                                                                                                                                                                               This invention describes novel nucleic acid sequences (A) that are expressed at high level in prostatic tumor tissue and encode gene products or their fragments. The products of the invention have antitumor activity. Polypeptides (I) encoded by (A) are used: (i) for identifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. AAY40215-Y48303 represent protein fragments encoded by the expressed sequence tags described in the method of the
                                                                                                                                                                                Matches 192;
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; 128; 166pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid expressed at high level in prostatic tumor tissue encoded polypeptides, useful for treating cancer and screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-519628/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tag; EST; prostate tumor; antitumor; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate
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                                                                                                                                                                                                Local
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 121
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                            125
                                                          61
                                                                                      65
                                                                                                                                      5 MAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLLSHQV 64
                                                                                                                                                                                                Similarity
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                 FDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFE 184
                                                                          LLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMONLAVIFDLLLDSYRTARE 124
FDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFE
                                                          LLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTARE
                                                                                                                    MAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLLSHQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQTFTALQPAVFPCISQLTCHVTDIRVRQAV 1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinzmann B,
                                                                                                                                                                                                                                            192 AA;
                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue specificity human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer-associated protein
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                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                             Score 192; DB 20; Pred. No. 7.8e-182;
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                                                                                                                                                                                                           Length 192;
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                                                                                                                                                                                                               expressed at high level in prostatic tumor tissue and encode gene products or their fragments. The products of the invention have antitumor activity. Polypeptides (I) encoded by (A) are used: (i) for identifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use encoded by the expressed sequence tags described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid expressed at high level in prostatic tumor tissue encoded polypeptides, useful for treating cancer and screening for therapeutic agents
                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel nucleic acid sequences (A) that are
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; 112-113; 166pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Specht T, Hinzmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed sequence tag; EST; prostate tumor; antitumor; treatment; gene therapy; tissue specificity human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate cancer-associated protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
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                                                                                                                  180;
   61
                            71
                                                                                       11
                                                                                                                               Similarity
                   DILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDTSPG 130
                                                                               MLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLLSHQVLLQNLY
   DILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDTSPG 120
                                                         MIDTOCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLLSHQVLLQNLY
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ilarity 100.0%;
Conservative (
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                                                                                                                              Score 180; DB 20; ; Pred. No. 5.9e-170;
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                                                                                                                  Mismatches
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LKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFEDDERST 190

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RESULT 9
AAO19169
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                                       Matches
                                                         Query Match
                                                                                               The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                 prognosticating, preven individual to diseases
                                                                                                                                                                                                   Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
                                                                                                                                                                                                                                                                             Billingel PA,
Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1998;
23-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate-specific PS118
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                                                                               Sequence
                                                                                                                                                                       Claim 17; Page 44; 58pp; English.
                                                                                                                                                                                                                                              WPI; 2002-665429/71
                                                                                                                                                                                                                                                                                                                              (KRAT/)
(ROBE/)
                                                                                                                                                                                                                                                                                                                                                   (HODG/)
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) ROBERTS-RAPP L.
) RUSSELL J C.
) STROUPE S D.
\mathbf{L}
                                        49;
                                                                                                                                                                                                                                                                                                                                                                       GORDAN J.
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         EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 441
                                                                               49 AA;
                                                                                                                                                                                                                                                                A, Cohen M,
Hodges SC,
Stroupe SD;
                                      9.5%; Solitarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0065383.
97US-0842385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e; prostate-specific sequence; prostate cancer; PS118;
sequence tag; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                            O. E
                                                                                                                                                                                                                                                                                                                                                                                         7 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                            Colpitts TL, Friedman Klass MR, Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
                                      Score 49; DB; Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein fragment
                                     1.8e-40;
hes 0;
                                                           멂
                                                           23;
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                                                                                                                                                                                                                                                                            'n,
                                                         Length 49;
                                       Indels
                                                                                                                                                                                                                                                                          Gordan J;
Roberts-Rapp
49
                                      0
                                      Gaps
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RESULT 10

Query Match Best Local S Matches 49

Similarity

100.0%;

Score 49; Pred. No. Mismatches

DB 1.8e-40 23;

Length 49; Indels

٥,

Gaps

0

49;

Conservative

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polypeptide (see AAM50809). A PS118 consensus sequence (see AAM508151) is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, polynucleotides, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostatic intraepithelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polynucleotides in transfected host cells, and immunogenic peptides are useful for raising PS118-specific invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the lease of energy in portant and unimportant prostate cancers
                                                                                                                                                                                                                                                                                                                                                                  Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS118 prostate marker immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM50813 standard; Protein; 49
                                                                                                                                                                                                                                                                              The present sequence is that of an immunogenic polypeptide comprising amino acids 393-441 of human prostate-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2001055758-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                         Claim 17; Page 44; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-187683/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BILL/)
(COHE/)
(COPL/)
(FRIE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1998;
                                without the use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GRAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HODG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GORD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                JC, Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GORDON J.
GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRATOCHVIL J
ROBERTS-RAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRIEDMAN P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPLPITTS T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BILLING-MEDEL P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLASS M R.
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   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen M, Coplpitts TL, Friedman ges SC, Klass MR, Kratochvil JD, upe SD;
                              surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PN, Gordon J
Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                   prognosticating,
                                                                                                                                                                                                                                                                                PS118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gordon J;
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393

441

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RESULT 11
ABG09729
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                                                                                                                                                                                               polypeptide (II) sequences. (I) is useful as hybridisation probes, comply probable (II) sequences. (II) is useful as hybridisation probes, comply probable (II) and for chromosome comply production of (II). The comply production of (II) and for chromosome comply production of (II) and in recombinant production of (II). The comply techniques comply probable (II) are also used in diagnostics as expressed sequence tags (II) are thereby techniques (II) are store normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in compositics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human the sequences of the invention.
                                                     Best Loc
Matches
                                                                                    Query Match
                                                                                                                       Sequence
                                                                                                                                                                       specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 40088; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT,
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #9720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG09729;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
                                                                   ьоса1
                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to isolated polynucleotide (I) and
460 MVLTVLNQIQILPDQTFTALQPAVFPCISQLTCHVTDIRVRQA 502
                                                                                                                                                                    The sequence data for this patent did not appear in the ication, but was obtained in electronic format directly
                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS73916.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                       50
                                                   8.3%;
llarity 100.0%;
Conservative (
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2000US-0649167.
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                                                   0,
                                                   Score 43; DB; Pred. No. 1.6
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                                                                 DB 22; I
1.6e-34;
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                                                                                 Length 50;
                                                     Indels
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from WIPO
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RESULT 12
AAO19166
ID AAO19
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                                           Matches
                                                   Best Local
                                                              Query Match
                                                                                                        The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                                  Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
                                                                                     Sequence
                                                                                                                                                                                    Claim 17; Page 43-44;
                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                              WPI; 2002-665429/71
                                                                                                                                                                                                                                                                                   Granados EN,
Russell JC,
                                                                                                                                                                                                                                                                                                       Billingel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                 (COLP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                       (COHE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1998;
23-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA019166;
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                                                                                                                                                                                                                                                                                                                                                                                             (GORD/)
(GRAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-2001; 2001US-0991681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002086316-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST; expressed sequence tag; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate-specific PS118 protein fragment
                                                                                                                                                                                                                                                                                                                                                     (ROBE/)
                                                                                                                                                                                                                                                                                                                                                               (KRAT)
                                                                                                                                                                                                                                                                                                                                                                         (KLAS/
                                                                                                                                                                                                                                                                                                                                                                                    (HODG/)
                    184 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate;
                                                                                                                                                                                                                                                                                                                             ROBERTS-RAPP I
RUSSELL J C.
STROUPE S D.
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BILLINGEL P A.
                                                                                                                                                                                                                                                                                                                                                                                                        GORDAN J.
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                                                                                                                                                                                                                                                                                                                                                              KRATOCHVIL J
                                                                                                                                                                                                                                                                                                                                                                       KLASS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                        COHEN M.
EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVLTVLNQIQILPDQTFTALQPAVFPCISQLTCHVTDIRVRQA 43
                                                                                     41
                                           Conservative
                                                                                                                                                                                                                                                                                   Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                     ΑĄ,
                                                                                                                                                                                                                                                                                             Hodges
                                                                                                                                                                                                                                                                                                          Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0842385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0065383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate-specific sequence; prostate cancer;
                                                     100.0%;
                                                                                                                                                                                                                                                                                    SC,
                                                                                                                                                                                                                                                                                                                                                   FO
                                                                                                                                                                                    58pp; English
                                                                                                                                                                                                                                                                                             Colpitts TL,
Klass MR,
                                                     Score 41;
; Pred. No.
                                           °,
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                                            Mismatches
                                                                                                                                                                                                                                                                                             Friedman PN,
Kratochvil JD,
                                                                  DB 23;
                                                     1.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #2
                                                              Length 41;
                                           Indels
 41
                                                                                                                                                                                                                                                                                            Gordan J;
Roberts-Rapp L;
                                          0
                                          Gaps
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RESULT 13 AAM50810

0

AAM50810 standard; Protein; 41 AA

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Consequence (see AMASORO). A PSIL® consensus sequence (see AMASORO). A PSIL® consensus sequence (see AMASORO) is found at least 12 times more often in prostate than in mon-prostate tissue. PSIL® polypeptides, polynucleotides, cantibodies, agonists and inhibitors are useful for detecting, it diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the prostate, such as benign prostatic hyperplasia, prostate conditions of the prostate, such as benign prostatic hyperplasia, prostate cancer, tumours and metastases. The PSIL® polypeptides can be produced by expression of PSIL® polymelectides in transfected host cells, and contibodies of diagnostic use. The methods and reagents of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers.
Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                                                                                                The present sequence is that of an immunogenic polypeptide comprising amino acids 184-224 of human prostate-specific
                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS118; prostate;
benign prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-187683/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Billing-Medel PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS118 prostate marker immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2002
                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KRAT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BILL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COHE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HODG/)
l Similarity 100.0%; | 41; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) GRANADOS E N.
) HODGES S C.
) KLASS M R.
) KRATOCHVIL J D.
) ROBERTS-RAPP L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JC,
                                                                                   the use of surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GORDON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRIEDMAN P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COPLPITTS T L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COHEN M
                                                          41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PA, Cohen M, Coplpitts TL, Friedman PN,
Hodges SC, Klass MR, Kratochvil JD, Robo
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0842385
                                                                                                                                                                                                                                                                                                                                                                         43; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marker; prostate cancer; tumour; hyperplasia; prostatic intraepith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rker; prostate cancer; tumour; metastasis;
perplasia; prostatic intraepithelial neoplasia;
diagnosis; therapy; vaccine; immunogen.
k; Score 41; DB
b; Pred. No. 1.3
0; Mismatches
DB 23; I
1.3e-32;
hes 0;
                          Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roberts-Rapp
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erts-Rapp L;
                                                                                                                                                                                                                                                                                                                                 PS118
0
0
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184 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 224

RESULT 15

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RESULT 14
AAO19168
ID AAO19
XX AAO19
XX AAO19
XX AAO19
XX Human
XX Human
XX Homo
DE Human
XX Homo
XX US20C
XX COH
PD 04-JU
XX 25-AI
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                                      S
                                                                                        Matches
                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                          monitoring and treatment of prostate diseases, particularly proceancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                     The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring prognosticating, preventing, treating, or determining predisposition individual to diseases and conditions of prostate, e.g. prostrate
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Granados EN,
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23-APR-1997;
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(COHE/)
(COLP/)
(FRIE/)
(GORD/)
(GRAN/)
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                                        332 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 371
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FRIEDMAN P N.
GORDAN J.
GRANADOS E N.
HODGES S C.
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STROUPE S D.
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97US-0842385.
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100.0%; Pr
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Pred. No. 1.2
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Roberts-Rapp
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comprising amino acids 332-371 of human prostate specific PS118

polypeptide (see AAM50809). A PS118 consensus sequence (see
ABA91651) is found at least 12 times more often in prostate than

in non-prostate tissue. PS118 polypeptides, polynuclectides,
antibodies, agonists and inhibitors are useful for detecting,
diagnosing, staging, monitoring, prognosticating, preventing and

treating (including by genetic immunisation), or determining the
predisposition of an individual to, diseases and conditions of the

predisposition of an individual to, diseases and conditions of the

prostate, such as benign prostatic hyperplasia, prostatitis,
prostatic intraepithelial neoplasia, prostate cancer, tumours and

metastases. The PS118 polypeptides can be produced by expression

of PS118 polynucleotides in transfected host cells, and

immunogenic peptides are useful for raising PS118 specific
antibodies of diagnostic use. The methods and reagents of the

cinvention may provide an early means of detecting diseases of the

prostate and may also provide new markers which can differentiate

between the clinically important and unimportant prostate cancers
     Best Loc
Matches
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate disease -
                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of an immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 44; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-187683/24.
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Granados EN, Hodg
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(FRIE/)
(GORD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS118 prostate marker immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2002
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                  Local
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) GRANADOS E N.
) HODGES S C.
) KLASS M R.
) KRATOCHVIL J D.
) ROBERTS-RAPP L.
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                  Similarity
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                                                                   40
7.7%; Score 40; DB 23; Length 40; ilarity 100.0%; Pred. No. 1.2e-31; Conservative 0; Mismatches 0; Indels
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    Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
    Stroupe SD;
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Qy 332 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 371

Search completed: July 24, 2003, 12:21:13 Job time : 133.965 secs

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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Word size
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US-09-065-383-30
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US-09-314-268-147
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US-08-474-728-34
US-08-474-040-34
US-08-484-537-34
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US-08-284-516C-47
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US-08-284-516C-67
US-08-284-516C-67
US-08-284-516C-67
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US-08-284-516C-67
US-09-537-911A-37
US-09-537-911A-47
US-09-537-911A-65
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                                                                                                                                    CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/842,38/
PILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/335-1729
TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acid
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                                                                                                                     TELEFAX: 847/938-2623
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US-09-252-991A-19154	US-09-308-345A-2	US-09-308-345A-4	US-09-252-991A-31461	US-09-220-528-63	US-09-252-991A-23334	US-09-252-991A-31554	US-09-198-452A-205	US-09-252-991A-24032	US-09-107-532A-6376	US-09-252-991A-26679	US-08-944-483-28	US-09-328-352-4310	US-09-011-769A-27	5189147-9	US-09-252-991A-31422	US-09-252-991A-17084	US-09-252-991A-29708
Sequence 19154, A	Sequence 2, Appli	Sequence 4, Appli	Seguence 31461, A	Sequence 63, Appl	Sequence 23334, A	Sequence 31554, A	Sequence 205, App	Sequence 24032, A	Sequence 6376, Ap	Sequence 26679, A	Sequence 28, Appl	Sequence 4310, Ap	Sequence 27, Appl	Patent No. 5189147	Sequence 31422, A	Sequence 17084, A	Sequence 29708, A

ALIGNMENTS

Sequence 27, Application US/09065383 Patent No. 6391543 GENERAL INFORMATION: ZIP: 60064-3500 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASESEQ for Windows Version 2.0 TITLE OF INVENTION: REAGENTS AND TITLE OF INVENTION: FOR DETECTING NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: ADDRESSEE: Abbott Laboratories APPLICANT: STREET: 100 Abbott CITY: Abbott Park COUNTRY: USA KRATOCHVIL, JON D. ROBERTS-RAPP, LISA RUSSELL, JOHN C. STROUPE, STEPHEN D. VENTION: REAGENTS AND METHODS USEFUL VENTION: REAGENTS AND METHODS USEFUL GRANADOS, EDWARD N. HODGES, STEVEN C. KLASS, MICHAEL R. FRIEDMAN, PAULA N. GRANADOS, BILLING-MEDEL, COHEN, MAURICE JULIAN FOR DETECTING DISEASES OF THE PROSTATE 33 Park Road PATRICIA

518 amino acids

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08/842,385

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                                                                                                                                                                                                                                                                                                                                                                Sequence 31,
                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 518;
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APPLICANT:
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TOPOLOGY: linear
MOLECULE TYPE: No.
                                                                                                 TITLE OF INVENTION: REAGENTS AND METHODS US TITLE OF INVENTION: FOR DETECTING DISEASES NUMBER OF SEQUENCES: 33
                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     APPLICANT:
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           COUNTRY:
                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                       Abbott Park
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                                                                                                                                                                                                                                                                                                                                                                Application US/09065383
                                                      E: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                          ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
                                                                                                                                                                                                       GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                  COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
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                                                                                                                                                                                            KRATOCHVIL, JON D.
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                                                                                                                                                                                                                                                        GORDON,
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Pred. No. 0;
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Patent No.
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Best Local Similarity
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APPLICANT: BILLIN
APPLICANT: COHEN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND
TITLE OF INVENTION: FOR DETECTION
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8.
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Disketto
COMPUTER: IBM Compat:
COMPUTER: DO:
COMP
SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
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                                                                                                                                                                                                                                                                                          STREET: 100 Abbott
CITY: Abbott Park
STATE: IL
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TYPE: amino acid
STRANDEDNESS: single
                                                                                 COMPUTER: IBM CON
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 847/938-2623
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539154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HODGES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRANADOS,
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                                                                                                                          IBM Compatible
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S, STEVEN C.
, MICHAEL R.
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                                                                                     Dos
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US-09-065-383-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
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APPLICANT:
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF
                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/84
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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Local Similarity 100.0%; Pred. No.
nes 41; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: lir
 NAME: Becker, Chery
REGISTRATION NUMBER:
                                                                                                   CLASSIFICATION:
                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                  CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 EDDERSTDSSOOCSSEDEDIFEETAQVSPPRGKEKROWRAR 224
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                                                                                                                                                                                                                                                                                                                                                                                       INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 amino acids
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STROUPE, STEPHEN D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GORDON, JULIAN
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                                                                                                                                                                                                                                                                                                                                                                    REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE PROSTATE 33
                                                                08/842,385
                                                                                                                                  US/09/065,383
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35,441
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
                                                               NAME: BECKEL, 35,441
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084
TELECOMMUNICATION INFORMATION:
THE PHONE: 847/935-1729
                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/842
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
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                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 100 Abbott CITY: Abbott Park
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                                                 TELEX:
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                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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    35 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR DETECTING DISEASES OF THE PROSTATE 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDWARD N.
                                                                                                                                                                                     08/842,385
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                                                                                                            6084.US.P1
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US-09-314-268-147
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CURRENT FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/314,268
EARLIER FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 147
LENGTH: 55
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Best Local Similarity
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TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
TITLE OF INVENTION: VIRUSES
FILE REFERENCE: 3789/80902
       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                              APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
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nes 35; Conservative (
                                                                                                                             COUNTRY: 1
ZIP: 9430:
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                                                                                                                                                                               CITY: Palo Alto
                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 317
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ANT: QUEEN, Cary L.
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                                                                                                                                                              California
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SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
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                                                                                                                                                                                            379 Lytton Avenue
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100.0%; Pred. No.
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US/07/634,278
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; Pred. No. 2.4e-2
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-UN-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 19-DEC-1
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REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SCHNEIDER, Wil. APPLICANT: SELICK, Harold
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HYPOTHETICAL:
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FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: QUEEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein LOCATION: 1..107 OTHER INFORMATION: OTHER INFORMATION:
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nes 7; Conserv
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                          California
                                                                                                                                                                                                                                                                                                                                          5: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
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light chain for humane Lay antibody."
                                                                      US 07/634,278
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%; Pred. No. 43;
0; Mismatches
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US 07/310,252

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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
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                                                            APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (415) 326-2400
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OTHER INFORMATION:
OTHER INFORMATION:
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                             FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: sin
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SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
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1..107
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light chain for humane Lay a
US 07/310,252
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0.0%; Pred. No.
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o. 43;
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                                                   CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/590,274
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
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REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
     APPLICATION NUMBER: US 07/590,27.

PILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/310,252
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NAME: Smith, William M
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TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
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ZIP: 94301
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SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
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13-FEB-1989
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light chain for humane Lay antibody."
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00.0%; Pred. No
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Mismatches
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Best Local Similarity
Marches 7; Conserva
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US-08-484-537-34
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APPLICANT: QUEEN, (
APPLICANT: CO, Man
APPLICANT: SCHNEID)
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
                                                                                                                                 CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US/07/634,278
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                   13-FEB-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%; Score 7; DB:
100.0%; Pred. No. 43
ative 0; Mismatches
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US 07/290,975
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RESULT 12
US-08-752-693A-2
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Best Local Similarity 100.0%;
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
                CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: PCT/US96/07321
APPLICATION NUMBER: PCT/US96/07321
APPLICATION NUMBER: 08/020,223
APPLICATION NUMBER: 08/020,223
APPLICATION NUMBER: 07/673,153
APPLICATION NUMBER: 07/673,153
FILING DATE: March 18, 1991
APPLICATION NUMBER: 07/327,765
APPLICATION NUMBER: 07/327,765
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REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein LOCATION: 1..107 OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,693A
FILING DATE: 19-NO. 6190640-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                   ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IEM PAULINE STASIAK, PH.D./2
OPERATING SYSTEM: PC-DOS
SOPTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD FOR TREATING NEOPLASIA USING HUMANIZED ANTIBODIES WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sydney Welt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 SSLSVSV 447
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FILING DATE: NUMBER: 07/32/,/00 APPLICATION NUMBER: 07/32/,/00 FILING DATE: March 23, 1989
FILING DATE: MIMBER: 07/118,411
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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(415) 370 NO: 34:
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Elizabeth Carswell Richards
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leonard Cohen
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light chain for humane Lay antibody."
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Best Local
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 318-300
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8615
                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/267,641
FILING DATE: 28-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael B.
TITLE OF INVENTION: Antibodie
TITLE OF INVENTION: Proteins
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                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/442,542 FILING DATE: 16-MAY-1995
                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
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5686600
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REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5381.1 CIP - JEL/MAS
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APPLICATION NUMBER: 06/724,991
FILING DATE: April 19, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human A33
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DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins and their Use
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Query Match
Best Local Similarity
Warches 7; Conserve
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                                                                                                                                                                                                                                                                                US-08-765-469-12
Sequence 37, Application US/08284516C PATENT NO. 6056957
GENERAL INFORMATION:
APPLICANT: Chou, Chuan-Chu
APPLICANT: Murgolo, Nicholas
APPLICANT: Abrams, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,469
FILING DATE:
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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; 100.0%; Pred. No.
-1ve 0; Mismatches
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o. 45;
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COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
COMPUTER: Application DATA:
APPLICATION UNMBER: PCT/US93/00759
FILING DATE: 04-FEB-1993
PRIOR APPLICATION UNMBER: 07/832,842
FILING DATE: 06-FEB-1993
PRIOR APPLICATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0233K
TELECOMMUNICATION STORMATION:
TELEPAX: 908 298 5388
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LEEGTH: 127 amino acids
TYPE: protein
US-08-284-516C-37
Search completed: July 24, 2003, 12:28:36 Job time : 60.9151 secs
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                                                                                                                                                                                             Query Match 1.4
Best Local Similarity 100.
Matches 7; Conservative
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APPLICANT: Silver, Jon
APPLICANT: Tindall, Stephen
APPLICANT: Windsor, William
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Design, Cloning and Expression of
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2000 Gallc
CITY: Kenilworth
STATE: New Jersey
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                                                                                                  28 SSLSVSV 34
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2000 Galloping Hill Road
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                                                                                                                                                                                                                             1.4%; Score 7; DB 3;
100.0%; Pred. No. 50;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

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Query
Match Length DB
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                                                                                                           SUMMARIES
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259	253	218	186	135	122	121	119	115	60	49	21	10	1031	32	Match Length DB ID
15	9	11	9	9	11	11	11	10	9	11	9	11	v	9	BG
US-10-128-714-3274	US-09-815-242-11842	US-09-925-179-67	US-09-729-674-30	US-09-916-790-31	US-09-305-736-142	US-09-974-879-143	US-09-764-891-3238	US-09-764-868-815	US-09-864-761-45360	US-09-768-235B-36	US-09-864-761-41759	US-09-572-404B-3170	US-09-815-242-10932	US-09-864-761-35805	ID
Sequence 3274, Ap		Sequence 67, Appl	Sequence 30, Appl	Sequence 31, Appl	Sequence 142, App	Sequence 143, App	Sequence 3238, Ap	Sequence 815, App	Sequence 45360, A	Sequence 36, Appl	Sequence 41759, A	Sequence 3170, Ap	Sequence 10932, A	Sequence 35805, A	Description

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Ü	707	596	596	596	596	596	596	596	596	581	578	569	477	454	445	438	414	405	400	400	365	359	352	342	320	314	314	314	287	272
t	7	15	15	15	15	14	14	14	11	9	10	10	15	10	9	10	15	15	9	9	10	9	15	10	10	15	11	9	15	15
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מפלחפוירם מדה, עלקה	2	100,	Sequence 310, App	e 310,	e 310,	Sequence 100, App	310		e 243	801,	2	617	14	Sequence 8, Appli	117	Seguence 28, Appl		e 120	Sequence 16, Appl	63,	æ	210,	966	Sequence 4170, Ap	e 6258,	e 472	Sequence 934, App	934,	Sequence 11165, A	Sequence 8274, Ap

ALIGNMENTS

PRIOR APPLICATION PRIOR APPLICATION PRIOR FILING DATE: PRIOR APPLICATION PRIOR PILING DATE: PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR PILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR PILING DATE: PRIOR PRIOR PILING DATE: PRIOR PRIOR PILING DATE: PRIOR PRIOR PILING DATE: PRIOR PRIOR PILING DATE:	RESULT 1 US-09-864-761-35805 ; Sequence 35805, Application US/09 ; Patent No. US20020048763A1 ; GENERAL INFORMATION: APPLICANT: Rank, David R. APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng TITLE OF INVENTION: GENE EXPRES FILE REFERENCE: Aeomica-X-1 ; CURRENT APPLICATION NUMBER: US/0 ; CURRENT FILING DATE: 2001-05-20 ; PRIOR APPLICATION NUMBER: US 60; ; PRIOR FILING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26 APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03 APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-09-27 FILING DATE: 2000-09-27 APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665 APPLICATION NUMBER: PCT/US01/00665 APPLICATION NUMBER: PCT/US01/00666 APPLICATION NUMBER: PCT/US01/00666 APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00668	ULT 1 09-864-761-35805 Application US/09864761 atent No. US20020048763A1 atent No. US20020048763A1 atent No. US20020048763A1 ENERAL INFORMATION: APPLICANT: Penn, Sharron G. APPLICANT: Hanzel, David K. APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE TITLE OF INVENTION: GENE EXPRESSION ANALYSIS B: FILE REFERENCE: Aeomica-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION DATE: US 60/180,312 PRIOR APPLICATION DATE: 2000-02-04
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	c ACID
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SACCOTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 35

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BH474, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BH474, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

TOTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9
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                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                       OR APPLICATION NUMBER: 60/207,727
DR FILLING DATE: 2000-05-26
DR APPLICATION NUMBER: 60/242,578
DR FILLING DATE: 2000-10-23
DR APPLICATION NUMBER: 60/253,625
DR FILLING DATE: 2000-11-27
DR FILLING DATE: 2000-11-27
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nes 8; Conserv
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: 60/257,931
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                             US-09-864-761-41759
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CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3170
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3170, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10932
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 41759, Application US/09864761
Patent No. US20020048763A1
                  PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                   FILE REFERENCE: Aeomica-X-1
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TITLE OF INVENTION: Complementary peptide ligands from the human genome
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APPLICATION NUMBER: US 60/236,359
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100.0%; Pred. No.
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FILING DATE: 2001-0: APPLICATION NUMBER: FILING DATE: 2001-0:

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PCT/US01/00664 PCT/US01/00667

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RESULT 5
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Best Local Similarity
Matches 7; Conserv
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SEQ ID NO 41759
LENGTH: 21
TYPE: PRT
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APPLICANT: Lerch1, Jens
APPLICANT: Reski, Ralf
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins
TITLE OF INVENTION: involved in the regulation of cell division, growth and
TITLE OF INVENTION: biomass formation in plants
FILE REFERENCE: 0093/000009
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN BRAI
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APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: US 60/234,687
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00661
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Cirpus, Petra
Lerchl, Jens
Reski, Ralf
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Bischoff, Friedrich
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Schmidt, Ralf-Michael
Freund, Annette
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100.0%; Pr
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DD IN ADULT LITER, SIGNAL = 2
ED IN ENER MARROW, SIGNAL = 1.6
ED IN FETAL LIVER, SIGNAL = 2.6
ED IN HELA, SIGNAL = 3
ED IN HEAT, SIGNAL = 3
ED IN LUNG, SIGNAL = 5.4
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k; Pred. No. 18;
0; Mismatches
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SQ ID NO 36
LENGTH: 49
TYPE: PRT
ORGANISM: Physcomitrella patens
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Best Local :
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PRIOR APPLICATION NUMBER: PCT/EP00/00675
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/608, PRIOR FILING DATE: 2000-06-30 PRIOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 2001-01-29 NUMBER OF SEQ ID NOS: 49117 SOFTWARE: Annomax Sequence Lissed ID NO 45360
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
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APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00666
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Pred. No.
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; ORGANISM: Homo sapiens
US-09-764-868-815
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Best Local Similarity luu.
Thes 7; Conservative
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SEQ ID NO 815
LENGTH: 115
                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 3238
                                                                                                                                                                                                                                          Sequence 3238, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
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Best Local Similarity
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                                                                                                                                                                   Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT232
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ORGANISM:
FEATURE:
                       NAME/KEY:
LOCATION:
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                                                                          TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                 ENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 PELLROD 431
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o. US20020168711A1
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                                        SITE
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0; Mismatches
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HIT: F06450.1, EVALUE 4.00e-26
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o. 88;
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o. 48;
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SIGNAL = 1.2
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; ORGANISM: Homo sapiens US-09-974-879-143
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                                                                                     SOFTWARE: Pa
SEQ ID NO 143
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Best Local
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR FILING DATE: 2000-10-13
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/066,095 PRIOR FILING DATE: 1997-11-17
                                                                                                                                   NUMBER OF SEQ ID NOS: 611
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                                         TYPE: PRT
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OTHER INFORMATION:
NAME/KEY: SITE
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                                                              LENGTH:
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o. US20030028003A1
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1997-11-17
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5. 91;
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NUMBER OF SEQ ID NOS: 612

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 142

LENGTH: 122

TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: SITE
LOCATION: (122)

OTHER INFORMATION: Xaa equals stop translation
US-09-305-736-142
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Best Local Similarity
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RESULT 11
US-09-916-790-31
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Best Local Similarity
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EARLIER APPLICATION NUMBER: POT/US98/23435
EARLIER FILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 60/064,911
                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60.066,095
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,090
EARLIER FILING DATE: 1997-11-17
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EARLIER APPLICATION NUMBER: 60/064,912
EARLIER FILING DATE: 1997-11-07
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TITLE OF INVENTION: 125 Human Secreted ProFILE REFERENCE: PZ020P1
CURRENT APPLICATION NUMBER: US/09/305,736
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                                                                                        297 SCKETPS 303
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APPLICATION NUMBER:
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APPLICATION NTTO---
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                                                            SCKETPS 76
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100.0%; Prr
                                                                                                                 100.0%; F1
                                                                                                                     1.4%; Score 7; DB 100.0%; Pred. No. 93 ive 0; Mismatches
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5. 93;
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; OTHER INFORMATION: Consensus amino acid sequence US-09-916-790-31
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                                   Best Loc
Matches
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SEQ ID NO 30
LENGTH: 186
TYPE: PRT
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                        Query Match
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                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
                                                                                                                                                                                                                                                                             APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/916,790 CURRENT FILING DATE: 2001-07-27 PRIOR APPLICATION NUMBER: 60/221,543 PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 18431 AND 32374, NOVEL HUMAN PROTEIN
TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 381552002700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Meyers, Rachael
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Silos-Santiago, Immaculada
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                              ORGANISM: Homo sapiens
                                                    Local
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286 SESSTPS 292
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                                   Similarity 7; Conserv
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Steininger II, Robert
Spaulding, Vikki
Wong, Gordon G.
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Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evans, Chery
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                                   1.4%; Score 7; DB 9; Lei larity 100.0%; Pred. No. 1.4e+02; Conservative 0; Mismatches 0;
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ilarity 100.0%;
Conservative
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                                                                      Length 186;
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123 SESSTPS 129

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US-09-815-242-11842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-925-179-67
                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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LENGTH: 218
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Publication No. US20030044858A1
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PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
FILE REFERENCE: P0718P2C1DIC1US
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
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nes 7; Conservative (
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APPLICATION NUMBER: US 07/744,768
FILING DATE: 1991-08-14
                                                                                APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23 APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US92/06860 FILING DATE: 1992-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1994-01-26
                                        APPLICATION NUMBER: 60/257,931
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                                                               LING DATE: 2000-11-27
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Xu, H. Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leonard G.
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60/269,308
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Best Local Similarity
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US-10-128-714-3274
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                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR PILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,086
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/316,362
                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 3274
LENGTH: 259
                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-08-31 NUMBER OF SEQ ID NOS: 8603
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APPLICANT: Hu, Wengi
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TYPE: PRT
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100.0%; Pred. No.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/paa/US06_0
2: /cgn2_6/ptodata/1/paa/US06_0
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/ cgn2_6/ptodata/1/paa/US094_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US095_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US095_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US095_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US095_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US099A_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US09A_COMB.pep: *
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US-09-629-469A-18627		-10-437-963-2037	-10-424-599-26545	-10-424-599-26545	-359-1756	-10-203-139-2772	-10-203-138A-128	-10-203-138-12879	-10-203-13/-2886	-10-203-136-2858	-10-203-135-2748	-10-203-134-2	-10-182-998-1257	-10-182-997-2092	-10-182-995-2227	-10-182-993-2801	9-864-761-3580	00663-2886	-09-107-433-447	16	-09-791-537-713	-09-991-681-	-08-842-385-	-09-991-681-	-08-842-38	-09-991-681-	2-385-	01-08631-4	۲	-08-842-38	-10-221-279-77	-10-131-48	-09-623-791A-8	-09-623-79	-US01-08	-08-842-385-	-10-144-198-3	PCT-US03-01943-30	-US03-04508-	US-10-416-993-495	-US01-4295	CT-US01-08631-40	-10-144-198-44
Sequence 18627, A	eductice vol.	0 2027	emience 26545	equence 26545	equence 17560	Sequence 27724, A	equence 1287	equence 128	equence 2886	equence 2858	equence 2/48	e 28	equence 1257	e 20929,	equence 2227	equence 28015,	Sequence 35805, A	quence 28863,	equence 4471,	e 5166,	equence 71315,	equence 29, App	equence	equence 30,	equence 9, A	equence 28,	equence	40088	e 31, Ap	equence 10,	equence	equence 87,	equence 87,	e 87	4009	equence 6, 1	ce 30,	e 30,	equence 32,	Sequence 495, App	quence 495, Ap	equence 40087	Sequence 44, Ap

ALIGNMENTS

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RESULT 1

US-09-991-681-27

Sequence 27, Application US/09991681

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA COHEN, MAURICE COLPRITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GORDON

GORDON, JULIAN

GORDON

GO
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHABL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
ROBERTS-RAPP, LISA
ROBERTS-RAPP, LISA
FOR DETECTING DISEASES OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                  CITY: Abbott Park
STATE: IL
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Result No.

Score 518 518

Query Match 100.0

Length DB 518 1770

Description

Sequence 27, Appl Sequence 44, Appl

SUMMARIES

25

US-09-991-681-27 PCT-US03-01943-44

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LENGTH: 518 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-991-681-27
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Best Local
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INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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481
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OPERATING
                 PAVFPCISQLTCHVTDIRVRQAVREWLGRVGRVYDIIV
                                                                                                                                                                                                                                                                        LVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE
                                                                                 FSAGPELLRODKRPRSGSTGSSLSVSVRDAEAQIQAWTNWVLTVLNQIQILPDQTFTALQ
                                                                                                                                            KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
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PAVFPCISQLTCHVTDIRVRQAVREWLGRVGRVYDIIV
                                                            FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ
                                                                                                                          KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 847/938-2623
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Pred. No. 0;
0; Mismatches
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RESULT 2 PCT-US03-01943-44; Sequence 44, App

Application PC/TUS0301943

RESULT 3
US-10-144-198-44
; Sequence 44, Application US/10144198
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies Inc
; TITLE OF INVENTION: Regulated Prostate

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CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 10/054,935
PRIOR FILING DATE: 2002-01-25
PRIOR PELICATION NUMBER: US 60/356,130
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 10/102,946
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 10/117,229
PRIOR APPLICATION NUMBER: US 10/144,198
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Best Local Similarity
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APPLICANT: ORIGENE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 10/197,824 PRIOR FILING DATE: 2002-07-19 NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CANCER GENES FILE REFERENCE: 3U 9U 901 PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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PAVFPCISQLTCHVTDIRVRQAVREWLGRVGRVYDIIV 518
                                                                                                          FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNWVLTVLNQIQILPDQTFTALQ 480
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                                                                                                                                                                   KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS 1672
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RESULT 4

PCT-US01-08631-40087

Sequence 40087, Application PC/TUS0108631

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
                                          PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 40087
TYPE: DET
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; ORGANISM: Homo sapiens
US-10-144-198-44
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CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
SEQ ID NO 44
LENGTH: 1770
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ORGANISM: Homo sapiens FEATURE:
                                  TYPE: PRT
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; ORGANISM: Homo &
PCT-US01-42950-495
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Best Local S
Matches 518
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Matches 518; Conserv
                                                                                                                                                                                                                                                                                                                       Sequence 495, Application PC/TUS0142950 GENERAL INFORMATION:
                                                                                                                                              NUMBER OF SEQ ID NOS: 682
SOFTWARE: PatentIn version 3.0
SEQ ID NO 495
                                                                                                                                                                                            APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: PCT/US01/42950
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
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OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX,
OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw scor
NAME/KEY: DOMAIN
LOCATION: (941)..(950)
OTHER INFORMATION: Helper component proteinase domain identified by PPam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0056, PFam scor
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; ORGANISM: Homo sapiens
US-10-416-993-495
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: US/10/416,993
CURRENT FILING DATE: 2003-11-16
PRIOR APPLICATION UNMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
SOFTWARE: PatentIn version 3.0
SEQ ID NO 495
LENGTH: 1839
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Best Local Similarity
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VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW 240
                             TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK
                                                                                          SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR
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CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-66-10
NUMBER OF SEQ ID NOS: 93
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GENERAL INFORMATION:
APPLICANT: IDEC PHARMACEUTICALS
APPLICANT: GATELY, DENNIS
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Local Similarity 100.0%;
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                                                                          VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW 240
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CURRENT APPLICATION NUMBER: US:10/54,935
PRIOR APPLICATION NUMBER: US:10/54,935
PRIOR APPLICATION NUMBER: US:10/54,935
PRIOR APPLICATION NUMBER: US:10/55,130
PRIOR APPLICATION NUMBER: US:10/102,946
PRIOR APPLICATION NUMBER: US:10/102,946
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US:10/117,229
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US:10/144,198
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-07-19
PRIOR FILING DATE: 2002-07-19
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
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PCT-US03-01943-30
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-01943-30
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Best Local
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TITLE OF INVENTION: CANCER GENES
FILE REFERENCE: 3U 9U 901 PCT
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TITLE OF INVENTION: Regulated Prostate Cance Genes
FILE REFERENCE: 9U 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
150 TD NO 30
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GENERAL INFORMATION:
APPLICANT: Russell, John
APPLICANT: Colpitts, Tracey
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASE OF THE
NUMBER OF SEQUENCES: 11
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SEQUENCE CHARACTERISTICS:
LENCTH: 467 amino acids
TYPE: amino acid
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NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6084.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/937-6365
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OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                  NKIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHL
                                                       NKIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHL
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MDQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQIL
                                                                                                      STGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAG
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100 Abbott Park Road
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CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILLING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/640,167
PRIOR PFLICATION NUMBER: 09/649,167
PRIOR PFLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
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PCT-US01-08631-40090
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APPLICANT: Hyseq, Inc
TITLE OF TANTONIAN
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SEQ ID NO 40090
LENGTH: 1982
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Best Local
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OTHER INFORMATION: Fusion glycoprotein F0 domain identified by eMATRIX,
OTHER INFORMATION: accession number PF00523D, p-value=7.188e-10, raw score
NAME/KEY: DOMAIN
ICCATION: (1065)..(1074)
OTHER INFORMATION: Helper component proteinase domain identified by PFam,
OTHER INFORMATION: accession name Peptidase_C6, E-value=0.0058, PFam score
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                                                                                                                                                                            KIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLM 412
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                      DQTFTALQPAVFPCISQLTCHVTDIRVRQAV 503
                                                                                                             DQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILP 472
                                                                                                                                                    KIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLM
                                                                                                                                                                                                                                                      TGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGN 352
                                                                                                                                                                                                                                                                                                                                     VSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPS
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                                                                         DQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILP
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US-09-623-791-87
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APPLICANT: HINZMAN
APPLICANT: SCHMITT
APPLICANT: PILARSK
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Best Local Similarity 100.0%; Pred. No. 1.2e-184;
Matches 192; Conservative 0; Mismatches 0;
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 Best Local Similarity
                   Query Match
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APPLICANT:
                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/DE99/00721
PRIOR FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 201
                                                                                                                                                                                                       FILE REFERENCE: ALBRE 11
CURRENT APPLICATION NUMBER: US/09/623,791A
CURRENT FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/623,791
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/DE99/00721
PRIOR FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 201
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APPLICANT: HINZMANN, BERND
APPLICANT: SCHMITT, ARMIN
APPLICANT: PILARSKY, CHRIST
                                                    09-623-791A-87
                                                                                                                    SOFTWARE: PatentIn
EQ ID NO 87
                                                                                                                                                                                                                                                                              APPLICANT:
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TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES
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TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TUMOR TISSUE
                                                                   LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
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SCHMITT, ARMIN
PILARSKY, CHRISTIAN
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37.1%;
100.0%;
Score 192; DB 20;
Pred. No. 1.2e-184;
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RESULT 14
US-10-131-487A-87
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US-10-221-279-7783
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; ORGANISM: Homo
US-10-131-487A-87
Sequence 7783, Application US/10221279
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-046
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APPLICANT: SPECHT,
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CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/623,791A
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: PCT/DE99/00721
PRIOR FILING DATE: 1999-03-09
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SCHMITT, ARMIN
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Pred. No. 1.2e-184;
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CURRENT APPLICATION NUMBER: US/10/221,279
CCURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-07

NUMBER OF SEQ ID NOS: 12360
SOFTMARE: Custom
SEQ ID NOS: 12360
SOFTMARE: Custom
SEQ ID NOS: 12360
SOFTMARE: Custom
SEQ ID NOS: 12360
SOFTMARE: Custom
SEQ ID NO 7783
LENGTH: 141
TYPE: PRT
CREAMINEM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 11, -(141)
COTHER INFORMATION: Xaa = any amino acid or nothing
US-10-221-279-7783

Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-69;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUETY MATCh
Best Local Similarity 100.0%; Pred. No. 1.8e-69;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUETY MATCh
Best Local Similarity 101.0%; Pred. No. 1.8e-69;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUETY MATCH
Best Local Similarity 101.0%; Pred. No. 1.8e-69;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUETY MATCH
Best Local Similarity 101.0%; Pred. No. 1.8e-69;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUETY MATCH
Best Local Similarity 101.0%; Pred. No. 1.8e-69;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUETY MATCH
Best Local Similarity 101.0%; Pred. No. 1.8e-69;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUETY MATCH
Best Local Similarity 102.0%; Pred. No. 1.8e-69;

Dest Local Similarity 102.0%; Pred. No. 1.8e-69;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUETY MATCH
Best Local Similarity 102.0%; Pred. No. 1.8e-69;

Dest Local Similarity 102.0%; Pred.
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Perfect score:
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140.227 Million cell updates/sec
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(cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

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                                                                         US-10-367-978-32
US-10-462-850-3170
US-10-273-573-687-79
US-09-291-417D-99
US-60-478-196-3273
US-10-273-573-10799
US-10-273-573-10799
US-10-462-850-3172
US-10-462-850-3184
US-10-462-850-3684
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US-10-273-573-7991
US-10-273-573-7991
US-10-273-573-7992
US-10-273-573-9240
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US-10-273-573-9240
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US-10-243-739A-44
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Sequence 3170, Ap
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10799, A
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104, App
3684, Ap
3685, Ap
111, App
7491, Ap
10762, A
107
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ALIGNMENTS	US-60-470-920-40	US-10-465-811-62	US-10-465-811-56	US-10-465-811-54	US-10-465-811-51	US-10-465-811-50	US-10-465-811-37	US-10-465-811-36	US-10-465-811-35	US-10-465-811-33	US-10-465-811-30	US-10-465-811-29	US-10-465-811-24	US-10-243-739A-71	US-10-243-739A-65	US-10-243-739A-63	US-10-243-739A-60	US-10-243-739A-59	US-10-243-739A-46
	Sequence 40, Appl	•	Sequence 56, Appl	•	•	•	•	•	Sequence 35, Appl	•	•	•	•	•	•	•	•	•	•

; LENGTH: 1872 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-367-978-32 US-10-367-978-32 Sequence 32, Application US/10367978 SEQUENCE INFORMATION: APPLICANT: GATELY, DENNIS INTLE OF INVENTION: PROSTATE SPECIFIC GENES INTLE OF INVENTION: OR THERAPEUTICS FILE REFERENCE: 037003-0301988 Query Match 100.0%; Score 518; Best Local Similarity 100.0%; Pred. No. 0; Matches 518; Conservative 0; Mismatches SOFTWARE: Pa PRIOR APPLICATION NUMBER: 60/357,140 PRIOR FILING DATE: 2002-02-19 PRIOR APPLICATION NUMBER: 60/396,082 PRIOR FILING DATE: 2002-07-17 PRIOR APPLICATION NUMBER: 60/386,759 PRIOR FILING DATE: 2002-06-10 NUMBER OF CEC TA NOC. CURRENT APPLICATION NUMBER: US/10/367,978 CURRENT FILING DATE: 2003-02-19 NUMBER OF SEQ ID NOS: 89 1595 1535 1475 1355 RIRAMAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLL 1415 SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR 121 TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK 180 241 181 61 SHQVLLQNLYDILLEEFVKGPSPGEEKTTQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR 1 RIRAMAQQVEMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLL PatentIn Ver. 2.1 VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK Mismatches DB AND THE USE THEREOF IN DESIGN 6 0, Length 1872; Indels . . Gaps 1654 1594 1534 1474 120 1414 300 240 60

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TPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD

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RESULT 3
US-10-273-573-8627
US-10-273-573-8627
; Sequence 8627, Application:
; GENERAL INFORMATION:
; GENERAL INFORMATION:
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                                                                          ; LOCATION: (1)...(151)
; OTHER INFORMATION: Xaa
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; OTHER INFORMATION: sequence located in Unknown at 6-15 and may interact with Sequenc
; OTHER INFORMATION: in this patent.
US-10-462-850-3170
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 Query Match 1.4%; Score 7; DB (Best Local Similarity 100.0%; Pred. No. 16, Matches 7; Conservative 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/10/462,850
CURRENT FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3170
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
SEQ ID NO 8627
                                                                                                                                                                                                                                                            APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
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TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(151)
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                                                                                                                                                                                      LENGTH: 151
TYPE: PRT
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                    DB 6;
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                                                                                         RESULT 6
US-10-273-573-10795
                                                                                                                                                                                                                                                                                                            ; ORGANISM: Aspergillus fumigatus US-60-478-196-3273
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US-60-478-196-3273
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                                                     Sequence 10795, Appl GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
SEQ ID NO 3273
LENGTH: 609
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                      Query Match
Best Local
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APPLICANT: Lemieux, Sebastien
APPLICANT: Hu, Wenqi
APPLICANT: Roemer, Terry
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF ASPERGILLUS FUMIGATUS AND
TITLE OF INVENTION: USE
 APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 10182-026-888
CURRENT APPLICATION NUMBER: US/60/478,196
CURRENT FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 4000
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APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
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                                                                        Application US/10273573
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100.0%; Pred. No. 56
ive 0; Mismatches
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0; Mismatches
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                    AND POLYPEPTIDES
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RESULT 8
.US-10-273-573-10799
; Sequence 10799, Application US/10273573
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SEQ ID NO 10795
LENGTH: 642
TYPE: PRT
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Best Local (
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APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                          Matches
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-10-273-573-10795
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CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Custom
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CURRENT FILING DATE: 2002-11-13
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                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                    LENGTH: 11
TYPE: PRT
                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR APPLICATION NUMBER: 09/989,600
OR FILING DATE: 2001-11-21
OR APPLICATION NUMBER: 09/577,408
OR FILING DATE: 2000-05-18
OR APPLICATION NUMBER: 10/115,831
OR FILING DATE: 2002-04-02
OR APPLICATION NUMBER: 09/677,298
OR APPLICATION NUMBER: 09/677,298
OR APPLICATION NUMBER: 09/695,781
OR APPLICATION NUMBER: 09/695,781
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 10/167,379
FILING DATE: 2002-06-10
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/775,330
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                                                                                                                    941 LLRODKR 947
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100.0%; Pred. No.
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RESULT 10
US-10-462-850-3172
US-10-462-850-3172
; Sequence 3172, Application US/10462850
; GENERAL INFORMATION:
APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the
FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/10/462,850
; CURRENT FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3172
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Best Local Similarity
Watches 6; Conserv:
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; OTHER INFORMATION: PROTEIN REPEAT MUSCLE CALCIUM-BI domain identified by
; OTHER INFORMATION: eMATRIX, accession number PD00301A, p-value=6.400e-09,
; OTHER INFORMATION: 10.24
US-10-273-573-10799
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CURRENT APPLICATION NUMBER: US/10/462,850
CURRENT FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 104, Application US/10462850
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
SEQ ID NO 10799
LENGTH: 1246
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Best Local
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ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: sequence located in BTF3L3 OTHER INFORMATION: in this patent.
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ORGANISM: Homo sapiens
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100.0%;
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Pred. No.
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                                                                                                                     human genome
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RESULT 12
US-10-462-850-3685
; Sequence 3685, Application US/10462850
; GENERAL INFORMATION:
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Best Local Similarity
Thes 6; Conserve
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US-10-462-850-3684
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Best Local Similarity
Thes 6; Conserve
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                                Query Match
Best Local S
Matches 6
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GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the PILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/10/462,850
CURRENT FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3684
                                                                                                                                                                                          FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/10/462,850
CURRENT FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3685
                                                                                                                                                                                                                                                                             APPLICANT: Proteom Ltd
                                                                                                   ORGANISM: Homo Sapiens .
FEATURE:
OTHER INFORMATION: sequence located in ATOH1 OR ATH1 at 315-324
OTHER INFORMATION: Sequence 3684 in this patent.
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ORGANISM: Homo Sapiens
FEATURE:
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                                            Local Similarity
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RESULT 15
US-10-273-573-10762
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US-10-273-573-7491
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US-10-273-573-7491
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US-10-369-060A-111
Sequence 10762, Application US/10273573
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 111
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GENERAL INFORMATION:
APPLICANT: Sallberg, Matti
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SEQ ID NO 7491
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CURRENT APPLICATION NUMBER: US/10/369,060A
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 09/839,447
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 09/556,605
PRIOR APPLICATION NUMBER: 09/556,605
PRIOR FILING DATE: 2000-04-21
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PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
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ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: CUSTOM
SEQ ID NO 10762
LENGTH: 97
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOWAIN
LOCATION: (8)..(25)
OTHER INFORMATION: ISLET AMYLOID PROTEIN (AMYLIN) SIGNATURE domain identified by
OTHER INFORMATION: eMATRIX, accession number PR00818C, p-value=9.024e-09, raw score
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US-10-273-573-10762
Search completed: July 24, 2003, 12:46:18 Job time : 15.3684 secs
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Result No. Minimum DB Maximum DB Database : Total number of hits satisfying chosen parameters: Word size Searched: Scoring table: Perfect score: Run Post-processing: Listing first 45 OM protein - protein search, using sw model 8 and is derived by analysis of the total score distribution. score Score seq length: 0
seq length: 2000000000 No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, Query Match US-09-991-681-27 518 1 RIRAMAQQVFMLDT July 24, 2003, 12:15:23; Search time 34.1288 Seconds (without alignments) 127863 seqs, 47026705 residues Gapop 60.0 , OLIGO SwissProt_41:* 0 RIRAMAQQVFMLDTQCSPKT.....VRQAVREWLGRVGRVYDIIV Copyright Length GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd. 멂 Gapext 60.0 PHAFTONAC
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suda I.; lacylase (E2b) subunit lacylase (E2b) subunit lydrogenase complex."; 1041(1989). Li, Derge J.G., Schuler Schaefer C.F., Bhat N Li, Wang J., Hsieh F Rubin G.M., Hong L., Casavant T.L., Schee	er D.J., transfer transfer	Euteleostomi; Homo. ox R.P., acylase (E2) complex.";	1 alpha-ke .3.1) (E	020219 020278 020280 020399 027439 047025 047026 047026 047026 047029 020221 098855 Q13892
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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human and mouse cDNA sequences.";
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Biochem. Biophys. Res. Commun. 174:804-809(1991).
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MEDLINE=88241022; PubMed=2837277;
LAU K.S., Griffin T.A., Hu C.-W.C., Chuang D.T.;
LAU K.S., Griffin T.A., Hu C.-W.C., Chuang D.T.;
"Conservation of primary structure in the lipoyl-bearing and dihydrolipoyl dehydrogenase binding domains of mammallan branched-chain alpha-keto acid dehydrogenase complex: molecular cloning of human and bovine transacylase (EZ) cDNAs.";
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Kinugasa A., Ishitsu T., Matsuda I., Indo Y.,
"Molecular basis of intermittent maple syrup urine disease
mutations in the E2 gene of the branched-chain alpha-keto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91128420; PubMed=1847055; Fisher C.W., Lau K.S., Fisher C.R., W. H. 17-bp insertion and a Phe215-->Cys
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Hum. Genet. 43:91-100(1998).
FUNCTION: THE BRANCHED-CHAIN ALPHA-KETO DEHYDROGENASE COMPLEX FUNCTION: THE BRANCHED-CHAIN ACTION OF ALPHA-KETO ACIDS TO ACYL-COA AND CO(2). IT CONTAINS MILTIPLE COPIES OF 3 ENZYMATIC COMPONENTS:
BRANCHED-CHAIN ALPHA-KETO ACID DECAMBOXYLASE (E1), LIPOAMIDE ACYLTRANSFERASE (E2) AND LIPOAMIDE DEHYDROGENASE (E3)
COPACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE SIMILARITY: Contains 1 lipoy1-binding domain.
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AND TO TRANSFER TO COENZYME A, ACYL GROUPS THAT ARE GENERATED
THE BRANCHED-CHAIN ALPHA-KETO ACID DECARBOXYLASE COMPONENT.
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DISEASE: Defects in DBT are a cause of maple syrup urine disease (MSUD); an autosomal recessive disorder characterized by mental and physical retardation, feeding problems, and a maple syrup odd
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                                                           X66785;
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AAA64512.1; ALT_INIT.
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532; PubMed=9621512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCTAHEDRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e: novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prange C.,
Mullahy S.J.,
Catne P.H.,
Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                            a collaboration
                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                syrup odor
                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.T.;
                                                                                                                                                                                                                                                      commercia
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ALT_SEQ

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RESULT 2
VATA_METBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         当日
REQUENCE FROM N.A.

RA INALOMI K.I., Eya S., Maeda M., Futai M.;

RA Inatomi K.I., Eya S., Maeda M., Futai M.;

RI "Amino acid sequence of the alpha and beta subunits of Methanosarcina barkeri ATPase deduced from cloned genes. Similarity to subunits of eukaryotic vacuolar and FOFI-ATPases.";

LJ. Biol. Chem. 264:10954-10959(1989).

C. -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON CONCESS ATP FROM ADP IN THE ARCHAEAL ALPHA CHAIN IS A CONTALYTIC SUBUNIT.

C. -!- CATALYTIC SUBUNIT.

C. -!- CATALYTIC SUBUNIT: ATP + H(2)O + H(+)(In) = ADP + phosphate + C H(+)(Out).
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004167; E3 binding.
InterPro; IPR003016; Lipoyl.
Pfam; PF00198; 2-oxoacid dh; 1.
Pfam; PF00364; biotin lipoyl; 1.
Pfam; PF02817; e3 binding; 1.
ProDom; PD001115; 20xoacid dh; 1.
PROSITE; PS00189; LIPOYL; 1.
                                                                                                                                                                                                                                                   VATA METBA
P22662;
01-AUG-1991
01-AUG-1991
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIW; 248610; -.
GO; GO:0005947; C:alpha-ketoglutarate
GO; GO:0005739; C:mitochondrion; TAS.
InterPro; IPR001078; 20xoacid dh.
InterPro; IPR001089; Biotin IIpoyl.
InterPro; TROMOTOR; As binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDING
ACT_SITE
ACT_SITE
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSIT CHAIN
                                                                                                                                                                                            Methanosarcina barkeri.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                        V-type ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A32422; A32422.
PDB; 1K8M; 04-DEC-02.
PDB; 1K8O; 14-NOV-01.
                                                                                                                                                                  NCBI_TaxID=2208;
                                                                                                                                                                                Methanosarcinales;
                                                                                                                                                                                                                     ATPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Acyltransferase; Mitochondrion; Transit peptide; Lipoyl;
Disease mutation; Maple syrup urine disease; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GK; P11182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:2698;
                                                                                                                                                                                                                                                                                                                                                               217 LPPSPKVE 224
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation; Maple syrup urine disease; 3D-structu
1 61 MITOCHONDRION (POTENTIAL)
62 482 LIPOAMIDE ACYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                     LPPSPKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      321
354
482
                                                                                                                                                                                                                                           synthase alpha
                                                                                                                                                                                                                                     Conservative
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452
456
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑĀ,
                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DBT
                                                                                                                                                                                                                                                                                                                                                                                    336
                                                                                                                                                                                eota; Euryarchaeota orders incertae
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
354
53487
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452
456
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      | I -> M (IN MSUD).
| FTIGAVAR 015099.
| F -> C (IN MSUD).
| FTIGAVAR 004978.
| G -> S (IN MSUD).
| FTIGAVAR 015100.
| FTIGAVAR 015100.
| Q -> P (IN REF. 4).
| L -> V (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEHYDROGENASE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRANCHED-CHAIN ALPHA-KETO ACID
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                     578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                          (V-type
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 482
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                           ATPase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPONENT
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                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 3
BPHY_DEIRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R InterPro; IPR003593; AAA ATPASSE.
R InterPro; IPR000194; ATPASSE a/bCC.
R InterPro; IPR000194; ATPASSE a/bCC.
R InterPro; IPR000100; ATPASSE a/bCS.
R InterPro; IPR004100; ATPASSE a/bN.
R Pfam; PP00306; ATP-synt_ab; 1.
R Pfam; PP00306; ATP-synt_ab N; 1.
R Pfam; PP00316; ATP-synt_ab N; 1.
R Pfam; PP03874; ATP-synt_ab N; 1.
R Pfam; PF03874; ATP-synt_ab N; 1.
R Pfam; PF03874; ATP-Synt_ab N; 1.
R Pfam; PF03874; ATPASSE ALPHA BETA; 1.
R TIGREAMS; TIGR01043; ATP Synthesis; Hydrogen ion transport; ATP-binding.
M Hydrolase; ATP synthesis; Hydrogen ion transport; ATP-binding.
NP_BIND 228 235
NTP (BY SIMILARITY).
SEQUENCE 578 AA; 63638 MW; 195019833C89552B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BPHY DEIRA
Q9RZĀ4;
16-OCT-2001
                                                                                                                                                                                                                        STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINB=20036896; PubMedc10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Dodson R.J., Haft D.H., Jiang L., Pamphile W., Crosby M., Shen M.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., DBM.J., Winton K.W., Fleischmann R.D.
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                   CHARACTERIZATION, AND MUTAGENESIS OF MET MEDLINE=20085458; PubMed=10617469; Davis S.J., Vener A.V., Vierstra R.D.; "Bacteriophytochromes: phytochrome-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bacteriophytochrome (EC 2.7.3.-) (Phytochrome-like protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                  Science 286:2517-2520(1999)
                                                                      nonphotosynthetic eubacteria.";
                                                                                                                                                                                         "Genome sequence of the radioresistant radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BPHP OR DRA0050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A34283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no waitfied and this statement is not removed. Usage by and for commercial statement is not removed.
FUNCTION: PHOTORECEPTOR WHICH EXISTS IN TWO REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE R MAXIMALLY IN THE RED REGION OF THE SPECTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MF_00309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conserv
                                                                                                                                                                           286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STGSSLSV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STGSSLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A34283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s; Score 8; DB 1; Pred. No. 10; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                       MET-259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               755 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                           bacterium
                                                                                   photoreceptors
                                                                                                                                         CYS-289 AND HIS-260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
   AND
                  FORMS THAT ARE
                                                                                                                                                                                                           Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
   THE FR FORM THAT
                                                                                      from
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GSSLSVSV

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                                                 Query Match
Best Local S
Matches
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PRINTS; PR01033; PHYTOCHROME.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00056; GAP; 1.
SMART; SM00387; HATPase c; 1.
SMART; SM000381; HiskA; 1.
SMART; SM00091; PAS; 1.
SMART; SM00091; PAS; FALSE NEG.
PROSITE; PS00112; PAS; FALSE NEG.
PROSITE; PS00146; PHYTOCHROME 1; FALSE NEG.
PROSITE; PS0046; PHYTOCHROME 2; 1.
Sensory transduction; Transferase; Kinase; Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004358; I
InterPro; IPR003018; C
InterPro; IPR003661; I
InterPro; IPR005467; I
                                                                                                                                                                                                                                                                                                                                                                                                                                     Photoreceptor;
DOMAIN 26
DOMAIN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the Buropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
BINDING
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase C; 1.
Pfam; PF00512; HisKA; 1.
Pfam; PF00360; phytochrome; 1.
                                                                                                                                                                                              MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001862; AAF12261.1; -. PIR; D75598; D75598.
                                                                                                                                                                                                                                             MUTAGEN
                                                                                                                                                                                                                                                                                            MUTAGEN
                                                                                                                                                                                                                                                                                                                                           MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000014; InterPro; IPR001294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; DRA0050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHROMOPHORE SIMILARITY: FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimer SIMILARITY: Contains 1 histidine kinase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEINOXANTHIN WHICH COULD PROTECT THE BACTERIUM FROM INTENSE VISIBLE LIGHT.

VISIBLE LIGHT.

PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE. IN HIGHE LACKS THE CONSERVED CYSTEINE WHICH BINDS CHROMOPHORE IN HIGHE PLANTS PHYTOCHROMES; THE ADJACENT HISTIDINE RESIDUE PROBABLY DELANTS PHYTOCHROMES; THE ADJACENT HISTIDINE RESIDUE PROBABLY AS A LIGATION SITE. ABLE TO BIND PHYCOCHROMOBILIN (PCB) AND PHYTOCHROMOBILIN IN VITRO, BUT THE IDENTITY OF THE NATURAL PHYTOCHROMOBILIN IN VITRO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHIFT FOR THE FAR-RED MAXIMUM. COULD ALSO ABSORB GREEN LIGHT. M
PARTICIPATE IN REGULATING PIGMENT SYNTHESIS LIKE THE CAROTENOID
DEINOXANITHIN WHICH COULD PROTECT THE BACTERIUM FROM INTENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABSORBS MAXIMALLY IN THE FAR-RED REGION. HAS ALSO A SLIGHT BLUE
                                                 Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transduction; Transferase; Kinase; Phosphorylation; reptor; Phytochrome; Chromophore; Complete proteome.
    GSSLSVSV 447
                                                                                                                                               755
                                                                                                                                                                                                                                                                                                                                         26
95
529
260
532
259
                                                    Conservative
                                                                                                                                                                                                                                           260
                                                                                                                                                                                                                                                                                            259
                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN.
THE N-TERMINAL SECTION;
                                                                                                                                                                                              289
                                                                                                                                                                                                                                           260
                                                                                                                                                                                                                                                                                            259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        His_kinA.
His_kinase.
PAS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ATPbind_ATPase.
; Bact_sens_pr_C.
; GAF.
                                                                                                                                                  81584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phytochrome
                                                                          100.0%;
                                                                                                                                                  ž
                                                    0
                                                                                                                                                                                                                  M->A: BINDS PCB (IN VITRO), BUT
DIFFERENCE SPECTRUM IS ALTERED.
M->C: BINDS PCB (IN VITRO), BUT
DIFFERENCE SPECTRUM IS ALTERED.
H->A: 100X REDUCTION OF CHROMOPHORE-
BINDING ACTIVITY.
                                                                                                                                                                                                                                                                                                                                 CHROMOPHORE (PROBABLE).
CHROMOPHORE (PROBABLE).
CHROMOPHORE (PROBABLE).
CHROMOPHORE (PROBABLE).
BUT

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Mismatches
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P44679;
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SEQUENCE FROM N.A
                                   NCBI_TaxID=727;
                                                             Pasteurellaceae;
                                                                                   Bacteria;
                                                                                                       Haemophilus influenzae
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28-FEB-2003
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SMART; SM00406; IGv; 1.
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                 Hypothetical
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15-JUL-1999 (Rel. 38, Last annotation updat
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MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMM!
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MISCELLANEOUS: THE SECOND AND THIRD
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COMPLEMENTARITY-DETERMINING-1.
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Best Local
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                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pathogenesis-related protein PR-4A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT SITE
SEQUENCE
This SWISS-PROT entry is copyright. It is proven the Swiss Institute of Bioinformatics
                                                                                                                                                        CTRAIN=CV. Xanthi; TISSUE=Leaf;
                                                          Friedrich L., Moyer M., Ward E., Ryals J.;
"Pathogenesis-related protein 4 is structurally homologous carboxy-terminal domains of hevein, Win-1 and Win-2.";
Mol. Gen. Genet. 230:113-119(1991).
-!- INDUCTION: By TMV infection.
-!- SIMILARITY: BELONGS TO THE BARWIN FAMILY.
                                                                                                                                                                                                                          Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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PROSITE; PS01328; 4HBCOA THIOESTERASE; 1.

Hypothetical protein; Hydrolase; Complete
ACT_SITE 18 18 BY SIMILARITY

ACT_SITE
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PIR; H64150; F
                                                                                                                                                   MEDLINE=92079884; PubMed=1745223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinf
the European Bioinformatics Institute
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Friedrich L., Moyer M., Ward E., Ryals J.;
"Pathogenesis-related protein 4 is structurally homologous
carboxy-terminal domains of hevein, Win-1 and Win-2.";
Mol. Gen. Genet. 230:113-119(1991).
-!- INDUCTION: By TMV infection.
-!- SIMILARITY: BELONGS TO THE BARWIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR4B TOBAC STANDARD; PRT; 147 AA.
P29063;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pathogenesis related protein PR-4B precursor.
Nicotiana tabacum (Common tobacco).
Dukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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PRINTS; PR00602; BARWIN.
PRODOm; PD004535; Barwin; 1.
PROSITE; PS00771; BARWIN 1; 1.
PROSITE; PS00772; BARWIN 2; 1.
Prodom; PD004535; Barwin; 1.

PROSITE; PS00771; BARWIN 1; 1.

PROSITE; PS00772; BARWIN 2; 1.

Plant defense; Pathogenesis-related protein; Plant defense; Pathogenesis-related protein; SIGNAL 1 25
                                                                                                                                                                                                        EMBL; X60282; CAA42821.1; -. HSSP; P28814; 1BW4.
                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                               PR00602; BARWIN.
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PATHOGENESIS-RELATED PROTEIN PR-4A.
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RESULT 9
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16-OCT-2001
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                                                                                                                                                                                                          Hypothetical protein; Complete SEQUENCE 158 AA; 17951 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21145866; PubMed=11248100; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., "Complete genomic sequence of Pasteurella multocida Pm70. Proc. Natl. Acad. Sci. U.S.A. 98:3460.3465(2001).
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Pasteurellaceae; Pasteurel
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InterPro; IPR002036; UPF0
Pfam; PF02130; UPF0054; 1
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RESULT 10
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Pfam; pf00936; Bact_microcomp; 1.
ProDom; pD003442; Bact_microcomp; 1.
PROSITE; PS01139; BACT_MICROCOMP; 1.
Signal; Complete proteome; 3D-structure.
SIGNAL 1 16
Onchocerca volvulus 
Eukaryota; Metazoa;
                                                     OV25-2
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                                                                                Small heat
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MEDLINE=99395039; PubMed=10464203;
Kofoid_E.C., Rappleye C.A., Stojil
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Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 181:5317-5329(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICROCOMPARTIMENT IN THE CELL IN POTENTIALLY TOXIC BY-PRODUCTS TAKE PATHWAY: Ethanolamine utilization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE CCHA/CCMK/CSOS1/PDUA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            LLSHQVL 65
                                                                                                                                                                                                                                                                                                                                            LLSHQVL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-02
                                                                                                   Rel. 25, (Rel. 25, 25, 25) (Rel. 25, 25, 25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
153
164
                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%; Sc. larity 100.0%; EConservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>Α</u>
                                                                                                                                                                                                              STANDARD;
                                                                             protein
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164
65
Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17486 MW;
                                                                        Last sequence update)
Last annotation update)
ein OV25-2 (Fragment).
                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
ETHANOLAMINE UTILIZATION PROTEIN
Q -> K (IN REF. 1).
LR -> FG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN THE FORMATION CELL IN WHICH THE UCTS TAKES PLACE.
Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R -> FG (IN REF. 1
9CA9F2DA4EACF2BC
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                              166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
o. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions in as its content is in
                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF A SPECIFIC METABOLISM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Latreille P., ou S., Layman D., Mulvaney E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTK.
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RESULT 11
OV21_ONCV
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                               PROSITE;
Heat shoc
                                                                                                                                                                                                                                                                                                                                                                                                                                OV21 ON
P29778;
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6282;
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                Small heat shock
                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONCVO
                                    SEQUENCE
                                                                                                                          EMBL; X68668; CAA48632.1;
                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         Submitted (OCT-1992) to -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                        Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X68669; CAA48633.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1992) to -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Onchocercidae; Onchocerca
                                                                         PRINTS; PR00299;
                                                                                    Pfam; PF00011; HSP20;
                                                                                                            InterPro; IPR001436;
                                                                                                                                                                                                                                                                                  Hoefle W
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Pfam; PF00011; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoefle W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                InterPro; IPR002068; Hsp20.
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                                                                                                                                                                                                                                               FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
7; Conserv
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSVSVRD
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                                                           PS01031; HSP20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS01031;
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(Rel.
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larity 100.0%;
Conservative
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                                   A,
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                                                                         ACRYSTALLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449
                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                      25, Createa, 25, Last sequence update, 25, Last annotation update, protein OV25-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P20; 1.
HSP20; 1.
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18636
                                    19935 MW;
1.4%;
100.0%;
                                                                                                           Crystallin_alpha
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TO 7
                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ databases TO THE SMALL HEAT SHOCK PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE SMALL HEAT SHOCK PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                             Chromadorea; Spirurida; Filarioidea;
                                    81F8BAA4DAC6F5FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      658690B4D0B946CD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 33;
DB 1;
                                                                                                                                                            (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 166;
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           Length 174;
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                                                                                                                                                                                                                                                           (HSP20)
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                                                                                                                                                                                                                       a collaboration
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                                                                                                                                                                                                             outstation
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                                                                                                                                                                          commercia.
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443

LSVSVRD 449

Matches

7;

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Mismatches

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RESULT TO SEE CASE OF THE SEE 
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                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RR4_BELCH
019990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methods using the plastid gene rps4.";

Plant Syst. Evol. 204:109-123(1997)
-:- FUNCTION: One of the primary rRNA binding proteins, it binds
directly to 16S rRNA where it nucleates assembly of the body of
the 30S subunit (By similarity).
-!- FUNCTION: With S5 and S12 plays an important role in translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOUZA-Chies T.T., Bittar G., Nadot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998
15-DEC-1998
28-FEB-2003
                                                                                                                                                                                       NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001912; Ribosomal_S4.
InterPro; IPR002942; S4.
InterPro; IPR002794; S4.
InterPro; IPR005709; S4_bact_org.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_01306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z68235; CAA92533.1; HSSP; P81288; 1C05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast
                                                                                                                                                                                                                                           DOMĀIN
                                                                                                                                                                                                                                                                   Ribosomal protein; RNA-binding; rRNA-binding; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                         FIGRFAM8;
                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00363; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=58944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Belamcanda chinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPS4
                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Phylogenetic analysis of Iridaceae with parsimony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: Contains 1 S4 RNA-binding domain.
SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accuracy (By similarity).

SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5.

The interaction surface between S4 and S5 is involved in control of translational fidelity (By similarity).
432 KRPRSGS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                     ; TIGR01017; rpsD_bact; pS00632; RIBOSOMĀL_S4; PS50889; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSVSVRD 89
                                                                                                                                                                                 82
182
182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
30S ribosomal protein S4 (Fragment).
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -; 1
                                                                                                                                                                                                                                     143
                                                                                                                                                                                 182
21048 MW;
                                                                       100.0%; +1
                                                                                                       1.4%; Score 7;
100.0%; Pred. N
                                                                                                                                                                                                                                        S4
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                                                                                                                                                                                    E3620B0641A04EF5
                                                                                                                                                                                                                                        RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s:
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No.
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                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carter L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ጅ
                                                                                                                                Length 182;
                                                                               0; Indels
                                                                                                                                                                                       CRC64;
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                                                                                                                                                                                                                                                                                                                Matches
                                            Query Match
Best Local
                                                                                                                                      HAMAP; MF_01306; -; 1.
InterPro; IPR001912; F.
InterPro; IPR002942; S.
InterPro; IPR005709; S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RR4 HEAMA
020231;
15-DEC-1998
15-DEC-1998
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                                                                                DOMAIN
NON TER
                                                                                                  Ribosomal
                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemanthus magnificeas.
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Souza-Chies T.T., Bittar G., Nadot S., Carter L., Besin
                                                                                                                   TIGRFAMS; TIGR01017; rpsD_bact; 1.
PROSITE; PS00632; RIBOSOMAL_S4; 1.
PROSITE; PS50889; S4; 1.
                                                                                                                                     SMART; SM00363; S4; 1.
TIGRFAM8; TIGR01017; r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lejeune B.P.;
                 432 KRPRSGS 438
                                                                                                                                                                                                               P81288;
17
                                                                                                                                                                                                                      Z68253; CAA92551.1; -.
                                  Similarity 7; Conserv
KRPRSGS
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HSSP; P81288; ICO5.
HAWAP; MF 01306; -; 1.
InterPro; IPR001912; Ribosomal_S4.
InterPro; IPR002942; S4.
InterPro; IPR005709; S4_bact_org.
Pfam; PF00163; Ribosomal_S4; 1.
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Plant Syst. Evol. 204:109-123(1997).
-!- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the body of the 30S subunit (By similarity).
-!- FUNCTION: With S5 and S12 plays an important role in translational accuracy (By similarity).
-!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5.
The interaction surface between S4 and S5 is involved in control
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Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
Hymenocallis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Souza-Chies T.T., Bittar G., Nadot S.,
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15-DEC-1998 (Rel. 37, Last Bequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein S4 (Fragment).
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SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: Contains 1 $4 RNA-binding domain.
SIMILARITY: BELONGS TO THE $4P FAMILY OF RIBOSOMAL PROTEINS
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-I- FUNCTION: With S5 and S12 plays an important role in translation accuracy (By similarity).
-I- SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5. The interaction surface between S4 and S5 is involved in control of translational fidelity (By similarity).
-I- SUBCELLULAR LOCATION: Chloroplast.
-I- SIMILARITY: Contains 1 S4 RNA-binding domain.
-I- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
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PROSITE; PS00632; RIBOSOMĀL_S4; 1.
PROSITE; PS50889; S4; 1.
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modified and this statement is not removed. Usage by an
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                                                                                                                     SEQÜENCE
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30S ribosomal protein S4 (Fragment).
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1.7%; Similarity 100.0%; 9; Conservative	e protein CelA [imported] :: Streptococcus pneumonia]-Aug-2001 #sequence_revi on: B95110 n, H; Nelson, K.E.; Paul Umayam, L.A.; White, O.; Hickey, E.K.; Holt, I.E. 193, 498-506, 2001 :: Loftus, B.J.; Yang, F.; Complete Genome Sequence cce number: A95000; MUID:2 on: B95110 preliminary e type: DNA s: 1-216 <kur> eferences: GB:AE005672; Peferences: GB:AE005672; Peental source: strain TICR 190954</kur>			178 179 179 196 196 201 201 221 233 233 234 253 253
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Score 9; DB 2; Pred. No. 0.82; 0; Mismatches] - Streptococcus ae ision 03-Aug-2001 lsen, I.T.; Eisen ; Salzberg, S.L.; ; Smith, H.O.; Ve of a virulent is 21357209; PMID:11 PIDN:AAK75075.1;	rision 26-May- rision 26-May- 1993 Lobulin chi ge 194080891; PMI on not shown on not shown region; immuno noglobulin Score 9; DB pred. No. 0 0; Mismatche	ALIGNMENTS	D71451 D71451 A75215 A75215 T39698 T411338 S41170 G71428 AC2201 T40730 E86425 C739142 E70962 E70962 E70962 F75272 F75272 F83440 T48058
Length 216; 0; Indels 0; Gaps 0;	pneumoniae (strain TIGR4) #text_change 03-Aug-2001 , J.A.; Read, T.D.; Peterson, S.; Heid Lewis, M.R.; Radune, D.; Holtzapple, i nter, J.C.; Dougherty, B.A.; Morrison, olate of Streptococcus pneumoniae. 463916 PID:g14972428; GSPDB:GN00164; TIGR:SP45	1995 #text_change 23-Jul-1999 nes and their hypermutation. D:8258341 PIDN:CAA51108.1; PID:g441349 globulin homology globulin homology 2; Length 108; 44; 0; Indels 0; Gaps 0;		MJ0653 homolog PH0 AV25 protein - nem MJ0653 homolog PAB blue copper bindin blue copper bindin ribosomal protein hypothetical prote hypothetical prote probable rna-bindi hypothetical prote mrkB protein precu probable magnesium ribosomal protein N-acetylglutamate probable short-cha RING-HZ zinc finge

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N;Alternate names: 3-methyl-2
C;Species: Homo sapiens (man)
C;Date: 25-Sep-1989 #sequence
C;Accession: A32422; A33362;
R;Nobukuni, Y.; Mitsubuchi, H
                                                                                          dihydrolipoamide S-(2\text{-methylpropanoy1})transferase (EC 2.3 N,Alternate names: 3-methyl-2-oxobutanoate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;HOSKINS, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E. J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            competence protein [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
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A;Introns: 317/1
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A;Accession: T48159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A97872; MUID:21429245; A;Accession: H97978
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A;Experimental source: cultivar Co
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    Date: 25-Sep-1989 #sequence revision 19-Oct-1995 #text change 18-Jun-1999;Accession: A32422; A33362; A28655; A28707; A45126; S27T94; S50200; S22865;Nobukuni, Y.; Mitsubuchi, H.; Endo, F.; Matsuda, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession:
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203
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vision 20-Apr-2000 #text_change 20-Apr-2000
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ase (lipoamide) (EC 1.2.4.4)
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A;Molecule type: mRNA
A;Residues: 6-313,'YYPSWKS' <LAU>
A;Residues: 6-313,'YYPSWKS' <LAU>
A;Cross-references: GB:M19301; NID:gl86635; PIDN:AAA59200.1; PID:g307078
A;Cross-references: GB:M19301; NID:g186635; PIDN:AAA59200.1; PID:g307078
A;Lau, K.S.; Herring, W.J.; Chuang, J.L.; McKean, M.; Danner, D.J.; Cox, R.P.; Chuang, D.J.; Biol. Chem. 267, 24090-24096, 1992
A;Title: Structure of the gene encoding dihydrolipoyl transacylase (E2) component of human A;Reference number: A45126; MUID:93054781; PMID:1429740
A;Accession: A45126
A;Molecule type: mRNA
A;Residues: 1-320,'Q',322-353,'L',355-482 <LA3>
A;Residues: 1-320,'Q',322-353,'L',355-482 <LA3>
A;Cross-references: EMBL:X66785; NID:g30489; PIDN:CAA47285.1; PID:g30490
R;Wynn, R.M.; Kochi, H.; Cox, R.F.; Chaang, D.T.
Biochim. Biophys. Acta 1201, 125-128, 1994
A;Title: Differential processing of human and rat E1-alpha precursors of A;Reference number: S50200; MUID:95002090; PMID:7918575
                                                                                                                                                                                         A; Map position: 1p31-1p31
C; Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
C; Keywords: acyltransferase; blocked amino end; mitochondrion; oxidoreductase
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R;Lau, K.S.; Chuang, J.L.; Herring, W.J.; Danner, D.J.; Cox, R.P.; Chuang, Biochim. Biophys. Acta 1132, 319-321, 1992
A;Title: The complete cDNA sequence for dihydrolipoyl transacylase (E2) of A;Reference number: S27194; MUID:93041936; PMID:1420314
A;Accession: S27194
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R;Lau, K.S.; Griffin, T.A.; Hu, C.W.C.; Chuang, D.T.
Biochemistry 27, 1972-1981, 1988
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A;Residues: 6-320,'Q','32-353,'L','355-482 <DAN'
A;Residues: 6-320,'Q','32-353,'L','355-482 <DAN'
A;Cross-references: GB:J03208; NID:g179353; PIDN:AAA35589.1; PID:g179354; GB:J04723
A;Hummel, K.B.; Litwer, S.; Bradford, A.P.; Aitken, A.; Danner, D.J.; Yeaman, S.J.
T. Biol. Chem. 263, 6165-6168, 11988
A;Title: Nucleotide sequence of a CDNA for branched chain acyltransferase with analysis
A;Reference number: A28655; MUID:88198156; PMID:3245861
                                                                                                                                                             F;1-61/Domain: transit peptide (mitochondrion) #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:118784; OMIM:248610
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A;Residues: 1-3;15-20;56-61;82-87;142-148;184-188;255-260;311-316;337-342;401-406;425-43(
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A; Residues: 6-313, 'YYFSWKS' <HUM>
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A; Accession: A32422
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A;Cross-references: GB:J04836; NID:g149819; PIDN:AAA72215.1; PID:g149820 C;Superfamily: vacuolar H+-transporting ATPsae 69K chain; H+-transporting C;Keywords: ATP biosynthesis; hydrolase; nucleotide binding; P-loop F;228-235/Region: nucleotide-binding motif A (P-Loop) F;251-431/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1223
                  RESULT
T22540
                                                                                                                                                                                                                                                                                                                                                                                                                                       H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - Methanosarcina barkeri C;Species: Methanosarcina barkeri C;Species: Methanosarcina barkeri C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Jun-2002
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A;Experimental source: strain EGD-e
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A; Residues: 1-483 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Listeria monocytogenes
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Accession: AD1223
                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                              Local
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                                                                                                              438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L.M.; Karst,
                                                                                 99
                                                                                                                                              Similarity
8; Conserv
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Similarity 100.0%;
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 protein F53B6.6 -
                                                                                                              STGSSLSV 445
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                                                                                 73
                                                                                                                                         100.0%; F1
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 Caenorhabditis elegans
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                                                                                                                                                            Score 8; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8; DB 2; Pred. No. 17;
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Dussurget, O.; En
                                                                                                                                                                           Length 578;
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Entian, K.D.; Fsihi, H.
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photoreceptor - Deinococcus radiodurans C; Species: Deinococcus radiodurans
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Marcins, E.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.F.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.R.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.R.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.R.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.R.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.R.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.R.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.R.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.R.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.M.; Silva, M.R.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettor
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A; Molecule type: DNA
A; Residues: 1-610 <WIL>
A; Residues: 1-610 <WIL>
A; Cross-references: EMBL: Z81086; PIDN: CAB03116.1;
A; Cross-references: clone F53B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein XF0752 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, October 1996 A;Reference number: Z19578 A;Accession: T22540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: E82768
R;anonymous, The Xylella fastidiosa Consortium of Nature 406, 151-157, 2000
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A; Introns: 38/1; 103/1; 192/2; 239/1; 268/2; 300/3; 532/2; 546/1
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                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A59328
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A;Experimental source: strain 9a5c
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R.Theologis, A.; Bcker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; pMID:11130712
  probable DNA-binding protein [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-Mar-2003
C;Date: 19-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-Mar-2003
C;Accession: H91246
R;Haysahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, 19 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, 10 DNA Res. 8, 11-22, 2001
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C;Superfamily: bacteriophytochrome; phytochrome homology
F:504-744/Domain: sensor histidine kinase homology <SHK>
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Science 286, 1571-1577, 1999
                                                                                                                                                                                                       RESULT 12
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A; Residues: 1-1532 <STO>
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A;Experimental source: strain R1
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A; Residues: 1-755 <WHI>
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Best Local
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Shinagawa, H.
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T.; Zalewski,
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                                                                                             R;Capra, J.D.; Klapper, D.G. Scand. J. Immunol. 5, 677-684, A;Title: Complete amino acid so
A; Accession: A01871
A; Molecule type: pro
A; Residues: 1-108 <0
                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984
C;Accession: A01871; F30609
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d sequence of the variable MUID:77038198; PMID:824717

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human IgM

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#text_change

21-Jan-2000

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A;Cross-references: GB:AE006469; PIDN:AAK64997.1; PID:g14523425; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hv
pela, D; Chain, P.; Cowie, A; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher,
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lel
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Ye
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: C95304

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilotu A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: C95304
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C;Superf
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/pocies: Sinorhizobium meliloti
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    Sinorhizobium meliloti

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N.A.; Fisher, R.F.;
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, K.; Yeh, K.
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R;Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic allowed a hyper-timinary; nucleic acid sequence not shown; translation not shown A; Ketatus: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-129 < KAW> A; Residues: 1-129 < KAW> A; Residues: 1-129 < KAW> A; Residues: this accession replaces an interim accession for a sequence replaced by GenBank A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin f;16-90/Domain: immunoglobulin homology <IMM> F;16-90/Domain: immunoglobulin homology <IMM>
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A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: F30609
A;Molecule type: protein
A;Residues: 1-104 <GON>
C;Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
Search completed: July 24, 2003, 12:27:11 Job time : 64.1903 secs
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C;Species: Pyrococcus horikoshii
C;Bate: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: H71014
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;Gene: PH1414
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Robertsrapp L;
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Matches 518
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Human; prostate;
                                   Human prostate-specific PS118 protein fragment #1.
                                                                 27-NOV-2002
                                                                                                 AA019165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Granados EN,
Russell JC,
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Granados F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FRIE/)
(GORD/)
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23-APR-1997;
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KLASS M R.
KRATOCHVIL J
ROBERTS-RAPP
RUSSELL J C.
STROUPE S D.
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  LVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE
              LVKRLHKLCMELCNNYIOMHLDLENCMEEPPIFKGDPFFILPSFOSESSTPSTGGFSGKE
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Kratochvil
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N-PSDB;
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Granados EN, Hod
Russell JC, Stro
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(COHE/)
(COPL/)
(FRIE/)
(GORD/)
                                                                                                                                                                                                                                                                      Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS118; prostate;
benign prostatic
                The present sequence is that of a human prostate-specific PS118 polypeptide, as predicted from a partial consensus cDNA sequence (see ABA91651), and lacking the N-terminal region. The PS118 consensus sequence is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, including derivatives of the present sequence, polynucleotides, anntibodies, agonists and inhibitors are useful for detecting,
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prognosticating,
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PAVFPCISQLTCHVTDIRVRQAVREWLGRVGRVYDIIV
                                                             FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ
                                                                                                                             KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
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Pred. No. 7.3e-254;
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CC diagnostic amino acid sequences of the invention.

CC observations of the sequence of the invention.

CC observations of the primerase of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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                                                  TPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD
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The present invention relates to novel human coding sequences are CC (ABQ99268-ABQ99608) and proteins (ABP65022). The sequences are CC (BADQ99268-ABQ99608) and proteins (ABP65022). The sequences are CC (Polynucleotides may be used in the field of molecular biology as CC (Polynucleotides may be used in the field of molecular biology as CC (Polynucleotides may be used in the field of molecular biology as CC (Polynucleotides may be used in the field of molecular biology as CC (Polynucleotides may be useful in diagnostics as expressed CC (Polynucleotides are useful in diagnostics as expressed CC (Polynucleotides and sequence in the proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or CC (Polynucleotides and proteins are useful                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID 495; 394pp; English.
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DB 22;

Length 1982;

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CC The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CPCR) primers of the production of (II) and the polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (III). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC of the polymer of the printed sequences of the invention.

CC art for wino introductions of the invention.
Sequence
                                            at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
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Matches 499; Query Match Best Local : Local Similarity 1408 1764 1704 1584 1464 1644 1524 361 301 241 181 121 61 1 RIRAMAQQVEMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLL LVKRLHKLCMELCNNYIQMHLDLENCMBEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS TPSEDDRSQSREHMGESLSLKAGGGDLLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD TAREFOTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK RIRAMAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKK----REIVVSLL FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ 480 TPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD LVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW Conservative 95.98; <u>,,</u> Score 2588; DI Pred. No. 3.1e 0; Mismatches .1e-242; Indels 4. Gaps 1583 1763 1703 1643 1523 120 1463 420 360 300 180 60

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel nucleic acid sequences (A) that are compressed at high level in prostatic tumor tissue and encode gene products or their fragments. The products of the invention have antitumor activity Polypeptides (I) encoded by (A) are used: (i) for dentifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. AAY48215-Y48303 represent protein fragments encoded by the expressed sequence tags described in the method of the
                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid expressed at high level in prostatic tumor tissue encoded polypeptides, useful for treating cancer and screening for therapeutic agents -
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N-PSDB; AAZ33451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate cancer-associated protein 34.
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                                     LLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTARE
                                                                                                         MAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLLSHQV
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                                                                                                                                                                                                                                                                                                                                192
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                                                                                                                                                                                                                                          36.4%; Score 982; DB 20; 100.0%; Pred. No. 3.7e-87;
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                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                 Length 192;
                                                                                                                                                                                                                   Indels
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180;

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MLDTQCSPKTPNNFDHAQSCQLIIELPPDEKFNGHTKKSVSFREIVVSLLSHQVLLQNLY 70

MLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLLSHQVLLQNLY 60

DILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDTSPG 130

Query Match Best Local Similarity

34.1%; Score 920; DB 20; ilarity 100.0%; Pred. No. 3.7e-81; Conservative 0; Mismatches 0;

Length 180 Indels

<u>,,</u>

Gaps

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RESULT 8
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                                     This invention describes novel nucleic acid sequences (A) that are expressed at high level in prostatic tumor tissue and encode gene products or their fragments. The products of the invention have antitumor activity. Polypeptides (I) encoded by (A) are used: (i) for identifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use encoded by the expressed sequence tags described in the method of the
                                                                                                                                                                                                                                                                                                                                              New nucleic acid expressed at high level in prostatic tumor tissue encoded polypeptides, useful for treating cancer and screening for
Sequence
                                                                                                                                                                                                                                                                                               Claim 22; 112-113; 166pp; German.
                                                                                                                                                                                                                                                                                                                                  therapeutic agents
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                                invention
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180 AA;
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EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS

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RESULT 9
AAO19169
ID AAO1
AX AAO1
AX AAO1
AX AAO1
AX AAO1
AX Huma
KW Huma
KW EST;
AX Homc
AX US2(
AX AO2
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AX AO3
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                                                                                        Query Match
Best Local
                                                                   Matches
                                                                                                                                                                                         The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                                                                                                                                                                                                                             Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
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23-APR-1997;
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393 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
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HODGES S C.
KLASS M R.
KRATOCHVIL J D.
ROBERTS-RAPP L.
STROUPE S D.
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                                                                                        Similarity
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Hodges
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                                                                   Conservative
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97US-0842385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tag; cytostatic; gene therapy
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צר
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate-specific sequence; prostate cancer;
                                                                                     9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SD, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colpitts TI
Klass MR,
                                                                                                                                                                                                                                                                                                                                                    English.
                                                            Score 260; DB 23;
Pred. No. 1.2e-17;
Pred. No. 1.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Friedman
Kratochvil
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                                                                                                       Length 49;
                                                                 Indels
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Roberts-Rapp
                        441
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RESULT 10
AAM50813
ID DAM50
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XX PS118
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XX PY081
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                                                                                                                                                                in non-prostate tissue. PS118 polypeptides, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostatic intraepithelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polynucleotides in transfected host cells, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the
                                                                                invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising amino acids 393-441 of human prostate-specific PS118 polypeptide (see AAM50809). A PS118 consensus sequence (see polypeptide (see AAM50809). It times more often in prostate than ABA91651) is found at least 12 times more often in prostate than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognostic preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 44;
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                                                           without the use of
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GORDON J.
GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s EN, Hodges
JC, Stroupe
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KRATOCHVIL J
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les SC,
lpe SD;
                                                           surgery
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Klass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
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Roberts-Rapp L
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o prostate
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Sequence

Query Match Best Local S Matches 49

h 9.6%; Similarity 100.0%; 49; Conservative (

<u>,</u>

Mismatches

Score 260; DB 23; Pred. No. 1.2e-17;

Length 49; Indels

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Gaps

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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II) The CC polymucleotides are also used in diagnostics as expressed sequence tags (II) is useful in gene therapy techniques (II) castore normal activity of (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as CC imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity amino acid sequences of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire polypublished_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 40088; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT,
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                   relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes.
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Query Match Best Local Similarity

98

Score Pred.

255; DB 22; No. 3.7e-17;

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                                                                                                The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treament of prostate these asses, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                                                                        Novel PS118 polypeptide for detecting, prognosticating, preventing, treating, individual to diseases and conditions of
                                                                               Sequence
                                                                                                                                                                          Claim 17; Page 43-44;
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                                                                                                                                                                                                                                                                              Granados
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23-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate;
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RUSSELL J C.
STROUPE S D.
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HODGES S C.
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FRIEDMAN
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KRATOCHVIL J
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                 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR
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EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR
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                                       Conservative
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97US-0842385.
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7 L
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                                                Score 216; DB 23;
Pred. No. 1.7e-13;
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                                       Mismatches
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                                                                                                                                                                                                       , diagnosing, staging, monitoring, or determining predisposition of of prostate, e.g. prostrate
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                                                          Length
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                   224
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RESULT 13
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XX PS118
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PR 23-AF
YX COHF
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PA (FORD
                                                                           The present sequence is that of an immunogenic polypeptide comprising amino acids 184-224 of human prostate-specific PS118 compounds of the consensus sequence (see ABA91651) is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, polynucleotides, and inhibitors are useful for detecting, antibodies, agonists and inhibitors are useful for detecting, it diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostate thyperplasia, prostatitis, prostatic intraepithelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of pS118 polynucleotides in transfected host cells, and immunogenic peptides are useful for raising PS118 specific antibodies of diagnostic use. The methods and reagents of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS118; prostate;
benign prostatic
prostatitis; huma
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Granados EN, Hod
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 43; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2001055758-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM50810 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GORD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (/TTIB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-187683/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GORDON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EN,
                                                         the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRATOCHVIL J D. ROBERTS-RAPP L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLASS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COPLPITTS T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BILLING-MEDEL P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HODGES S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRIEDMAN P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COHEN
      41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l PA, Cohen M, Coplpitts TL, Friedman
Hodges SC, Klass MR, Kratochvil JD,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0842385
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hyperplasia; prostatic intraepithelial neoplasia;
an; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gordon J;
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Query Match

0

Score

216;

DB 23;

Length 41;

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RESULT 14
AAO19168
ID AAO15
XX AAO15
XX AAO15
XX AAO15
XX AAO15
XX Humar
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                         Ś
                                                                     Matches
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                            The present invention relates to a number of prostate-specific sequences derived from the human PS118 gene. These can be used in the detection, monitoring and treatment of prostate diseases, particularly prostate cancer. The present sequence is a PS118 protein fragment of the invention. The coding sequences of the invention were isolated from a prostate tissue expressed sequence tag (EST) library.
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel PS118 polypeptide for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating, or determining predisposition of individual to diseases and conditions of prostate, e.g. prostrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Granados EN,
Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Billingel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1998;
23-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA019168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAO19168 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 44; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-665429/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-2001; 2001US-0991681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST; expressed sequence tag; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COHE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GRAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRIE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROBE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRAT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLAS/
                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate-specific
                                                                  l Similarity
40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROBERTS-RAPP
RUSSELL J C.
STROUPE S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLPITTS T L.
FRIEDMAN P N.
GORDAN J.
GRANADOS E N.
HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate; prostate-specific sequence; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRATOCHVIL J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COHEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BILLINGEL P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLASS M R.
SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR
                                                                                                                                                          40
                                                                ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen
Hodges
                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0065383.
97US-0842385.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colpitts TL,
Klass MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
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                                                                                            Score 215;
Pred. No.
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                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.7e-13; thes 0;
                                                                                     2.1e-13;
                                                                                                                DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n,
                                                                                                              Length
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                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordan J;
Roberts-Rapp
                                                                                                                40;
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RESULT 15
AAM50812
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                                         The present sequence is that of an immunogenic polypeptide comprising amino acids 332-371 of human prostate-specific PS118 comprising amino acids 332-371 of human prostate-specific PS118 comprising amino acids 332-371 of human prostate sequence (see polypeptide (see AM50809). A PS118 consensus sequence (see in the polypeptide) are polypeptides, polymulate than in non-prostate tissue. PS118 polypeptides, polymulate tides, and inhibitors are useful for detecting, attacking, staging, monitoring, prognostidenting, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benjum prostatic typerplasia, prostaticing, the prostate, such as benjum prostatic secretary prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polymucleotides in transfected host cells, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                            Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate disease -
                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 44; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-187683/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Billing-Medel PA, Cohen
Granados EN, Hodges SC,
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS118; prostate; marker; prostate cancer; tumour; metástasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM50812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM50812 standard; Protein; 40
                                 without the use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GORD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRIE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) GORDON J.
) GRANADOS E N.
) HODGES S C.
) KLASS M R.
) KRATOCHVIL J D.
) ROBERTS-RAPP L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BILLING-MEDEL P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRIEDMAN P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPLPITTS T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COHEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PN, Gordon J;
Roberts-Rapp L;
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Sequence

40

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                    ş
                                            Matches 40;
                                                       Best Local Similarity
                                                                  Query Match
                332 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 371
Ц
SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
                                             Conservative
                                                       100.0%;
                                            0,
                                                       Score 215; DB 23;
Pred. No. 2.1e-13;
                                            Mismatches
                                                                 Length 40;
                                             Indels
                                             0;
                                           Gaps
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Search completed: July 24, Job time: 170.369 secs 2003, 11:53:36

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
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ALIGNMENTS

RESULT 1 US-09-065-383-27 Sequence 27, Appli Patent No. 6391543 ZIP: 60064-3500 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/065,383 FILING DATE: CLASSIFICATION: DATA: APPLICATION TO DATA: APPLICATION TO DATA: CLASSIFICATION TO DATA: FILING DATE: CLASSIFICATION: DATA: APPLICATION TO DATA: APPLICATION TO DATA: APPLICATION TO DATA: CLASSIFICATION: DATA: APPLICATION TO DAT PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/842,38 APPLICATION NUMBER: 09/842,38 APPLICATION NUMBER: 1997 ATTORNEY/AGENT INFORMATION: NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 518 amino aci GENERAL INFORMATION APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: REFERENCE/DOCKET NUMBER: 60 TELECOMMUNICATION INFORMATION: TELEPHONE: 847/935-1729 CORRESPONDENCE ADDRESS: ADDRESSEE: Abbott Laboratories TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: APPLICANT: APPLICANT: STREET: 100 Abbott CITY: Abbott Park STATE: IL TELEX: TELEFAX: 847/938-2623 COUNTRY: Application US/09065383 KRATOCHVIL, JON D. ROBERTS-RAPP, LISA RUSSELL, JOHN C. STROUPE, STEPHEN D. 100 Abbott BILLING-MEDEL, PATRI COHEN, MAURICE COLPITTS, TRACEY L. FRIEDMAN, PAULA N. 518 amino acids USA GRANADOS, EDWARD N. HODGES, STEVEN C. KLASS, MICHAEL R. JULIAN REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF TI Park Road 08/842,385 PATRICIA 6084.US.P1 DISEASES OF THE PROSTATE 2.0

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                                                              TITLE OF INVENTION: REAGENTS AND MITTLE OF INVENTION: FOR DETECTING NUMBER OF SEQUENCES: 33
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                E: Abbott Laboratories
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
                                                                                                           ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
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HODGES, STEVEN C.
KLASS, MICHAEL R.
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US-09-065-383-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                     TITLE OF INVENTION: REAGENTS AND TITLE OF INVENTION: FOR DETECTING NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: ADDRESSE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                          ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: No. 6391543e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                        STREET: 100 Abbot
CITY: Abbott Park
STATE: IL
                                       COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 49 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICATION NUMBER:
                                                                                                                          COUNTRY:
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10. 639154
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                                                                                                                                                                                                                                                    KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
NVENTION: REAGENTS AN
                                                                                                                                                                        100 Abbott Park Road
                                                                                                                           USA
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
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                                                           IBM Compatible
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S, STEVEN C.
, MICHAEL R.
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100.0%; Pred. No. 2.9e-20;
vative 0; Mismatches 0;
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                                                                                                                                                                                                                                      THE PROSTATE
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FILING DATE:

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
                                                                                                                                                                                                                                                                                                                                                      TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                     SOFTWARE: FASTISE FOR WINDOWS VERSION 2.0 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/065,383
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: No. 6391543e
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APPLICATION NUMBER:
                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/84
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 60064-3500
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TOPOLOGY: lir
                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09065383
                                                                                                                                                                                                                                                                                          100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 amino acids
                                                                                                                                                                                                                                                                                                                                                                         RUSSELL, JOHN C.
STROUPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                          GRANADOS, EDWARD N. HODGES, STEVEN C. KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GORDON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BILLING-MEDEL, PATRICIA
                                                                                                                                                                              IBM Compatible
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35,441
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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APPLICANT
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                                                                          REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-APR-
                                                                                                                                                                                                                                                                                                                             ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
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                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 100 A
CITY: Abbott
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                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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   35 amino acids
                                                               847/938-2623
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KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RUSSELL, JOHN C.
STROUPE, STEPHEN D.
PENTION: REAGENTS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRANADOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BILLING-MEDEL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%; Score 215; DB 4;
.00.0%; Pred. No. 1.3e-15;
                                                                                                                                                                                     08/842,385
                                                                                                                                                                                                                                                 US/09/065,383
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                                29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LISA
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                                                                                                           6084.US.P1
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STRANDEDNESS: single; TOPOLOGY: linear; MOLECULE TYPE: No. 6391543eUS-09-065-383-29
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US-08-729-416C-1
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                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARAE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,416C
FILING DATE: 11-OCT-1996
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                            Best Local Similarity
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TITLE OF INVENTION: NOVE
TITLE OF INVENTION: THER
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO: 1:
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NAME: PERRY, GLENN J.
REGISTRATION UNMER: 20458
REFERENCE/DOCKET NUMBER: 7899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPAX: 202-822-0944
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acids
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Local Similarity 100.0%; Pred. No. 5.2e-12;
les 35; Conservative 0; Mismarchen
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
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219 RQWRARMPLLSVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPF 278
                                        129
                                                                              177 QVKKVLFED----
                                                                                                                                                      125 FDTSPGLKCLLKK------VSGIGGAANL-YRQSAMSFNIYFHALVCAVLTNQETITAE 176
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                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                    HMRSISFASGGDPDTTDYVAYVAKDPVNRRACHILECCDGLAQDVIGSIGQAFELRFKQY 188
                                                                                                                  CEAVPGAKGAFKKRKPPSKMLSSILGKSNLQFAGMSISLTISTASLNLRTPDSKQIIANH 128
                                                                                                                                                                                            PGDEPLPRPPRGTPHASDQVLGPGVTYVVKYLGCIEVLRSMRSLDFSTRTQITREAISRV 68
                                                                                                                                                                                                                                  PGEEKTIQVPE------AKLAGFLRYI-SMQNLAVIFDLLLDSYRTARE 124
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                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                    4.1%; Score 111; DB 3; Length 474; 18.5%; Pred. No. 0.0086; Indels 120;
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NOVEL BRAIN-SPECIFIC ADAPTER MOLECULE GENE
THEREOF, AND ANTIBODY THERETO
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                                                                          --DERSTDSSQQCSSEDEDIFEETAQVSPPRGKEK 218
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Qy 279FIRSFQSESSTFSTGGFSGKETSSEDDRSQSREIMGESISSLKAGG 324
279FILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLSLKAGG

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US-08-729-416C-7
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Best Local (
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                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 594 amino
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pept:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME: PERRY, GLENN J.
REGISTRATION NUMBER: 28458
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PILLSBURY, MADISON & SUTRO, L.L.P. STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 20005-3918
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                                         219 ROWRARMPLLSVOPVSNADWVWLVKRLHKLCMELCNNYIOMHLDLENCMEEPPIFKGDPF 278
                                                                                                                                                                                                                                                                                                                         90; Conservative
                                                                                                                                                                                                                                                                                                                     h 4.1%; Score 111; DB 3; Length 594;
Similarity 18.5%; Pred. No. 0.012;
90; Conservative 71; Mismatches 205; Indels 1
                                                                                                                                                              CEAVPGAKGAFKKRKPPSKMLSSILGKSNLQFAGMSISLTISTASLNLRTPDSKQIIANH 248
                                                                                                                                                                                                   FDTSPGLKCLLKK------VSGIGGAANL-YRQSAMSFNIYFHALVCAVLTNQETITAE 176
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                                                                                 HMRSISFASGGDPDTTDYVAYVAKDPVNRRACHILECCDGLAQDVIGSIGQAFELRFKQY 308
                                                                                                                                                                                                                                                                                    PGEEKTIQVPE----
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      LQCPTKIPALH-DRMQSLDEPW--
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                                                                                                                                                                                                                                                                                -----AKLAGFLRYI-SMQNLAVIFDLLLDSYRTARE 124
                                                                                                                      -DERSTDSSQQCSSEDEDIFEETAQVSPPRGKEK 218
      ---TEEEGDGSDHPYYNSIPS 347
                                                                                                                                                                                                                                                                                                                       Indels 120;
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APPLICANT: NAKAWINA, TAKESHI
TITLE OF INVENTION: NOVEL, BRAIN -SPECIFIC ADJ
TITLE OF INVENTION: AND ANTIBODY THERETO
FILE REFERENCE: 7898/262241
CURRENT APPLICATION NUMBER: US/09/433,353
CURRENT FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 08/729,416
PRIOR APPLICATION NUMBER: 08/729,416
PRIOR APPLICATION NUMBER: 08/729,416
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PACENTIN VET: 2.1
SEQ ID NO 7
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US-09-433-353-7
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Patent No. 6545141
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EVKVEKKG------EPLGPRGQDSPLLQRPQ-HLMDQGQMRHSFSAGPELLRQD
                                                                                                                                           KMPPPGGFLDTRLKPRPHAPDTAQFAGKEQTYYQGR-----HLGDTFGEDWQQTPLRQGS
                                                                                                                                                                                                                        LOCPTKIPALH-DRMQSLDEPW-----
                                                                                                                                                                                                                                                             ROWRARMPLLSVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPF
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                                                              SDIYSTPEGKLHVA-PTGEAPTYVNT-QQIPPQAWPAAVSS--AESSPRKDLFDMKPFED
                                                                                                 GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYKKRKQQHNLSAFPK 384
                                                                                                                                                                              -----FILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLS-----LKAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                               MOLECULE IN HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/670,611 FILING DATE: 19910313 CLASSIFICATION: 435.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kagan, Sarah A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                           ORGANISM:
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ETERLNSRIEHLKSQNDLLTITLE-----ECKSNAERMSMLVGKYESNATALRLALQY 451
                                DERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVWLVKRL 245
                                                                    EISSIGVSSSVAEHLAHSLQDCSNIQEIFQTLYSHG-
                                                                                                          KVSGIGGAANLYRQSAMSF-----
                                                                                                                                             PSTGELSTSSSSNDIPIAKIAERVK---
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Gene Mutated in Colorectal Cancer
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                                                                                                                                                                                                                   Score 110; DB 1; Length 829; 
Pred. No. 0.028; 
1; Mismatches 198; Indels 1
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                                                                                                        --NIYFHALVCAVLTNQETITAEQVKKVLFED 185
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                                                                                                                                             -LSKTRSESSSSDRPVLGS
                                                                      --SAISESKIRE--FEV
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US-08-220-674-2
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                                                                                                                                                                                                                                                                                    FILING DATE: 31-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 07
FILING DATE: 13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                              MOLECULE TYPE:
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 829 amino acid
                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                 NAME: Kagan, Sarah A
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    TOPOLOGY:
                                                                                     STRANDEDNESS:
                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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SOURCE
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1001 G Street
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White, Raymond
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RESULT 12
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US-08-220-674-2
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Patent No. 5576422
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Best Local :
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                                                                                 COUNTRY: U.S...
ZIP: 20001-4597
ZOUNTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPEM PC-DOS/MS-DOS
MEDIUM TYPEM: PC-DOS/MS-DOS
MEDIUM TYPEM: PC-DOS/MS-DOS
MEDIUM TYPEM: PC-DOS/MS-DOS
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APPLICANT: Kinzler, Ke
APPLICANT: White, Rayn
APPLICANT: White, Rayn
APPLICANT: Nakamura, )
TITLE OF INVENTION: Ge
TITLE OF INVENTION: Ha
                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                      STREET:
                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 KVSGIGGAANLYRQSAMSF------NIYFHALVCAVLTNQETITAEQVKKVLFED 185
 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PSPGEEKTI----QVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDTSPGLKCLLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VR--QAVREWLGRVGRVYDII 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRLDLENAVLMQELMAMKEEMAELKAQLYLLEKEKK-----ALELKLSTREAQEQAY 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSSTASSCOTEFTKEDEQ-RIKDYIQQLKNDRAAVKLTMLELESIHIDPLSYDVKPRGDS 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQCIEAYELLL------ALAESEQSLILGQFRAAGVGSSPGDQSGDENITQM 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEFTNAIRREKKLKARVQELV 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPL-LQRP---QHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAW 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKG-----EPLG----PRGQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EISSIGVSSSVAEHLAHSLQDCSNIQEIFQTLYSHG-----SAISESKIRE--FEV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVHIEHLKSEVEEQKEQRMRSLSSTSSGSKDKPGKECADAASPALSLAELRTTCSENELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DDRSQSREHMGESLSLKAGG--GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMA 358
                                                                                                                                                                                                                                                                      1001 G Street
                                                                                                                                                                                                                                                                                                                                                                                                     Kinzler, Kenneth W. White, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                          Vogelstein, Bert
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                                                       US/08/445,186
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Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                   Colorectal
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                                                                                               #1.25
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; ORGANISM: Hom
US-08-445-186-2
                                                                                                                                   RESULT 13
US-08-446-549-2
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                                                                                           Sequence 2, Application US/08446549 Patent No. 5693536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202-508-9100 INFORMATION FOR SEQ ID NO: 2:
                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: Y
ANTI-SENSE: NO
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kagan, Sarah A. REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
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                                                                                                                                                                                                                                                                                       LVHIEHLKSEVEEQKEQRMRSLSSTSSGSKDKPGKECADAASPALSLAELRTTCSENELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TSSTASSCOTEFTKEDEQ-RLKDYIQQLKNDRAAVKLTMLELESIHIDPLSYDVKPRGDS
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   Nakamura,
                 White, Raymond
                                                       Vogelstein,
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13-MAR-1991
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31-MAR-1994
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660

549

304 451 Gaps

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; TOPOLOGY: linear; MOLECULE TYPE: protein; HYPOTHETICAL: YES ANTI-SENSE: NO; ORIGINAL SOURCE: ORGANISM: Homo sapiens US-08-446-549-2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/446,549
FILING DATE: 19-MAY-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 07/670,611
FILING DATE: 13-MAR-1991
APPLICATION INFORMATION:
APPLICATION INFORMATION:
APPLICATION SATAN
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REGISTRATION NUMBER: 32,141
REGERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFOAMATION:
TELECOMMUNICATION INFOAMATION:
TELECOMMUNICATION INFOAMATION:
TELECOMMUNICATION INFO
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LENGTH: 829 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 20001-4597
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609 QRLDLENAVLMQELMAMKEEMAELKAQLYLLEKEKK---
                                         402 SPL-LORP---OHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAW 457
                                                                                            550
                                                                                                                                   359 ADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKG-----EPLG----PRGQD
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                                                                                                                                                                                                                                                                                                                                                                                                                            186
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                                                                                          TSSTASSCDTEFTKEDEQ-RLKDYIQQLKNDRAAVKLTMLELESIHIDPLSYDVKPRGDS 608
                                                                                                                                                                                                                                   ----DDRSQSREHMGESLSLKAGG--GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMA 358
                                                                                                                                                                                                                                                                                                                                                                           ETERLNSRIEHLKSQNDLLTITLE-----ECKSNAERMSMLVGKYESNATALRLALQY 451
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1001 G Street
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--ALELKLSTREAQEQAY 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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S	B &	Db Qy	Query Best 1 Match	US-08-	Дb	Qy	망	9
186 DERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVWLVKRL 245 : : : : : : : : : :	137 KVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFED 185	81 PSPGEEKTIQVDEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDTSPGLKCLLK 136	4.1%; Score 110; DB 2; Length 829; Best Local Similarity 18.4%; Pred. No. 0.028; Matches 92; Conservative 81; Mismatches 198; Indels 130; Gaps 19;	SULT 14 -08-446-550-2 Sequence 2, Application US/08446550 Septicant Witte Raymond Applicant White Raymond Applicant White Raymond Applicant Invention: Humans Under Graph Under Carrier US/08100000000000000000000000000000000000	721 AEFTNAIRREKKLKARVQELV 741		661 LVHIEHLKSEVEEQKEQRMRSLSSTSSGSKDKPGKECADAASPALSLAELRTTCSENELA 720	458 TWMVLTVLWQIQILPDQTFTALQ

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RESULT 15
US-08-923-992A-8
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                                                              US-08-923-992A-8
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Query Match
Best Local Similarity
                                                                                                                                                                TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION UNDER: US 60/024,707
PILLING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC
TITLE OF INVENTION: Streptococcal Beta
                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                   TYPE: amin
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ZIP: 20005
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1100 New York Avenue,
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Score 103; DB Pred. No. 0.25;
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EIPSNPEYGIQKSI
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Search completed: July 24, 2003, 12:16:20 Job time: 48.2635 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

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10: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

13: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

14: /cgn2 6/ptodata/2/pubpaa/US10 PUBCOMB.pep:*

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16: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

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18: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
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US-10-106-698-5604
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US-10-162-435-2
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US-10-162-698-5295
US-10-106-698-5295
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                 US-09-823-187-88
US-09-764-864-823
US-09-764-864-116
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Sequence 28, Appl
Sequence 5604, Appl
Sequence 5604, Appli
Sequence 2, Appli
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Sequence 88, Appli
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Sequence 823, Appl
Sequence 823, App
Sequence 8161, Ap
Sequence 1161, Ap
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US-10-225-486-57	US-09-745-763-19	US-10-144-649A-425	US-09-854-133-425	US-09-738-973-425	US-09-908-500A-2	US-10-154-386-2	US-10-029-217A-4	US-09-925-301-1094	US-10-017-754-1934	US-09-902-941-1934	US-09-864-761-37015	US-09-934-455-164	US-09-987-107-58	US-09-987-107-7	US-09-815-242-12173	US-09-815-242-5680	US-09-771-161A-220	US-09-771-161A-219	US-10-102-806-678	US-10-200-154-4	US-09-954-043-4	US-09-764-864-1282	-10-156-	-368-	-10-	US-10-153-668-468	US-09-823-187-87	US-10-171-311-113	US-10-151-569-2
Sequence 57, Appl	\mathbf{H}	425	429	425		2	Sequence 4, Appli	109	1934,	Sequence 1934, Ap	37019		58,	e 7, 1	121	5680,	Sequence 220, App	219,	67	о 4		<u></u>	14518	e 20	e 357,	e 468,	e 87, J	e 113,	Sequence 2, Appli

ALIGNMENTS

PUBLICACTOR.

REPEREAL INFORMATION:

APPLICANT: Takaaki Sato and Junn Yanagisawa

APPLICANT: Takaaki Sato and Junn Yanagisawa

TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN

TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF

TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Verent Application DATA:
APPLICATION NUMBER: US/08/681,219
FILING DATE: 22-UUL-1996
CLASSIFICATION: 435 TELEFAX: (212) 391-05 INFORMATION FOR SEQ ID NO: ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/48962/JPW/JKM
TELECOMMUNICATION INFORMATION: SEQUENCE CHARACTERISTICS:
LENGTH: 828 amino acids CORRESPONDENCE ADDRESS: CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036 STREET: TELEPHONE: (212)
TELEFAX: (212) 39 STRANDEDNESS: ADDRESSEE: amino acid E: Cooper & Dunham LLP 1185 Avenue of the Americas 391-0525 -- NO: 28: single 278-0400

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RESULT 2
US-09-816-669A-14
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09816669A Patent No. US20020137019A1
                                                                                                                           SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                 APPLICANT: MARKUS, Steven
TITLE OF INVENTION: TRANSCRIPTION FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL
TITLE OF INVENTION: TRANSCRIPTION FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL
TITLE OF INVENTION: PROTEINS AS TARGETS FOR ANDROGEN RECEPTOR-DEPENDENT DISEASES
FILE REFERENCE: GARABEDIAN=1.1A
CURRENT APPLICATION NUMBER: US/09/816,669A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/225,618
PRIOR APPLICATION NUMBER: 60/25,618
PRIOR PILING DATE: 2000-08-15
PRIOR FILING DATE: 2000-03-24
NUMBER: 60/191,768
PRIOR FILING DATE: 2000-03-24
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                                                                LENGTH: 2783
TYPE: PRT
ORGANISM: Human
                                                                                                                                                SOFTWARE: PatentIn version 3.1
                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GARABEDIAN, Michael APPLICANT: TANEJA, Samir
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      4.0%; Score 108.5;
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      DB
      10;
  Length 2783;
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; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (327)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5604
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US-10-106-698-5604
Sequence 5604, Application US/10106698
Publication No. US20030109690A1
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Best Local (
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NUMBER OF SEQ ID NOS: 8564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/163,280
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                              202 DIFEETAQVSPPRGKEKRQWRARMPLLSVQP--
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252 LCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKETPSEDDRSQSR 311
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                                                                                                                       49 KALKGYIKHEARKGN---
                                                                                                                                                                                                                                            82 SPGEEKTIQVPEAKLAGFLRYISMONLAVIFDLLLDSYRTAREFDTSPGLKCLLKKVSGI 141
                                                                                                                                                                                                                                                                                       78;
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tive 45; Mismatches
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                                                                                                                                                                                                                                                                                   Score 102.5; D
Pred. No. 0.79;
3; Mismatches
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                                                                              -VSNADWVWLVKRLHKLCME 251
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                                                                                                                                                                                                                                                                                                                         Length 453;
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                                        ----TE 127
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RESULT 4 US-09-836-499-2

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; ORGANISM: Homo sapiens US-09-836-499-2
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TITLE OF INVENTION: 16051A AND 16051B, NOVEL HU
TITLE OF INVENTION: FAMILY MEMBERS AND USES THI
FILE REFERENCE: 10448-043001
CURRENT APPLICATION NUMBER: US/09/836,499
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 60/197,507
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                           146 NLYRQSAMSFNIYFHALVCAVLTNQETITA----EQVKKVLFEDDERSTDSSQQCSSEDE 201
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                                                                                                                                                                                                                                256 YIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMG 315
                                                                                                                                                                                                                                                                                                                                202 DIFEETAQVSPPRGKEKRQWRARMPLLSVQP-----VSNADWVWLVKRLHKLCMELCNN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     893 SLLSHTQDQDRNTEELDMAGVQSLVPRLRHQLSFLPLKGAGSSCPPSPPEISAGEIYFVE 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 839 FNMAVRMIQNSPDNI-----ELIISQSKGVGGNNPDEEKNGTANSGVSSTDILSFGYQG
                                            368 TEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 FMLDTQCSPKTPNNFDHAQSCQLIIELP-----PDEKPNGHTKKSVSFREIVV----
                                                                                                                                                                                      FVQM--EKESCSH----LKSDLVRIKRLFPGQPAEENGAIAAGDIILAVNGRSTEGLIFQ 1146
                                                                                                                                                                                                                                                                                      SMGDERTAVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LA---GFLRY-----ISMONLAVIFDLLLDSYRTAREFDTSPGLKCLLKKVSGIGGAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRKQQHNLSAFPKEVKVEKKG--EPLGPRGQ----DSPLLQRPQHLMDQGQMRHSFSAGP 425
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  DQEDSWRD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVKEDGTLGFSVTGGINTSVPYGGIYVKSIVPGGPAAKEGQILQGDRLL--QVDGV---- 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLLSH-----PSPGEEKTIQVPEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASQSTLGLKGSLKRSAISAAKTGVRFSAATKDNE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE----SSKPGKNKRTAITTPNFKKLHEAHFKEM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FONHEKOESODLRATAKVP----SP----PDEHOEAENAVSSGNRDSKVPSEGKKSLYT 178
                                                                                                                                                                                                                                                                                                                                                                               -----ILCG-LTHKQAVQCLKGPGQVARLVLE--RRVPRSTQQCPSAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KHFEEHNSMNELKQQPINKGGVRTPVPPRGRLSVASTPISQR----RSQGR---
                                                                                             EVLHLLRGAPQEVTLLLCRPPPGAL---PEMEQEWQTPELSADKEFTRATCTDSCTSPIL
                                                                                                                                       ESLSLKAGGGD----LLLPPSPKVEKKDPSRKKEWW--ENAGNKIYTMA--ADKTISKLM 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.7%;
-SASP-----DAGEGLGLRPESS----QKAIREAQWGQNRERPWASSLT 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100.5; D
Pred. No. 6.2;
66; Mismatches
                                                                                                                                                                                                                                                                                    ----LVTALPGRPSSCVSVTDGPKFEVKLKKNANGLGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN PDZ
THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo
US-10-162-435-2
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CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/836,499
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: PCT/US01/12420
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 60/197,507
PRIOR APPLICATION NUMBER: US 60/197,507
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                         SEQ ID NO 2
LENGTH: 1294
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                                                                                             Matches
                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Leiby , Kevin R.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE-ASSOCIATED PROTEIN AND
TITLE OF INVENTION: CELL SURFACE PROTEIN FAMILY MEMBERS
FILE REFERENCE: 10448-189001
                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/891,008 PRIOR FILING DATE: 2001-06-25 PRIOR APPLICATION NUMBER: PCT/US01/19963
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                                                                                           Local Sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-06-25
APPLICATION NUMBER: US 60/214,220
FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/934,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 10/041,406 FILING DATE: 2002-01-08
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APPLICATION NUMBER: US 09/886,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/205,674 FILING DATE: 2000-05-19
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APPLICATION NUMBER: PCT/US01/16013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/260,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US02/00275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/20059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                   Similarity
FNMAVRMIQNSPDNI-----ELIISQSKGVGGNNPDEEKNGTANSGVSSTDILSFGYQG 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSFSAGPELLRQDKRPRSGSTGSSLSVSVR
                                       FMLDTQCSPKTPNNFDHAQSCQLIIELP-----PDBKPNGHTKKSVSFREIVV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curtis , Rory A.
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                                                                                             Conservative
                                                                                                                                                                                                            sapiens
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                                                                                                            3.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60/213,963
                                                                                                                                                                                                                                                                                                          Version
                                                                                                            Score 100.5;
Pred. No. 6.2;
                                                                                             Mismatches
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                                                                                                                                       DB 15;
                                                                                             194;
                                                                                             Indels
                                                                                                                                       Length 1294;
                                                                                           139;
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Matches

111;

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Query Match Best Local Similarity

LENGTH: 1294 TYPE: PRT

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US-09-836-499-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09836499 Publication No. US20030027316A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5
                                                                                                                                                                                                                                        Matches 111;
                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 10448-043001
CURRENT APPLICATION NUMBER: US/09/836,499
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 60/197,507
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 16051A AND 16051B, NOVEL TITLE OF INVENTION: FAMILY MEMBERS AND USES
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \PPLICANT: Meyers, Rachel
                                                                                                                                                                                                                                                                                                                                           LENGTH: 1309
                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1204
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                                                                                                                                                                                                        10 FMLDTQCSPKTPNNFDHAQSCQLIIELP-----PDEKPNGHTKKSVSFREIVV----
                          NLYRQSAMSFNIYFHALVCAVLTNQETITA----EQVKKVLFEDDERSTDSSQQCSSEDE
                                                                                    LA---GFLRY-----ISMQNLAVIFDLLLDSYRTAREFDTSPGLKCLLKKVSGIGGAA 145
                                                                                                                   SLLSHTQDQDRNTEELDMAGVQSLVPRLRHQLSFLPLKGAGSSCPPSPPEISAGEIYFVE
                                                                                                                                                SLLSH----
                                                                                                                                                                            FNMAVRMIQNSPDNI-----ELIISQSKGVGGNNPDEEKNGTANSGVSSTDILSFGYQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSFSAGPELLRODKRPRSGSTGSSLSVSVR 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQEDSWRD----SASP-----DAGEGLGLRPESS---QKAIREAQWGQNRERPWASSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVIHILIRGAPQEVTLLICRPPPGAL---PEMEQEWQTPELSADKEFTRATCTDSCTSPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESLSLKAGGGD----LLLPPSPKVEKKDPSRKKEWW--ENAGNKIYTMA--ADKTISKLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVQM--EKESCSH----LKSDLVRIKRLFPGQPAEENGAIAAGDIILAVNGRSTEGLIFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIFEETAQVSPPRGKEKRQWRARMPLLSVQP-----VSNADWVWLVKRLHKLCMELCNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLYRQSAMSFNIYFHALVCAVLTNQETITA----EQVKKVLFEDDERSTDSSQQCSSEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVKEDGTLGFSVTGGINTSVPYGGIYVKSIVPGGPAAKEGQILQGDRLL--QVDGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LA---GFLRY-----ISMQNLAVIFDLLLDSYRTAREFDTSPGLKCLLKKVSGIGGAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLLSHTQDQDRNTEELDMAGVQSLVPRLRHQLSFLPLKGAGSSCPPSPPEISAGEIYFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLLSH--
                                                       LVKEDGTLGFSVTGGINTSVPYGGIYVKSIVPGGPAAKEGQILQGDRLL--QVDGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSPESHPHLCKLHQERDESTLATSLEKDVR 1280
                                                                                                                                                                                                                                       Conservative
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ILCG-LTHKQAVQCLKGPGQVARLVLE--RRVPRSTQQCPSAND
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                                                                                                                                             ----QVLLQNLYDILLEEFVKG-----PSPGEEKTIQVPEAK 95
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Pred. No. 6.4;
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APPLICANT: Meyers,
APPLICANT: Glucksm
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CURRENT APPLICATION NUMBER: US/10/162,435
CURRENT FILING DATE: 2002-06-04 PRIOR APPLICATION NUMBER: US 09/836,499 PRIOR FILING DATE: 2001-04-17 TITLE OF INVENTION: NOVEL HUMAN MEMBRANE-ASSOCIATED PROTEIN AND TITLE OF INVENTION: CELL SURFACE PROTEIN FAMILY MEMBERS PRIOR APPLICATION NUMBER: US 60/197,507 PRIOR APPLICATION NUMBER: PCT/US01/12420
PRIOR FILING DATE: 2001-04-17 FILING DATE: 2000-04-18
APPLICATION NUMBER: US 09/891,008 APPLICATION NUMBER: US APPLICATION NUMBER: US 60/214,220 APPLICATION NUMBER: PCT/US01/19963 FILING DATE: 2001-06-25 APPLICATION NUMBER: APPLICATION NUMBER: PCT/US02/00275 FILING DATE: 2000-06-23
APPLICATION NUMBER: US 10/041,406 APPLICATION NUMBER: US 60/213,963 APPLICATION NUMBER: APPLICATION NUMBER: US 09/886,429 APPLICATION NUMBER: US APPLICATION NUMBER: PCT/US01/16013 APPLICATION NUMBER: US 09/860,868 FILING DATE: 2000-06-23 Curtis , Rory A. J. Kapeller-Libermann, Rosana Bandaru, Rajasekhar 10448-189001 NUMBER: PC: 2001-08-2 2001-01-08 2001-05-18 2001-06-25 2001-06-21 2000-05-19 2002-01-08 2001-05-18 2001-08-2 2002-01-08 2001-06-21 PCT/US01/20059 PCT/US01/41811 US 09/934,268 60/260,286 60/205,674 60/226,612

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; SEQ ID NO 5295
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-5295
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US-10-106-698-5295
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-435-5
                                                                                         CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR TILING DATE: 2000-09-28
PRIOR PPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
PRIOR PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
                                                                                                                                                                                                                                                                                     Sequence 5295, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
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NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows
SEQ ID NO 5
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Best Local Similarity 21.8%;
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Pred. No. 6.4;
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RESULT 9
US-09-788-600-5
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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: PCT/US00/22351
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/189,026
PRIOR APPLICATION NUMBER: 60/189,026
PRIOR APPLICATION NUMBER: 60/148,757
PRIOR PILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 7
PRIOR PILING DATE: 1999-08-16
                                                                                                                                                                                                                                                                      US-09-788-600-5
                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
SEQ ID NO 5
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Shi et
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                                                                                                                                                                      Matches
                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Retinoid Receptor Interacting Polynucleotides, Polypeptides, TITLE OF INVENTION: Antibodies FILE REFERENCE: PT017P1
                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 SDAP
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411
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                                                                                                                                                                                             Similarity
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                                                                         IKSLKEKLLLEE---EPTT----SHGQSSQGIVEETSEE-----GNSVPASQSVAALTS
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                                                                                                                                                                 ; Score 98; DB 9; Le
; Pred. No. 1.8;
54; Mismatches 115;
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PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 4700
LENGTH: 446
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   Matches
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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246 HKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTP-----STGGF 296
                                       138 SGGQKQRLALAGVIAMGARLILLD-EPTANLDPQGQKDVVAAVDRVVQETGATLIVVEHR 196
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                                                                                  --GKEKR----QWRARMPLLSVQPVSNAD---
                                                                                                                         SIGLVLQDPDSQVIASRIGDDVAFGCENLQIPREEIWPRVERALELVGLDLPLSHPTKYL 137
                                                                                                                                                                   QVKKVLFEDDER-----STDSSQQCSS---EDEDIFEETAQ------VSPPR---
                                                                                                                                                                                                            FEIAPGERILLTGASGAGKSTLL--
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OCHIAI, KEIKO
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TATEISHI, NAOKO
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21.1%; Pred. No.
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APPLICANT: DUNPHY, William
TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS OF USE THEREOF
FILE REFERENCE: CTI1120-1
CURRENT APPLICATION NUMBER: US/09/982,091A
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/241,246
PRIOR APPLICATION NUMBER: US 60/241,246
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                       442 SLSVSVRDAEAQIQAWTNMVL--TVLNQIQILPD----QTFTALQPAVFPCISQLTCH 493
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                                                                                                                                                                   240 VKNKVKKHKKKEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 SDEEIFVSKKLKNRKVLQDSDSETEDTNASPEKTTYDSAEEENKENLYAGKNTK-----
                                                                                                                                                                                                                                                   MEKIRQLKKKETKNQEDDVEQPFNDSGCLLVDKDLFETGLEDENNSPLEDEESLESIRAA 239
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                                                                                  -KEALKQLHSETQRLIRESALNLPYHMPENKTIHDFFKRKP
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US-09-823-187-88
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 88
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APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/823,187
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PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
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FILING DATE: 2000-04-06
APPLICATION NUMBER: 60/195,005
FILING DATE: 2000-04-06
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APPLICATION NUMBER: 60/195,343
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                                                                                                                                                                                                                                                                              299 KETPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRK-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                               184 EDDERSTDSSQQCSSEDEDIFEETAQVSPPR-----GKEKRQWRARMPLLSVQPVSNADW 238
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QKEKRGRPDEKPRARPVKVERTRKRSEGLSLE---RKGEKKKEP-----SVEERLQKLH 475
                                   -----RQDKRPRS-----GSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILP 472
                                                                                                                                                          DRISEW-----KRRDEERRRELEARRREQEEELRRLREQEREEKERRKERAERG 364
                                                                                                                                                                                                ---KEWWENAGNKIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVKVEK-----KGEPL 395
                                                                                                                    GPRGO----DSPLLQRPQHLMDQGQMRHSFS-----AGPELL-----
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                                                                                                                                                                                                                                                                                                                                                                                                           EEDSESPSESEKTSDQDFTPEKKTA-ARPPRRGPLGGRKKKK-----VPSASDSD-
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Shimkets, Richard A
Spaderna, Steven K
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Padigaru, Muralidhar
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                                                                                                                                                                                                                                                                                                                           --SKADSDGAKEEPVV-----
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Pred. No. 4.
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COTHER INFORMATION:
US-09-764-864-823
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 823
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APPLICANT: Rosen et al.
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OTHER INFORMATION: )
NAME/KEY: SITE
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CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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OTHER INFORMATION:
NAME/KEY: SITE
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ORGANISM: Homo
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OTHER INFORMATION:
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OTHER INFORMATION:
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 G----GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYKKRKQQHNL 379
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                                                                                                                                  VKRLH-----KLCMELCNN---YIQMHLDLENCMEEPPIFKGD-----PFFILPSFQS 286
                                                                                                                                                                      KEDPSLKDVEDTMVETIALCQRNSHNLNQQQREALW---FPLLEAMMAPQKLSSS----A 491
                                                                                                                                                                                                      SQQCSSED-EDIFEETAQV----SPPRGKEKRQ--WRARMPLLSV----QPVSNADWVWL 241
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                                 EQTLLETTTSLLNQDLHWSLCNLRASVTRGLNPKQDYCSICLQQYKRRQEMADEIIVFSC
                                                                                                   IPHLHSEALKSLTMQVLNSMAAFIALPSILQRILQDPVYGKGKLGEIQGLILGMLDTFNY
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US-09-764-864-1161
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                                                           Sequence 1574 Application US/09764864
Patent No. US2002012753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1161
LENGTH: 555
TYPE: PRT
ORGANISM: Homo sapiens
S-09-764-864-1161
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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Best Local Similarity
Matches 64; Conserv
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
'SQFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAA-----DKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQH 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DFATVRE-----TLEAGNYE-----SPMELCKDVRLIFSNSKAYTPSKRSRIYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6%; Score 96; DB 10; Length 555; ilarity 21.0%; Pred. No. 4.4; Conservative 46; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              PQL--KSESSTSAFSTPTRSIPPRHNAAQINGKTESSSVVRTRSNR
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LENGTH: 555
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                                                                                                                           411
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245 VVVDP 249
                                         468 IQILP 472
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                                                                                                                        LMDQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWT----NMVLTVLNQ 467
                                                                                                                                                                                                             MAA-----DKTISKIMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQH 410
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                                                                                                                                                                                                                                                             -----DFATVRE-----TLEAGNYE-----SPMELCKDVRLIFSNSKAYTPSKRSRIYS 139
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21.0%; Pred. No. 4.4;
                                                                                    POL--KSESSTSAFSTPTRSIPPRHNAAQINGKTESSSVVRTRSNR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Mismatches 113; Indels 82;
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Search completed: July 24, 2003, 12:18:14 Job time : 63.1151 secs

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Result
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Maximum DB seq length: 2000000000
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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228	168 1485	1383 115 115	<u> </u>		submitted to GenBank, A; Description: FAB1: a A; Reference number: A5 A; Accession: A55997 A; Molecule type: DNA A; Residues: 1-2274, 'R' A; Cross-references: GB (C. Cenerics)	Accession: 856274 Molecule type: DNJ Residues: 1-2278 Cross-references: Yamamoto, A.; Kosl	74 Propro		30 100. 31 100. 32 100. 33 100. 33 99. 35 99. 36 99. 36 99. 37 99. 39 99. 40 98. 41 98. 42 98.
		LMLQD	σ	ri 1	bmitted to GenBank, Augu Description: FAB1: a nov Reference number: A55997 Accession: A55997 Molecule type: DNA Residues: 1-2274,'R',227 Cross-references: GB:U01		SULT 1 6274 6274 Alternate names: prottAlternate names: prottSpecies: Saccharomyce: Date: 10-Sep-199 #setAccession: S56274; AS: Murakami, Y.; Nattou, bmitted to the EMBL Description: Analysis Reference number: S56		2
ADWVWLVKRLI	TNQETITAEQVKKVLFED : : : : TDISRITAKQLKKLFY	LESROY - LOWER LEGENCY -LYYKILEKINNFYGSVLSRLERIKLD -LYYKILEKINNFYGSVLSRLERIKLD -LYYKILEKINNFYGSVLSRLERIKLD -LYYKILEKINNFYGSVLSRLERIKLD -LUYKILEKINNFYLD -LUYKILEKINNFYLD -LUXHILLELL	DHAQSCQI	5 4 2 1 − 1 − 1 − 1 − 1 − 1 − 1 − 1 − 1 − 1 −	el ge 6-227	:D506	acch sein sein sein sein sein sein sein sein		453 2 484 2 947 2 1268 2 649 2 1534 2 1534 2 1207 2 1207 2 1207 2 1750 2 960 2 1750 2 1750 2 1750 2
LSVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCME :: : :	TNOETITAEQVKKVLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKE : : : :	:: :	< ⊢	MIPS:YFR019w osphatidylinosit linositol-4-phos Score 126; DB Srod, No. 0.98;	3 e required for <yam> ID:g392993; PID</yam>	NID:g836685;	wrenisiae) YFR019w YFR019w xrevisiae rec_revisiae 10-Sep-1999 # Hagiwara, H.; Shibata, T Library, May 1995 the nucleotide sequence o	ALIGNMENTS	\$50248 \$60943 \$70657 \$44125 \$456710 \$56734 \$62962 \$141622 \$184781 \$721931 \$721931 \$741812 \$141812 \$141812 \$141812 \$141812 \$141812
EPPIFKG	KRQWRARMPL LPL	LDTFYADSPCDQHLPLNLVIKSLY-DKAVNWNSTFALFAKSYLPSE 1	Gaps FREIVVS	4-phosphate 5-kinase te 5-kinase homology Length 2278;	endocytic-vacuolar pathway and N:AAA81360.1; PID:g398498	PIDN:BAA09258.1; PID:g836774;	text_change 16-Jun-20 .; Ozawa, M.; Sasanum f chromosome VI from		SSF2 protein - yea RUD3 protein - yea probable adi - Myc high density lipop homeocic protein H DNA topoisomerase ribosome receptor, hypothetical prote probable ABC trans hypothetical prote hypothetical protein - F4489.6 protein - DNA polymerase orf hypothetical protein hypothetical protein - DNA polymerase orf hypothetical
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114; CONSERVATIVE 63; MISMATCHE 33 IIELPPDEKPNGHTKKSVSFREIVVSLL 34 IIELPPDEKPNGHTKKSVSFREIVVSLL 177 IERLSEDQLLGDQGSEDISFEEIQVDLLLESG 80 GPSPGEEKTIQ-VPEAKLAGFLRYISN	Qy 433 RPRSGSTGSSL-SVSVRDAEAQI 454 Db 1707 PLHSRSGNILSSANVKTLEAPV 1729 RESULT 2 Sinc finger protein - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 08-Dec-2000 C;Accession: A45172; S27802 C;Accession: A45172; S27802 C;Ritein, R.D.; Meyer, B.J. Cell 72, 349-364, 193 A;Title: Independent domains of the Sdc-3 protein control sex determination and dosage d A;Reference number: A45172; MUID:93161411; PMID:8431944 A;Accession: A45172 A;Status: preliminary A;Accession: A45172 A;Rocession: A45173 A;Cross-references: EMBL:M85149; NID:g156440; PIDN:AAA28144.1; PID:g156441 A;Experimental source: strain N2 A;Roces: sequence extracted from NCBI backbone (NCBID:124842) C;Genetics: A;Genetics: A;Genetics: A;Genetics: D;A binding; nucleus; zinc finger Query Match Query Match A;&; Score 124; DB 1; Length 2150; Best Local Similarity 20.6%; Pred. No. 1.3;	1531 EGLKDVE
HPEQLPVSASEKANNQIVPEVEVEGSVVPVTNQQETITAEQ LLKKVSGIGGAANLYRQSAMSFNIYFHALLVCAVLTNQETITAEQ	RESULT 3 T19450 Typothetical protein C25D7.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T19450 R;Ainscough, R. submitted to the EMBL Data Library, October 1996 A;Reference number: Z19125 A;Accession: T19450 A;Reference number: Z19125 A;Reference n	Qy 360 DKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPR 398

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T41551

hypothetical protein SPCC70.05c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41551
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z22001
A;Accession: T41551
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A;Residues: 1-781 <WOO>
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A; Map position: 2
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A; Molecule type: mRNA
A; Residues: 1-1148 <ZHA>
A; Cross-references: EMBL: APO30234;
A; Experimental source: HeLa cells
C; Keywords: pre-mRNA splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           splicing factor Sip1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
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Mol. Cell. Biol. 18, 676-684, 1998
Mol. Cell. Biol. 18, 676-684, 1998
A;Title: Sipl, a novel RS domain-containing protein essential A;Reference number: Z16554; MUID:98107652; PMID:9447963
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                                                                                                                                                                                                                                                                                          94;
                                                                                                                                                                                                                                                    1 RIRAMAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELP---PDEKPNGHTKKSVSFREIVV
                                                                                                                                                                                                                                                                                                           Similarity
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EKNESLTEHPRSTELPKTHIEQIQKHFSEDNNEMIPMECDSFCSDQNES----
                                TNOETIT-----
                                                                                                        LAVIFDLLLDSYRTAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVL 167
                                                                                                                                                                            SLLSHQVLLQNLYDILLEEFVKGP----SPGE-----EKTIQVPEAKLAGFLRYISMQN 107
                                                                                                                                                                                                                QISGLSQSEVKTDV-CTVHLPNDFPTCLTSESKVYQPVSCPLSDLSENVESVVNEEKITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPST-----GGF-----
                                                                    IATCDTFGNEDFNNIQDSENN----
                                                                                                                                          SSLV-EITEHKDFTLKTEELIESPKLESSEGEIIQTVDRQSVKSPEVQLLGHVETEDVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLVSRVRDNYANTSYESWPHSTEFDMFTYAVSGSLKLTPQGTGFDCINPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNREGGNGSYFDGPLTASPTPSSPTG-TPNSMSKSPSL----SSLASTGASYRPGPSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHKNTSSHPSSPVNGKS--SDIHKSQSYQHLKNS-----PPNSRTARKPVPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PHHSGLKNLLEKA-----MHPGHKSNANSPTSESPSKGFGSFINNHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LSVSVRD--AEAQIQAWTN-----MVLTVLNQIQILPDQT-FTALQPA 482
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - ANSASHNLGSTKSPNGNAKESLSRSAELPSKAKPMEINNGYRKKPSPLSPNSSI
                                                                                                                                                                                                                                                                                 4.1%; sc.
/ 18.5%; Pre/
**** 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.1%; Score 111; DE 21.4%; Pred. No. 2.9; ative 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGSS------
                                ----AEQVKKVLFEDDER--STDSSQQCSSEDEDIFEETAQVSPP 213
                                                                                                                                                                                                                                                                                                       Score 111; DB 2;
Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         from
                                                                                                                                                                                                                                                                                                                                                                                                  NID:g2822459; PIDN:AAC39565.1;
                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                          183;
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                                                                                                                                                                                                                                                                                                                          Length 1148;
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                                                                                                                                                                                                                                                                                          Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                    NLLNTKLEKSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pre-mRNA splicing
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colorectal tumor suppressor protein - human
(7.Species: Homo sapiens (man)
(7.Species: Homo sapiens (man)
(7.Species: Homo sapiens (man)
(7.Species: Homo sapiens (man)
(7.Species: A38434; A331.66
(7.Species: A38434; MUID:91164855; PMID:1848370
(7.Species: A38434; MUID:91164855; PMID:18484870
(7.Species: A38434; MUID:91164855; PMID:18484870
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(7.Species: A38434; MUID:91164855; PMID:18484870
(7.Species: A38434; MUID:9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVSGIGGAANLYRQSAMSF------NIYFHALVCAVLTNQETITAEQVKKVLFED 185
    QRLDLENAVLMQELMAMKEEMAELKAQLYLLEKEKK-----ALELKLSTREAQEQAY
                                               SPL-LQRP---QHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAW
                                                                                            TSSTASSCOTEFTKEDEQ-RLKDYIQQLKNDRAAVKLTMLELESIHIDPLSYDVKPRGDS
                                                                                                                                          ADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKG-----
                                                                                                                                                                                         LKRAHDCRKTAENAAKALLMKLDGSCGGAFAVAGCSVQP-----WESLSSNSHTST
                                                                                                                                                                                                                                  ----DDRSQSREHMGESLSLKAGG---GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMA
                                                                                                                                                                                                                                                                                    SEQCIEAYELLL
                                                                                                                                                                                                                                                                                                                            HKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKETPSE-
                                                                                                                                                                                                                                                                                                                                                                         ETERLNSRIEHLKSQNDLLTITLE-----ECKSNAERMSMLVGKYESNATALRLALQY
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ilarity 18.4%;
Conservative 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
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Pred. No. 3.8;
81; Mismatches
                                                                                                                                                                                                                                                                                    ·ALAESEQSLILGQFRAAGVGSSPGDQSGDENITQM
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                                                                                                                                            ----EPLG----PRGQD
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                                 A41948
alpha-fetoprotein enhancer-binding pr
N;Alternate names: ATBF1 protein
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revisic
C;Date: 31-Dec-1993 #sequence_revisic
C;Accession: A41948
R;Morinaga, T.; Yasuda, H.; Hashimoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data A; Reference number: Z19841 A; Accession: T24103
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                                                                                                                                                                                                            RESULT 9
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A;Map position: 4
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Best Local
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                                                                                        31-Dec-1993 #sequence_revision
iga, T.; Yasuda, H.; Hashimoto, T.; Higashio,
l. Biol. 11, 6041-6049, 1991
A human alpha-fetoprotein enhancer-binding )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VR--QAVREWLGRVGRVYDII
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20.7%;
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  enhancer-binding protein, ATBF1, contains four homeodo
                                                                                                                                                             protein -
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                                                                                            31-Dec-1993
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hypothetical protein R102.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T24103 R;Berks, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-587 <WIL>
A;Cross-references: EMBL:Z70309; PIDN:CAA94361.1; GSPDB:GN00022; CESP:R102.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 19/2; 111/3; 147/1; 270/2; 407/1; 481/3; 529/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 SSQQCSSEDEDIFEETAQVSPPR----GKEKRQWRARMPLL-SVQPVSNADWVWLVKRLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 KCLLKKVSGIGGAANLYROSAMSFNIYFHALVCAVLTNOETITAEQVKKVLFEDDERSTD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKLIKLVK--EGETNNLKQGSKLFDDL--TMSCGSLI------
                                                                                                                                                                                     MAADKTISKLMTE---YKKRKQQHNLSAFPKEVKVEKK-----
                                                                                                                                                                                                                                               VSVQPTLEDDMTQKK---------VVKKPSSRPHKK-PSTTRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVKG---PSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTA--REFDTSPGL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVHIEHLKSEVEEQKEQRMRSLSSTSSGSKDKPGKECADAASPALSLAELRTTCSENELA 720
                                                                                                                       LSVQKTVEDDMTQKKVVKKPSSRPHKKPSTMEVILKKKKSAATISKETCQLHTKFGKLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TMDQFDNEEAAVIEDLVQLKRSKEEKEKKKKKKKTKERMDALDELTHVTSNDRISLLSR--
TVTEPNNSPYQNLLDLSFRPSKVQDNPQMFLPPSINPKTATEIKK
                                                          --PRGQDSP----LLQRPQHLMDQGQMRHSFSAGPELLRQDKR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                 KLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESS-----TPSTGGFSGKET 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRKGVQLPISSRKRTLQNLEKKAARFVRSLVFREVG----FLDRHDTCHEREYQLTEDD
                                                                                                                                                                                                                                                                                                         EDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109.5;
Pred. No. 2.5
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                                                                                                                                                                                                                                                                                                                                                                       -IIPDLHNQSRKGLKLAPST---IREHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132;
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   329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129;
                                                                                                                                                                                                                                                  ----HT 224
                                                                                                                                                                                     -GEPLG 396
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                                                                                                                                                                                                                                                                                                                                                                       189
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#text_change 15-Oct-1999

K.; Tamaoki,

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F;128-150/Region: zinc finger CCHH motif F;176-198/Region: zinc finger CCHH motif F;311-332/Region: zinc finger CCHH motif F;340-361/Region: zinc finger CCHH motif F;448-471/Region: zinc finger CCHH motif F;489-509/Region: zinc finger CCHH motif F;517-538/Region: zinc finger CCHH motif F;633-655/Region: zinc finger CCHH motif F;634-706/Region: zinc finger CCHH motif F;684-706/Region: zinc finger CCHH mo
                                                                                                                           RESULT 10
T41788
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A;Molecule type: mRNA
A;Residues: 1-2783 <MOR>
global transactivator orf42 - Bombyx mori nuclear polyhedrosis virus (isolate C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV A;Variety: isolate T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;809-958/Region: glutamine-rich
F;1071-1092/Region: zinc finger CCHH motif
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C;Superfamily: alpha-fetoprotein enhancer-binding protein; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation; zinc f
E;72-94/Region: zinc finger CCHH motif
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F;1799-1820/Region:
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F;1329-1385/Domain:
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A;Map position: 16q22.3-16q23.1
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F;2545-2566/Region:
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;2611-2633/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       376 TTPEMVMPSSMFLPAAVPDRDGNSNLEEAGK--QPETSEDLGKNILPSASTEQSGD--LK 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 KHLQQHESGVEGE-----SCYYHCVLCNYSTKAKLNLIQHVRSMKHQRSESLRK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 LQRLQKGLPEEDEDLGQIFTIRRCPSTDPEEAIEDVEGPSETAADPEELAKDQEGGASSS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 4.0%; Score 108.5;
Similarity 20.6%; Pred. No. 28;
73; Conservative 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                             PSPKVEKKDPSRKKE-----WWENAGNKIYTMAADKTISKLMTEYK----KRKQ 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D----VNRLRVHAMTQHSVQPMLRCPLCQDMLNNKIHLQLHLTHLHSVAPDCVEKLIMTV 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QAEKELTDSPATSKRISPPGSSES----PLSSKRPKTAEEIKPEQMYQCPYCKYSNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DWVWLVKRLH-----KLCMELCNN--YIQMHLD----LENCMEEPPIFK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQP-----
                                                                                                                                                                                                                                                                                   PSP----ADPGSVREDSGFICWKKGCNQVF----KTSAALQTHFNEVHAKRPQ 476
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zinc finger CCHH motif
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homeobox homology <HOX1>
homeobox homology <HOX2>
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zinc finger CCHH motif
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R;Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus A;Reference number: 222020; MUID:99281911; PMID:10355780
A;Accession: T41788
                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1173 <CON>
A;Cross-references: EMBL:U70844; PIDN:AAB09095.1; GSPDB:GN00028; CESP:ZK154.5
A;Experimental source: strain Bristol N2; clone ZK154
A;Experimental source: strain Bristol N2; clone ZK154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: isolate C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-506 <KAM> A;Cross-references: EMBL:L33180; PIDN:AAC63717.1 A;Experimental source: isolate T3
                                                                                                                                                                             A; Map position: X
A; Introns: 48/3; 126/3; 163/1; 628/3; 833/3; 915/2; 1105/2
                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, September 1996
A;Description: The sequence of C. elegans cosmid ZK154
A;Reference number: Z20119
A;Accession: T25985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ZK154.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T25985
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                                                                                                                                                                                                                                        ;Gene: CESP:ZK154.5
                                                                                                                                                                                                                                                                 Genetics:
                                                                                              Matches
                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 DSTNRIKSIIKKIV------LKRDKSEISFNIPKH------TVEYV-HVNFN
                                           167 LTNQETITAEQVKKVLFEDDERSTDSSQQCSSEDEDIF-----EETAQVSPPRGKEK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 DTSPGLKCLLKKVSGIGGAANLYR-QSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFE
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66; Conserv
                                                                                                                  Similarity
LAKVAVIRAANVQKILEKRSLGKISTGGQAAAQDEEIFRYVTSNGNSELLNKMPNRG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FQS--ESSTPSTGGFSGKETPSED-----DRSQSREHMGESLSLKAGGGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LROIC---CHPYLAMHGRNLLETNDCFKMDYMSSKCKRVLDLVDDILNTSDDKIILVSQW 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHKLCMELCNNYIQMH----LDLENCME------EPPIFKGDPFFILPS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.0%; Score 108; DB ilarity 21.6%; Pred. No. 2.7; Conservative 53; Mismatches
                                                                                              Conservative
                                                                                         4.0%; Score 108; DB 22.2%; Pred. No. 8.8; tive 31; Mismatches
                                                                                                                                    DB 2;
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                                                                                                                                         Length 1173;
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	Db 1125STPSTGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPPS 332 Qy 288SSTPSTGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPPS 332 Db 1147 FGDSSSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	
	Query Match 4.0%; Score 108; DB 2; Length 1912; Best Local Similarity 20.3%; Pred. No. 18; Matches 73; Conservative 39; Mismatches 137; Indels 110; Gaps 176 EQVKKVLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSN :- - : : : 1076 KRVKKILDDTDNQATRNSRSSSSASSISESSESTTSTPSSSSDSDNRAS	
	A;Reference number: S55680; MUID:95322425; PMID:7599159 A;Accession: S55681 A;Status: preliminary A;Molecule type: protein A;Residues: 1628-1639 <yam> C;Superfamily: vitellogenin C;Keywords: egg yolk; glycoprotein; liver; phosphoprotein C;Keywords: egg yolk; glycoprotein; liver; phosphoprotein F;1-15/Domain: signal sequence #status predicted <sig> F;16-1912/Product: vitellogenin I #status predicted <mat></mat></sig></yam>	
<u>. j.</u> .	A;Accession: T29088 A;Accession: T29088 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Rolecule type: mRNA A;Residues: 1-1912 <mab> A;Residues: 1-1912 <mab> A;Cross-references: EMBL:D89547; PIDN:BAA13973.1 A;Cross-references: liver A;Cross-reference: liver A;Cross-reference: liver R;Yamamura, J; Adachi, T; Aoki, N.; Nakajima, H.; Nakamura, R.; Matsuda, T. Biochim. Biophys. Acta 1244, 384-394, 1995 A;Title: Precursor-product relationship between chicken vitellogenin and the yolk prote</mab></mab>	
	RESULT 12 T29088 Vitellogenin I precursor [validated] - chicken Vitellogenin I precursor [validated] - chicken N;Contains: lipovitellin I; lipovitellin II; phosvitin; yolk glycoprotein 42K C;Species: Gallus gallus (chicken) C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000 C;Accession: T29088; S55681 R;Mabuchi, N.; Yamamura, J.; Adachi, T.; Aoki, N.; Nakamura, R.; Matsuda, T. submitted to the EMBL Data Library, November 1996 A;Bescription: cDNA cloning and estrogen-induced expression of chicken vitellogenin I. A;Reference number: Z20557	
	Qy 409 -QHLMDQGQMRHSFSAGPELLRQDKRPRS 436	
	QY 382 FPKEVKVEKKGEPLG-PRGQDSPLLQRP	
	Qy 332SPKVEKKDPSRK-KEWWENAGNKIITMAADKTISKLMTEYKKRKQQHNLSA 381	
	Qy 219 RQWRAMPLLSVQPVSNADWVWLVKKLHKLCMELCNNYIQMHLDLENCMEEEPIFKG 275 Db 247 -SFAKGIPLNNKPATSSSSNPKFVPLMNRTIAVPPSTSS 284 Qy 276 DPFFILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPP 331 Qy 276 DPFFILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPP 331 Db 285 RPPIPIFPVVTSAPRPNQRPLPHMAPKLPVKVFIPSLARK 324	
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peptide synthetase [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_cha C;Accession: AE2136
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AE2136
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A;Molecule type: DNA
A;Molecule type: CNA
A;Residuss: 1-2617 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74343.1; PID:g17131737; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2136
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: all2644
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Best Local S
Matches 75
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es 75; Conserv
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                                                                            2593 SGFTPSDFPQMD 2604
                                                                                                                                                                                    2556 DWTY-SKQLHHRQTIATLAENYQQILLSLIQHCL----
                                                                                                                                                                                                                                                                                                                                                                                                     2460 GISLKAIKEQLRQIPDRGISYGLLRYLASP------TIRDTIKAIPLPQVRF- 2505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2288 IDGISWRVFLEDLQLAYQQLSQGQQIQLPPKTTSYQQWANKLQEHTWSADLQAAFNYWTS 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1306 WKQDREAETKRVKSQFNSHSSYDIPNEWETYL-PKVY-----RLRPRSAHTHW 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2348 PTWQQIPPLPVDYAPGSNTMADVDTYSTFLSVTDTQNLLQEVPHAYRTQINDVLLTALVL 2407
                                                                                                                                 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 SPGLKCL---LKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  450 AEAQIQAWTNMYLTVLNQIQI--LPDQTFTALQPAVFPCISQLTCHVTDIRVRQAVREW 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 G--PSPGEEKTI------QVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 QSCQLIIELPPDEKPNGHTKKSVSFREIVVSLLSHQVLLQ-----NLYDILLEEFVK 79
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- - -
                                                                                                                                                                                                                                    DWVWLVKRLH--KLCMELCNNYIOMHLDL-ENCMEEPPIFKGDPFFILPSFQSESSTPST 293
                                                                                                                                                                                                                                                                                                                                                DDERSTDSSQQCSSEDEDIFEETAQVSPPR---GKEKRQWRARMPLLSVQPV-----SNA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFQTWTGENRLLVELEGHGREDLFPSINLSRTMGWFTS-----LFPVLLDIYPSA---DL 2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRAMAQQVEMLDTQCS-----PKTEN----PKTEN-27
                                                                                                                                                                                                                                                                                             -----NYLGQSDQIFSENSLFTPASESIGHSRSSRGKRNTLIEINSIVTGGKLRC 2555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Mismatches 125; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106.5;
Pred. No. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anabaena sp. strain PCC 7120 #text_change 09-Dec-2002
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                                                                                                                                                                                       TPEV 2592
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global transactivator-like protein - Autographa californica nuclear polyhedrosis virus G;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV A;Note: dsDNA virus C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999 C;Accession: B72855

KLAG 98 	Qy 58 SLLSHQVLLQNLY-DILLEEFV	u 0
EIVV 57 :::: KVLI 435	Qy 1 RIRAMAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVV	n o
aps 15;	Query Match 3.9%; Score 104.5; DB 2; Length 830; Best Local Similarity 18.3%; Pred. No. 9.9; Matches 66; Conservative 64; Mismatches 138; Indels 93; G	
; 666/1; 736/1; 80	A;Gene: CESP:F32A6.3 A;Introns: 31/2; 69/3; 111/3; 146/2; 247/3; 290/2; 352/3; 416/3; 632/3	> > (
1388.1; CESP:F32A6	A;Residues: 1-830 <wux> A;Residues: 1-830 <wux> A;Cross-references: EMBL:U40409; NID:g1065447; PID:g1065450; PIDN:AAA813 A;Experimental source: strain Bristol N2 C;Genetics:</wux></wux>	0222
	A;Accession: T16236 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	> > >
	K;WU, X. submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid F32A6. A;Reference number: Z18483	>> o ×
-1999 .	RESULT 15 T16236 Typothetical protein F32A6.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep- C;Accession: T16236	K F COOD
	RÓDKK	۵
·	Qy 372 KRKQQHNLS 380	O
YI 475	Db 420 VGLNLIGGNHIVMLEPHWNPQIELQAQDRISRMGQTKNTYVYKMLNVEDNSIEK	U
TEYK 371	LPPSPK	O
KAGG 324 (CGG 419	Db 362 QWVEYLKIFENFFKQKNIATLMYTGQLKVEDRILAETTFNDAANTOHRILLLSIKCGG	0 0
	307 ĹRQIĆĊHPYLAMHGKNILETNDCFKMDYMS	
FILPS 283	WELCNNYIQMHLDLENCMEEPPIFKGDPF	O
	261	0 ,
	185 DDERSTDSSOOGSSEDENTERERTAOVSBRACKROWRARMSTISVOVV	0
VLFE 184 	Qy 126 DTSPGLKCLLKKVSGIGGAANLYR-QSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFE :: : ::	0 O
Gaps 18;	Query Match 3.9%; Score 105; DB 2; Length 506; Best Local Similarity 22.3%; Pred. No. 4.5; Matches 69; Conservative 49; Mismatches 91; Indels 100; G	
11	A;SCATUB: preliminary A;Molecule type: DNA A;Residues: 1-506 <ayr> A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66672.1; PID:g5591 C;Genetics: A;Gene: Ac-GTA</ayr>	>0>>>
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665 KDQNDPDLWIHLLGVVAEFPAHFSQLIIEASNCLDPLLIMDKLPDDSDIP 714	Db
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607 PFLRKNANYNVNKARKLCSDKGYIEETIYLLAKSGNHYDAVKMMVREYRNMEKVIDYC 664	DЪ
190TDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQ 231	Q
556 SVEPSFVMEKIGRQPKLQLAYLTKLMSRNEGTEFADKAVQLYAEYDQKKLL 606	Db
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496 LYLYERKYESALKILMSCODFQIFNVIDKHQLFDLVKDQITELMNINSERALKLLLDNAD 555	Db
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SUBCELLULAR LOCATION: VACUOLE-ASSOCIATED (POTEN
SIMILARITY: BELONGS TO THE PTDINS(4)P-5-KINASE
SIMILARITY: Contains 1 FYVE-type zinc finger.
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01-FEB-1994
15-SEP-2003
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ZN_FING
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00096; zf-C2H2; I.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M85149; AAA28144.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: CONTROLS BOTH SEX DETERMINATION AND X CHROMOSOME DOSAGE COMPENSATION. THESE TWO FUNCTIONS ACT INDEPENDENTLY.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Developmental protein; Zinc-finger; Metal-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYONIC AND EARLY LARVAL
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Pfam; PF00096; zf-C2H2; 1.
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                                                               TLQEGSSIPSSSHIY---
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                                                                                                     LIKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQ-----ETITAEQ------
                                                                                                                                                                                      GP----SPGEEKTIQ-VPEAKLAGFLRYISMONLAVIFDLLLDSYRTAREFDTSPGLKC 133
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SEX DETERMINATION DOMAIN.
DOSAGE COMPENSATION DOMAIN 2.
C2H2-TYPE 1.
C2H2-TYPE 2.
WW; 7430D77AC784EA46 CRC64;
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Pred. No. 1
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Mismatches
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Q09950;
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                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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                                                                                                     SEQUENCE
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                                                                                                                                                                                                                  PIR; T22981;
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                          Lloyd C.
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  81
                                                    85;
                                                                Similarity
                        SYRTAREFDTS-----PGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTN 169
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SLKDIRELRNSIDQSLIKPPELKMLRSKAAG-----EESKRHAHFESIQEEEKIS
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11 54.6 kDa
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                                                  Conservative
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384
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                                                                                                    54641 MW;
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protein F59Bl0.2 in chr
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                                                  46;
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POLY-SER.
POLY-SER.
POLY-SER.
ARG-RICH.
POLY-ARG.
                                                 Pred. No. 1;
5; Mismatches
                                                              Score 113;
Pred. No.
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                                                                                                    1BD7D31E9DDAA74B CRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91335211; PubMed=1651563;
Nishisho I., Nakamura Y., Miyoshi Y., Miki Y., Ando H., Horii A.,
Koyama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J.
Koyama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J.
Petersen G., Hamilton S.R., Nilbert M.C., Levy D.B., Bryan T.M.,
Preisinger A.C., Smith K.J., Su L.-K., Kinzler K.W., Vogelstein B.;
"Mutations of chromosome 5q21 genes in FAP and colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinzler K.W., Nilbert M.C., Vogelstein B., Bryan T.M., Levy D.B., Smith K.J., Preisinger A.C., Hamilton S.R., Hedge P., Markham A., Carlson M., Joslyn G., Groden J., White R., Miki Y., Miyoshi Y., Nishisho I., Nakamura Y.; "Identification of a gene located at chromosome 5q21 that is mutated in colorectal cancers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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01-NOV-1991 (Rel.
16-OCT-2001 (Rel.
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P23508;
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                                                                                                                                                                                                                                                  GENE LOCATED AT 5021.
TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES TYPES.
DISEASE: IS PROBABLY INVOLVED IN EARLY STAGES OF COLORECTAL
NEOPLASIA IN BOTH SPORADIC AND FAMILIAL TUMORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308
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                                                                                                                                                                                                                                                                                                                                                               253:665-669(1991).
TION: CANDIDATE FOR THE PUTATIVE COLORECTAL TUMOR
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40, Last annotation update)
cancer protein (MCC protein)
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Eukaryota; Metazoa;
                Homo sapiens (Human)
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                             HOXC10
                                       Homeobox protein Hox-C10.
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R -> Q (IN COLORECTAL CANCER)

/FTId=VAR 005144.

A -> V (IN COLORECTAL CANCER)
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S -> L (IN COLORECTAL
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     EMBL; AF255675; AAF67759.1; -.
EMBL; BC001293; AAH01293.1; -.
EMBL; X99684; CAA67999.1; -.
EMBL; X99685; CAA68000.1; -.
HSSP; P02833; 9ANT.
TRANSPAC; T03328; -.
Genew; HGNC:5122; HOXC10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         origin.";
                         PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                               HOXB and HOXC homeogenes in human carcinoma cell lines."; FEBS Lett. 415:263-267(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20296799; PubMed=10835276; de Stanchina E., Gabellini D., Norio Riva S., Falaschi A., Biamonti G.;
                                                                        GO; GO:0003702; F:RNA polymerase II t: GO; GO:0008284; P:positive regulation InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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[1]
                                                             Pfam; PF00046; homeobox; 1.
                                                                                                             MIM; 605560;
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                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear.
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  PS00027; HOMEOBOX_1;
PS50071; HOMEOBOX_2;
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                                     Homeobox; 1.
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RC TISUE Cervix;

RC MEDLINE-22388257; PubMed=12477932;

RX MEDLINE-22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

RA Babas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rahas S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Rahas S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Holtzingez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). SEQUENCE OF 94-106 AND 258-297 FROM N.A.
MEDLINB-98019011; PubMed-9357979;
Flagiello D., Gibaud A., Dutrillaux B., Poupon M.F.,
"Distinct patterns of all-trans retinoic acid depend
HOXB and HOXC homeogenes in human embryonal and smal Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WIT SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR Giacca dependent ы 3 small-cell human DNA replication Peverali Malfoy B.; expression lung \mathbf{s} 엺

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Best Local Similarity
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Q13435;
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DNA_BIND 26
CONFLICT 11
CONFLICT 26
Das R., Zhou Z., Reed R.;

"Functional association of U2 snRNP with the ATP-independent spliceosomal complex E.";

Mol. Cell 5:779-787(2000).

-!- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3B REQUIRED FOR 'A'

COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO TH BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX. BELONGS ALSO TO THE MINOR U12-DEPENDENT SPLICEOSOME, WHICH IS INVOLVED IN THE SEMBLY OF THE 'E' COMPLEX. BELONGS ALSO TO THE MINOR U12-DEPENDENT SPLICEOSOME, WHICH IS INVOLVED IN THE SPLICEOSOME.
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28-FEB-2003 (Rel. 41, Last annotation update)
Splicing factor 3B subunit 2 (Spliceosome associated protein 145)
145) (SF3b150) (Pre-mRNA splicing factor SF3b 145 kDa subunit).
                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                    Gozani O., Feld R., Reed R.;
"Evidence that sequence-independent binding of highly c
snRNP proteins upstream of the branch site is required
of spliceosomal complex A.";
                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eucheria; Primates;
                                                                                                                                                                                                                                                                                              SF3B2 OR SAP145.
                                                                                                                        MEDLINE=20337962;
                                                                                                                                    CHARACTERIZATION OF THE SPLICEOSOME
                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=96154048; PubMed=8566756;
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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118
265
271
342
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                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                         PubMed=10882114;
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265
271
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19.3%;
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A -> G (IN REF. 3).
MISSING (IN REF. 3).
W; BD8127FD43C2A37B C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKEKROWRARMPLLSVOPVSNADWVWLVKRLHKLCMELCNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109.5;
Pred. No. 1.
                                                                                                                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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; Homo.
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Matches 63
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GO; GO:0008248;
GO; GO:0006371;
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SMART; SM00513; SAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF04037; DUF382; 1. Pfam; PF04046; PSP; 1. Pfam; PF02037; SAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spliceosome; mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF RARE CLASS OF NUCLEAR PRE-MRNA INTRON.
SUBUNIT: COMPONENT OF SPLICING FACTOR SP3B WHICH IS COMPOSED FOUR SUBUNITS; SF3B4/SAP49, SF3B3/SAP130, SF3B2/SAP145,
SF3B1/SAP155. SF3B ASSOCIATES WITH THE SPLICING FACTOR SF3A A 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEINS COMPLEX (U2 SMRNP). SF3B2 INTERACTS DIRECTLY WITH SF3B4.
SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: TO YEAST CUS1. SOME, TO C.ELEGANS ZK632.11.
SIMILARITY: Contains 1 SAP domain.
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                                                                                                                                                                                                                                                                                                                                                QWRARMPLLSVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFF
                                                                                                                                                                                                                                                                                                                                                                                                                        TNOETITAEQVKKVLFEDDERSTDSSQQCSSEDEDIFEETAQVSPP-----RGKEKR
ALQEKEEQKTMKSKMREKVRPKMG
                                  SFSAGPE-----LLRQDKRPRSG
                                                                          DVTAQDPKLLVHLKATRNSVPVPRHWCFKRKYLQGKRGIEKPPFELPDFIKRTGIQEMRE
                                                                                                              NLSA-FPK---EVKVEKKGEPL-----
                                                                                                                                                  -----FTVAE----LKQLVARPDVVEMH
                                                                                                                                                                                         LSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYKKRKQQH
                                                                                                                                                                                                                               FKRIFEAFKLTDDVKKEKEFEKLDKLENSAAPKKKGFEEEHKDSDDDSSDDEQEK---
                                                                                                                                                                                                                                                                       ILPSFQS-----
                                                                                                                                                                                                                                                                                                         PQRVR----GVSSESSGD-----REKDSTRSRGSDSPAADVEIEYVTEEPEIYEPNFIF
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872 AA;
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81
106
226
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308
676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAP;
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73
109
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19.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
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POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 108.5;
Pred. No. 4.7;
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POLY-GLU.
POLY-GLU.
POLY-GLU.
POLY-GLU.
POLY-GLU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
  539
                                    437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity;
                                                                                                            GPRGQDSPLLQRPQHLMDQG--QMRH 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                118;
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RESULT 7
SUUR_DROME
                                                                                                                            RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Hit R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Hit R.A., Sabburner M.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boltshakov S.,
RA Bertis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Ghorya D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bertis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport D.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport D.B., Davies S.M.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Herrandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Inang Y., Lin X.,
Lin X., Mattet B., Kolira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lin X.,
RA Hostin D., Houston K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Hostin D., Palteman G.S., Pan S., Pollard J., Woshrefi A.,
RA Houth S.M., Wolfer B., Wolfer R.D.C., Scheeler F., Shen H.,
Ra Holling S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A
Misra S., Cr.
Hradecky P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUUR
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Drosophila suppressor of underreplication protein binds to late-replicating regions of polytene chromosomes."; Genetics 160:1023-1034(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Makunin I.V., Volkova E.I., Pirrotta V., Zhimulev I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suppressor of Underreplication protein. SUUR OR SU(UR)ES OR CG7869.
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15-SEP-2003 (Rel. 42, Last
15-SEP-2003 (Rel. 42, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VTE2;
                                            MEDLINE=22426069;
                                                                     STRAIN=Berkeley
                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
                                                                                    REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21898319;
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                                                                                                                        nome sequence of Dro
287:2185-2195(2000)
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         Crosby M. P., Huang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL
         PubMed=12537572;
M.A., Mungall C.J., Matthews B.B.,
Y., Kaminker J.S., Millburn G.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11901119;
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L STAGE.
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                                                                                                                                                                                                                                                                                    Query Match
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Nanayev R.A., Demakova O.V.;
"Influence of the SuUR gene on intercalary heterochromatin
Drosophila melanogaster polytene chromosomes.";
Chromosoma 111:377-398(2003).
                                                                                                                                                                                                                                                                                                                    InterPro; IFR000330; SNF2_N.
Pfam; PF00176; SNF2_N; 1.
Chromatin regulator; Nuclear pr
SEQUENCE 962 AA; 107624 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Be Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q. Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ277592; CAB89187.1; -. EMBL; AE003546; AAF50110.3; -. FlyBase; FBgn0025355; SuUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhimulev I.F., Belyaeva E.S., Semeshin Makunin I.V., Volkova E.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Overexpression of the SuUR gene induces reversible pericentric, telometic and intercalary heterochromat melanogaster polytene chromosomes.";
J. Cell Sci. 116:169-176(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alekseyenko A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhimulev I.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           systematic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22344761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22530965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lewis S.E
                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosomes.
TISSUE SPECIFICITY: Expressed throughout development. Weakly expressed. Expressed at higher level in embryos and adult female expressed. Expressed both maternally and zygotically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBLEMANUMAR LOCATION: Nuclear. Binds to polytene salivary glands; localized at late-replicating in heterochromatin and pericentric heterochromatin. many Polycomb Group proteins binding sites on polytomosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Required for underreplication of many late replicating euchromatic regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polytene chromosomes.
                 230
                                                                                                                                                                                                                                                    106;
                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                   VIFDLLLDSYRTAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTN
                                                                                                                                                                                                                     LYDIL-----LEEFVKG------PSPGE--EKTIQVPE-AKLAGFL-RYISMQNLA
                 VQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENC-MEEPPIFKGDPFFILPSFQSES
                                                                                                                                                                                      LYNVLRLGGRLEHQYKSFASFDRKFHLPDPKEVFSKRIDLEEYYKQRGFLSEYIK-----
                                                  IDNNPAQQNKTGLFEETDRLSEHSVDDVAMSPLIFEYSESDDEP
                                                                               QETITAEQVKKVLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the
                                                                                                                    DFRLRRFR--HOFDKSLPLVAPEQYKHNL----NLWLASKNSQSTISGSDVCSTIAS
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belyaeva E.S., Makunin I.V., Pirrotta V., Volkova E
A., Andreyeva E.N., Makarevich G.F., Boldyreva L.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=12456726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=12644953;
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                                                                                                                                                                                                                                                                    4.0%;
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                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                      protein; Developmental protein.
W; 5063FB88E875C4F9 CRC64;
                                                                                                                                                                                                                                                                      Pred. No. 5.
                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on polytene
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                      Indels 153;
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n. Colocalizes
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n in polyte
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RESULT ABENUT IN COMMENT OF THE COME
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ABF1 HUMAN STANDARD;
Q15911; Q15101; Q13719;
                                                                                                                                                                                                                                      SEQUENCE OF 1-1190 FROM N.A. (ISOFORM A).

MEDLINE=99455270; PubMed=10493829;

Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,

Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,

Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,

Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;

"Genome duplications and other features in 12 Mb of DNA sequence human chromosome 16p and 16q.";

Genomics 60:295-308(1999).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Alpha-fetoprotein enhancer binding protein
(AT-binding transcription factor 1).
                                                                                                               <del>:</del>
                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM TISSUE=Hepatoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tamaoki
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                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rinaga T., Yasuda H., Higashio K., Tamaoki T.;
human alpha-fetoprotein enhancer-binding protein,
ur homeodomains and seventeen zinc fingers.";
l. Cell. Biol. 11:6041-6049(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol.
                                                             ENCE OF 112-2/03......
LOWICZ A., McQuerry Y., Hotic M.;
LOWICZ A., McCarry Y., LOWICZ A., LOWI
                              sequence of the enhancer element SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
     Event=Alternative splicing; Named
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and characterization of an ATBF1 isoform differentiation-dependent manner."; Chem. 270:26840-26848 (1995).
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Catarrhini; Hominidae;
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     isoforms=2;
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     InterPro; InterPro; 14.

Pfam; PF00046; homeobox; 4.

Pfam; PF00096; zf-C2H2; 18.

ProDom; PF000010; Homeobox; 4.

PROSITE; PS00027; HOMEOBOX 1; 2.

PROSITE; PS00027; HOMEOBOX 2; 4.

PROSITE; PS00028; ZINC FINGER C2H2 1; 14.

PROSITE; PS00028; ZINC FINGER C2H2 2; 9.

PROSITE; PS0016; ZINC FINGER C2H2 2; 9.

PROSITE; PS0016; ZINC FINGER C2H2 2; 9.

PROSITE; PS0016; ZINC FINGER C2H2 2; 9.
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GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003705; F:RNA polymerase II transcription factor acti...
GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS
GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS
InterPro; IPR007087; Znf C2H2.
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                                                                                                                                                                                                                      DOMAIN
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                                                                        P87498;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vitellogenin I precursor (Minor vitellogenin) [Contains:
I (LVI); Phosvitin (PV); Lipovitellin II (LVII); YGP42].
VTG1 OR VTGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
SEQUENCE FROM N.A.
TISSUE=Liver;
                            NCBI_TaxID=9031;
                                              Archosauria;
                                                       Eukaryota; Metazoa;
                                                                 Gallus gallus (Chicken)
                                                                                                                                       VITI
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                                                                                                                                                                                  PSP----ADPGSVREDSGFICWKKGCNQVF----KTSAALQTHFNEVHAKRPQ
                                                                                                                                                                                                   PSPKVEKKDPSRKKE-----WWENAGNKIYTMAADKTISKLMTEYK----KRKQ
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-> GEWSHRHGRPRLGLGVHLLETSRGLLFEGDVTDPAGPH
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                                                       Craniata; Vertebrata;
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                                              Galliformes;
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                                              cebrata; Euteleostomi;
Phasianidae; Phasiani
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                                               Phasianinae;
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Matches

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Pred. No. 15; 9; Mismatches

Indels

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1076 KRVKKILDDTDNQATRNSRSSSSSASSISESSESTTSTPSSSDSDNRAS

176 EQVKKVLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSN 235

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Query Match
Best Local
                                             CARBOHYD
CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                          EMBL; D89547; PIR; T29088;
                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Precursor-product relationship between chicken vitellogenin anyolk proteins: the 40 kDa yolk plasma glycoprotein is derived; the C-terminal cysteine-rich domain of vitellogenin II."; Biochim. Biophys. Acta 1244:384-394(1995).

-i-FUNCTION: PRECURSOR OF THE EGG-YOLK PROTEINS THAT ARE SOURCES OF NUTRIENTS DURING EARLY DEVELOPMENT OF OVIPAROUS
                                  SEQUENCE
                                                                  CARBOHYD
                                                                                                                                 DOMAIN
                                                                                                                                          DOMAIN
                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                           SMART;
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                                                                                                                                                                                                                                                              Pfam; PF01347; Vitellogenin_N; Pfam; PF00094; vwd; 1.
                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mabuchi N.,
Matsuda T.;
                                                                                                                                                                                                                                                                                    InterPro; IPR001846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95322425;
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                                                                                                                                                                                                                                                                                                                                                                                                                               PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESPECTIVE YOLK COMPONENTS:
INDUCTION: BY steroids (estrogen).
PTM: PHOSVITIN, AN EGG YOLK STORAGE PROTEIN, IS
HIGHLY PHOSPHORYLATED (10%) PROTEINS IN NATURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: PRODUCED BY THE LIVER, SECRETED INT AND THEN SEQUESTERED BY RECEPTOR MEDIATED ENDOCYTOSIS I COCYTES, WHERE IT IS GENERALLY CLEAVED, GIVING RISE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISMS. PHOSVITIN IS BELIEVED TO
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SM00216; VWD; 1.
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                                  MW;
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SER-RICH.
SER-RICH.
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N-LINKED
                                                                                                                                                                                                                    ); Storage POTENTIAL.
            Score 108;
                                                                                                                                                                        VITELLOGENIN I.
LIPOVITELLIN I (BY SIMILARITY).
PHOSVITIN (BY SIMILARITY)
LIPOVITELLIN II (BY SIMILARITY)
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            DB
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           Length 1912;
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HUMAN
DPOO HUMAN
075417; 095
                                                                                                                                                                                                                                                                             SEQUENCE OF 60/-1/04 FROM HARTIS F.V., Kaelin C.B., Burtis K.C.;

"Catalytic activity of Pol eta, a new human DNA polymerase related the bacterial DNA polymerase I family and Drosophila Mus308.";

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-1998) TO THE REPAIR OF INTERSTRAND
                                                                                                                                                                                                                                                                                                                                                           Genomics [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA polymerase theta (EC 2.7.7 POLO OR POLH. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                      Sharief F.S., Vojta P.J., Ropp P.A., Copeland "Cloning and chromosomal mapping of the human (POLO), the eighth human DNA polymerase."; Genomics 59:90-96(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39,
30-MAY-2000 (Rel. 39,
28-FEB-2003 (Rel. 41,
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                             EMBL; AF052573; AAC33565.1;
EMBL; AF043628; AAD05272.1;
HSSP; P00582; 1KFS.
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99326527; PubMed=10395804;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
InterPro; IPR001098; DNA pol.
InterPro; IPR002298; DNA polI.
Pfam; PF00476; DNA pol_A; 1.
                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                 GO:0005654; C:nucleoplasm; TAS.
GO:0003686; F:DNA repair enzyme;
GO:0006281; P:DNA repair; TAS.
                                                                                                                                                                                                                                                           CROSSLINKS.

CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393
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                                                                                  HGNC: 9186; POLQ
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L, Last annotation update
L (BC 2.7.7.7) (DNA polym
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Catarrhini; Hominidae;
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DR PROSITE; PS00447; DNA POLYMERASE A; 1.

W Transferase; DNA-directed DNA polymerase; AT PBIND 175 182 ATP (POTENTIAL)

T CONFLICT 1185 1185 L -> F (IN REF. CONFLICT 1685 1685 R -> Q (IN REF. CONFLICT 175 179 V -> A (T. REF. CONFLICT 175 179 V -> A (T. REF. RECONFLICT 1756 1750
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                         genes.";
                                                                                                             Steelman S., Moskow J.J., Muzynski K., North C., Druck Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.; "Identification of a conserved family of Meisl-related
                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS MEIS1-1 AND MEDLINE=97202105; PubMed=9049632;
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vej
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                      Homeobox protein Meisl (XMeisl).
Xenopus laevis (African clawed frog)
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                                                                         Genome Res.
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                                   ome Res. 7:142-156(1997).
SUBCELLULAR LOCATION: NU
ALTERNATIVE PRODUCTS:
                   Event=Alternative splicing; Named isoforms=2;
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Comment=Additional isoforms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPVLDEHHQGDQDGGDQDERAEKSKLTG-----TRQNHSFIW-----SGASFDLSPG
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R -> Q (IN REF. 2).
V -> A (IN REF. 2).
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MW; AECD17A2103F6BDA C
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Pred. No. 16;
71; Mismatches
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                                                                                                                                                                                                                                                                    Pipoidea;
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ANC1_CAPEL STANDARD;
IP ANC1 CAPEL STANDARD;
AC Q9N4M4; O61841; O61842;
DT 15.5EP-2003 (Rel. 42, Created)
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EMBL; U68387;
HSSP; P41778;
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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DOMAIN
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DOMAIN 194 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T03390; -.
TRANSFAC; T03391; -.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Meis1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Meis1-1;
                                                                                                                    378
                                                                                                                                             255
                                                                                                                                                                      318
                                                                                                                                                                                                 198
                                                                                                                                                                                                                         269
                                                                                                                                                                                                                                                 138
                                                                                                                                                                                                                                                                                                                         181 VLFEDDERSTDSSQQ------CSSE--DEDIFEETAQVSPPRGKEKRQWRARMPLLSV
                                                                                                                                                                                                                                                                                                   6B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P79937-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P79937-1;
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00027; HOMEOBOX_1;
PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00027;
                                                                                            LTHPYPSEEQKKQLAQDTGLTILQVNNWFINARRIVQPMIDQSNRAVSQG
                                                                                                                    NLSAFPKEVKVEKKGEPLG-
                                                                                                                                                                      LSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYKKRKQQH
                                                                                                                                                                                              SEDLTRSAPLTDQPSWSRDHDDAASIRSGGTPGPSSGGHT---SHSGDNSSEQGDGLDNS
                                                                                                                                                                                                                       EPPIFKGDPFFILPSFQSE-
                                                                                                                                                                                                                                                 NPELDNLMIQAIQVLRFHLLELEKVHELCDNFCHRYISCLEGKMPIDLVIDDRDGGSKSD
                                                                                                                                                                                                                                                                        QPVSNADWVWLV------KRLHKLCMELCNNYI-----QMHLDL------ENCME
                                                                                                                                                                                                                                                                                                LIFEKCELATCTPREPGVAGGDVCSSESFNEDIAVFSKQI-----RAEKPLFSS
                                                                                                                                                                                                                                                                                                                                                                                                      390
                                                                                                                                                                                                                                                                                                                                                                                                                              34
91
178
273
275
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262
272
373
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB19197.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB19196.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269
267
334
390
                                                                                                                                                                                                                                                                                                                                                                3.9%;
19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                      42887
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3S TO THE TALE/MEIS HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                      ₹
;
                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                             --DDPDKEKK--RNKGRGIFPKVATNIMRAWLF---
                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP_002241.

K -> Q (IN MEIS1-2).
F -> L (IN MEIS1-2).
E -> K (IN MEIS1-2).
N -> H (IN MEIS1-2).
G -> K (IN MEIS1-2).
MISSING (IN MEIS1-2).
                                                                                                                                                                                                                                                                                                                                                                                                                 F -> L (
E -> K (
N -> H (
G -> K (
                                                                                                                                                                                                                                                                                                                                                                 Score 106;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMEOBOX (TALE-TYPE).

PMSGMGMNMGMEGQWHYM -> LQGMPGSYISPSGPMGMSM
AQPSYTTSQWPLHHAQLRHGISVHTYLPGHHHHPAVMMHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SER/THR-RICH.
ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPQPGMPISASSPSVLNTGDPSMSGHVMNIHAQ
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homeobox; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soform Meis1-2
                                                                                                                                                                                                                                                                                                                                                                                                     D0D98637D08CF32F CRC64;
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                   -----SSTPSTGGFSGKETPSEDDRSQSREHMGES
                              8545 AA
                                                                                                                    --PRGQDSPLLQRPQHLMDQG
                                                                                                                                                                                                                                                                                                                                                                            ВB
                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                          Length 390;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                    415
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                      377
                                                                                                                                                                                                                      317
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Waterston
Submitted
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Submitted
EMBL; AY157938; AAN35200.1; -. .

EMBL; AC006834; AAF40010.3; -.

EMBL; AY126454; AAM95163.1; -.

HSSP; P46939; 1QAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Znang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts "The nesprins are giant actin-binding proteins, orthologous Drosophila melanogaster muscle protein MSP-300.";
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Starr D.A., Han M.; "Role of ANC-1 in tethering nuclei to the actin cytoskeleton.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Nuclear anchorage protein 1 (Anchorage 1 protein)
ANC-1 OR ZK973.6 OR T03A1.3/T03A1.4.
                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: Contains 1 actin-binding domain.
-!- SIMILARITY: Contains 2 calponin-homology (CH)
-!- SIMILARITY: Contains 1 Klarsicht domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 80:473-481(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 689-1243
MEDLINE=22296983; Pul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22264052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-1751 FROM N.A., INTERACTION WITH F-ACTIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 298:406-409(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: First expressed in L1 larvae, and thereafter. DOMAIN: The large coiled coil domains are composed of 6 nearly exact repeats of 903 residues. The last repeat is partial. These repeats are conserved in Hawai (CB4856), Australia (AB4) and Germany (RC301) strains. The length of the repeat may be maintained because of a selective advantage to keep the protein large and allow a single molecule to extent more than 0,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type IV membrane protein (Poter largest part of the protein is cytoplasmic, while it part is associated either with the nuclear envelope, the outer nuclear membrane, or with mitochondrial membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the cytoplasm, creating a bridge across the nuc-
between the cytoskeleton and the nucleus.
SUBUNIT: Interacts with F-actin via its N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Plays a central role in nuclear and mitochondrial anchoring. Probably connects nuclei to the cytoskeleton by interacting with unc-84 at the nuclear envelope and with F-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         targeting.
SIMILARITY: Belongs to the Nesprin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Ubiquitously expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interacts indirecty with unc-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S., Goela D.,
1 (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Klarsicht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 FROM N.A.
PubMed=12408964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=12169658,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Broy M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain, which contains a potential is essential for the nuclear envel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.;
e EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., FUNCTION, O UNC-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nuclear envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in all
                                                                                                                                                                                                                                                                                                                                                                                                         domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Nesprin homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nuclear envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roberts R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        postembryonic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
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                                                                                                                                                                                                                                                                                                                      a collaboration
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                                                                                                                                                                                                                                                                                           outstation
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Pfam; PF00307; CH; 2.

SMART; SM00264; BAG; 6.

SMART; SM00033; CH; 2.

SMART; PS00019; ACTININ 1; 1.

PROSITE; PS00020; ACTININ 2; FALSE |

PROSITE; PS50021; CH; 2.

Structural protein; Cytoskeleton; Av
DOMAIN
DO
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REPEAT
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InterPro; IPR001589; Actbind actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
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NNANDAI KRLGDALDDAEKTVVPSSVPAL--SEFKDRIAPHLATLVEAVNDVPASVE
                                                            NKIYTMAADKTISK------LMTEYKKRKQQ--HNLSAFPKEV--KVEKKGEPLGPR | : | : | : | : | : | : | : | : |
                                                                                                                                               LDDAIKTSDEHDKEQLILSLKLNISQFEQIPLDQLKSDDLKTAEKEITNSLKPEEAEPLL
                       GODSPLLORPOHLMDQGOMRHSFSAGPELLRODKRPRSGSTGSSLSVSVRDAEAQIQ
                                                                                               AKIQELREAKRVGDEARSAAH-DQIVALEKEAEDVTAKESAKKKKKDKKKSPQEMIDELS
                                                                                                                      GGFSG-KETPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRK-KEWWENAG
                                                                                                                                                                        LENCM-----FILPSFQSESSTPST
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                                                 AKV--VEAKALIPKIEEAAKNENLPADDKPKAEQLVSNLEAFVKDVETQVSEKQDELDKL
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RESULT 13
GTA_NPVAC
ID 741447;

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence updat of the control 
                    SEQUENCE FROM N.A.

STRAIN=C6;

MEDLINE=94303173; PubMed=8030224;

Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., P
"The complete DNA sequence of Autographa californica
polyhedrosis virus.";

Virology 202:586-605(1994).

-i- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lear polyhedrosis virus (A
RNA stage; Baculoviridae;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Bromodomain and PHD finger-containing
BRPF3 OR KIAA1286.
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Pfam; PF00176; SNF2 N; T.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1
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                                                     Ohara O.
                                                                          MEDLINE=20039619; Po
Nagase T., Ishikawa
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               Homo
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"Prediction of the coding
                                                                                                                             TISSUE=Brain;
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                               sapiens (Human)
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IPR000330; SNF2_N.
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157
506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQS--ESSTPSTGGFSGK-----ETPSEDDRSQSREHMGESLSLKAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHPYLAMH -- GKNILETNDCFKMDYMSSKCKRVLDLVDDILNTSNDKIILVS
                                                                          PubMed=10574462;
va K.-I., Kikuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160
59058 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.9%;
  sequences of unidentified human genes. 100 new cDNA clones from brain which co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 105; DB Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (BY SIMILARITY).
DEAH BOX.
; 84E0CC24A85984AE CRC64;
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y protein 3
                                                                            Hirosawa
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                                                                                                                                                                                                                                                                                                                           (Fragment)
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                                                                            Nomura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for large proteins in vitro.";
DNA Res. 6:337-345(1999).
-!- SIMILARITY: Contains 1 bromodomain.
-!- SIMILARITY: Contains 1 PHD-type zinc
-!- SIMILARITY: Contains 1 PWWP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00249; PHD; 2.
SMART; SM00293; PWWP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001487; Bromodomain.
InterPro; IPR000313; PWWP domain.
InterPro; IPR001965; Znf PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00633; BROMODOMAIN_1; PROSITE; PS50014; BROMODOMAIN_2; PROSITE; PS50812; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00439; bromodomain; 1. Pfam; PF00628; PHD; 1. Pfam; PF00855; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:14256; BRPF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01359; ZF_PHD_1; 1. PROSITE; PS50016; ZF_PHD_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q92831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB033112;
                              876
                                                                                                                                               777
                                                                                                                                                                                                         723
                                                                                                                                                                                                                                    196
                                                                                                                                                                                                                                                                   899
                                                                                                                                                                                                                                                                                            146
                                                                                                                                                                                                                                                                                                                         626
                                                                                                                                                                                                                                                                                                                                                                                 569
                                                                                                                                                                                                                                                                                                                                                                                                                                        109;
 386
                                                                                                                 299
                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00297; BROMO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
VKVEKKGEPLGPRGQDSPLLQR-PQHLMDQGQMRHSFSAGP-----ELLRQDKRPRSG 437
                                                                                    AVLEQALQEEPEDDGDRDDSKLPPPPTLEPTGPAPSL----SEQESPPEPPTLKPINDSK 875
                                                                                                                                                                           LHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTG----GFSG--
                                                                                                                                                                                                                                    CSSED----
                              PPSRFLKPRKVEEDELLEKSPLQLGNEPLQRLLSDNGINRLSLMAPDTPAGTPLSGVGRR
                                                                                                                                                                                                                                                                                            NLYROSAMSFN----IYFHALV-----CAVLTNQETITAEQVKKVLFEDDERSTDSSQQ 195
                                                                                                                                                                                                                                                                                                                                                    TIQVPEAKLAGFLRYISMQNLAVIFDLLLDS--YRTAREFDTSPGLKCLLKKVSGIGGAA 145
                                                                                                                                                                                                                                                                                                                                                                                ERARLLIELIRKREKLKREQVKVQQAAMELELMPFNVLLRTTLDLLQE---KDPAHIFAE 625
                                                                                                                 -----KETPSED-DRSQSR-----EHMGESLSLKAGGGDLLLPPSPKV----EKK
                                                                                                                                               VRLLRREI - - NALROKL
                                                                                                                                                                                                        PKLEDFYRFSWEDVDNILIPENRAHLSPE--VQLKELLEKLDLVSAMRSSGA----RTRR
                                                                                                                                                                                                                                                                 NLIVTNCMKYNAKDTIFHRAAVRLRDLGGAILRH----ARROAENIGYDPERGTHLPES
                                                                                                                                                                                                                                                                                                                        PVNLSE--VPDYLEFISKPMDFSTMRRKLESHLYRTLEEFEED-----F
                                                                                                                                                                                                                                                                                                                                                                                                          OSCOLITELPPDEKPNGHTKKSVSFREIVVSLLSHQVLLQNLYDILLEEFVKGPSPGEEK
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1214
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415
615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA; 136598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BROMODOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
271
441
685
                                                                                                                                                                                                                                -ED----IFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVWLVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%;
                                                        KKEWWENA----GNK-IYTMAADKTISKLMTEYKKRKQQHNLSAFPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                               ----AQPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHD-TYPE.
GLU-RICH.
BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 105; D
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PWWP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,
                                                                                                                                               PQPPSLNKTVSNGELPAGPQGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        130;
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MBL outstation -
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VP41_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              유
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                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vacuolar assembly protein VPS41 homolog.
F32A6.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; ZinG-finger.
Hypothetical protein; ZinG-finger.
ZN_FING 814 868 RING-TYPE.
SROHENCE 876 AA; 99987 MW; 8D4B0E2AD4211C06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00299; CLH; 1.

SMART; SM00184; RING; 1.

SMART; SM00184; RING; 1.

FROSITE; PS50089; ZF_RING_2; 1.

PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as lon modified and this statement is not removentities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute. Ther the European Bioinformatics Institute. There is non-profit institutions as long a not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q19954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000547; Clathrin_repeat.
InterPro; IPR001841; Znf_ring.
Pfam; PF00637; Clathrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U40409; AAA81388.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE VPS41 FAMILY.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
Submitted (SEP-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
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  140
                                                       542 LYLYERKYESALKILMSCODFQIFNVIDKHQLFDLVKDQITELMNINSERALRLLLDNAD
                                                                                                                                                                                                                                                                                   425
                                                                                                                                                                 482 ACLFNNVKOFRKLVOTWSPDLYMTSFIIDRTQWRIQQISKSGNLADVDETERVLMDALAH 541
                                                                                                                  99 FLRY----
                                                                                                                                                                                                    58 SLLSHQV-----LQNLY-DILLEEFV-------KGPSPGEEKTIQVPEAKLAG 98
                                                                                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                                                                       1 RIRAMAQQVFMLDTQCSPK---TPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVV 57
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
GIGGA---ANLYRQSAMSFNIYFHALVCAVLT----NQETITAEQVKKVLFEDDERS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSV--
                                                                                                                                                                                                                                                                             RARAAASRIPLICGECKEEWEWAVNQFEEVKLCTLLAEVLPDGTP---TLDPECYQKVLI 481
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CE29305
                                                                                                            ----ISMONLAV-----IFDLLLDSYRTAREFDTSPGLKCLLKKVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                         3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases.
ED FOR VACUOLAR ASSEMBLY AND VACUOLAR TRAFFIC (BY
                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 104.5; DB 1; Length Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                            138;
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761 N 761
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                                                                    KDQNDPDLWI--HLLGVVAEFPAHFSQLIIEASNCL-----DPLLIMDKLPDDSDIP
                                                                                                                                     PFLRKNANYNVNKARKLCS--DKGYIEETIYLLAKSGNHYDAVKMMVREYRNMEKVIDYC
                                                                                                                                                                       ----TDSSQQCSSEDEDIFEETAQVSPPRGKE-----KRQWRARMPLLSVQ 231
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Search completed: July 24, 2003, 11:54:17 Job time : 28.511 secs

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Result
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1: sp_archea:*
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1159.539 Million cell updates/sec
                                               Q9ulh6 homo sapien
Q8n4y4 homo sapien
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Q9vxt5 drosophila
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Q8wzv3 neurospora
Q8te71 homo sapien
Q8jip0 oryzias lat
Q8tap2 homo sapien
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Best Local Similarity
Matches 518; Conserv
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413080; AAL04174.1; -.
InterPro; FR000904; Sec7.
SMART; SM00222; Sec7; 1.
Hypothetical protein.
Hypothetical protein.
1770 AA; 195845 MW; 5E996E36A6F92AB4 CRC64;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                    TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK
                                                                                                                                                                                               SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR
TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK 1432
                                                                                                                                                      SHOVLLONLYDILLEEFVKGPSPGEEKTIOVPEAKLAGFLRYISMONLAVIFDLLLDSYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2698; DB 4; Length 1770; llarity 100.0%; Pred. No. 1.4e-225; Conservative 0; Mismatches 0; Indels 0;
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Best Local Similarity
Matches 516; Conserv
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O1-CCT-2002 (TrEMBLrel. 22, L:
O1-CCT-2002 (TrEMBLrel. 22, L:
O1-CCT-2002 (TrEMBLrel. 22, L:
Similar to KIAA1244 protein (
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUN-2002) to the
EMBL; BC033191; AAH33191.1;
NON_TER 1
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                                                                                VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKROWRARMPLLSVQPVSNADWVW
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99.6%;
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Pred. No. 2
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Matches 516
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Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

NCBI TaxID=9606;

[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96CH9 PRELIMINARY; PRT; 592 AA.
Q95CH9; PTT; 592 AA.
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence up
O1-OCT-2002 (TrEMBLrel. 22, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (SEP-2001) to the
EMBL; BC014227; AAH14227.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
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                                                                                                                                                                                                                                                                   TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK 180
                                                                                                                                                                                                                                                                                                                   SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR
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             FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ
                                                               KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
                                                                                                                                                   LVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE
                                                                                                                                                                   LVKRLHKLCMELCNNYIOMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE
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FSAGPELLRODKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ
                                                KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
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PAVFPCISQLTCHVTDIRVRQAVREWLGRVGRVYDIIV

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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Hich R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Hich R.A., Shahburner M., Henderson S.N.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Barli J.F., Agbayani A., An H.-J., Andrews Ffannkoch C., Baldwin D.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokatein P., Brottier P.,
RA Borkova D., Botcher A., Dong Z., Mays A.D., Davies P.,
RA Borkova D., Botcher A., Dong Z., Mays A.D., Davies P.,
RA Ge Pablos B., Delnher A., Dong Z., Mays A.D., Dav I., Dietz S.M.,
RA Golder C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Herrandez J.R., Houck J.,
RA Harris N.L., Wattei B., McIntosh T.C., McLeod M. H., Nelson D.A., Ketchum K.A.,
RA Hasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA McMulto G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murphy L., Murphy L., Rushy D. L.,
RA Mang Z.-Y., Wassarman D.A., Weinster R.D.C., Scheeler F., Shen H.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Sine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Gibbs R.A., Whosh G. N., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Gibbs R.A., Wars E.M., Wars E.N., Weissenbach J.,
RA Gibbs R.A., Wars E.W., Zhong W., Zhong W., Zhong Y., Zhon Y., Smith H.O.,
RA Gibbs R.A., Zhong F.N., Zhong W., Zhong W., Zhou X., Smith H.O.,
RA Gibbs R.A., Shong F.N., Zhong W., Zhon Y., Zho X., Smith H.O.,
RA Gibbs R.A., Shong F.N., Zhong W., Zhou X., Smith H.O.,
RA Gibbs R.A., Shong F.N., Zhong W., Zhou X., Smith H.O.,
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Q9W444;
01-MAY-2000
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Baradon R.C., Rogers Y. Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dreenek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Paragas V., Park S., Patel S., Pfeiffer B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                           SEQUENCE FROM N.A.
Celniker S.E., Adams M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006;
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22,
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Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

Pterygota;

MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., E. Amanatides P.G., Scherer S.E., Li P.W.,

Evans

n ins R.A.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stapleton M., Strong R., Svirekas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003436; AAF46115.2; FlyBase; FBgn0029834; CG5937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2000)
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InterPro; IPR000904; Sec7.
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D., Celniker
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                                                                                                                                                                     PGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDTSPGLKCLLKKVSGIG 142
                                                                                                                                                                                                                                                                            KK----SVSFREIVVSLLSHQVLLQNLYDILLEEF--
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A; 223895
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23895 MW; 94F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 177.5;
Pred. No. 7.2
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RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beason K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cawley S., Dahlke C., Davenport L.B., Davies P., Davoles M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Cherry J.M., Cawley S., Dahlke C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbatt W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Liang Y., Lin X., Katush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., McIntosh T.C., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Stapleton M., Skupski M.P., Smith T., RA Williams S.M., Woodary C., Turner R., Venter E., Wang A.H., Wang X., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., "The genome sequence of Drosophila melanogaster.";

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A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

A Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Tyler D.,

A Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

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                            FlyBase;
Submitted
                                                                                                                                                                                                                                                                                                 Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Dietz S.M.,
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InterPro; IPR006768; CwfJ C 1.
InterPro; IPR006767; CwfJ C.2.
Pfam; PF04677; CwfJ N 1; 1.
Pfam; PF04676; CwfJ N 2; 1.
SEQUENCE 687 AA; 78148 MW; 7
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01-DEC-2001
                                                                                                     Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY061596; AAL29144.1; -. FlyBase; FBgn0032678; CG12750. InterPro; IPR003891; IF_EIF4G_MA3. Pfam; PF02847; MA3; 1. SMART; SM00544; MA3; 1.
                                                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu.C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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l C.J.,
, Wan K.,
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                       Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Andams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards I.M.D., Zhang Q., Chen L.X.,
A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Barandon R.C., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter B.D., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter B.D., Helson C.R., Miklos G.L.G.,
A Bariti J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
A Ballew R.M., Botchan M.R., Bouck J., Brokstein P., Borttier P.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Borttier P.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Borttier P.,
A Burtis K.C., Busam D.A., Butler H., Gavenport L.B., Davies P.,
A Burtis K.C., Busam D.A., Butler H., Caddieu E., Center A., Chandra I.,
A Burtis K.C., Busam D.A., Butler H., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Durbin K.J., Evangelista C.C., Ferriaz C., Ferriaz S., Munn P.,
A Durbin K.J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W.,
A Bablew R., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
A Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
A Bartin R., McChert R., Levitsky A.A., Li J., Liang Y., Lin X.,
A Bartin R., McChert R., Levitsky R.A.
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Ephydroidea; Drosophilidae; Drosophila.
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   Mobarry C.,
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A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.B., Doyle C., Dreenek D., Farfan D.,

Perriera S., Friee E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

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A Gonzalez M., Houck J., Hoskins R.A., Nattei B., Moshrefi A.,

A Gonzalez M., Wou M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A Pacleb J., Paragas V., Park S., Patel S., Pfeifer B.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

"Sequencing of Drosophila melanogaster genome.",

"Sequencing of Drosophila melanogaster genome.",
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Pfam; PF02854; MIF4G; 1.
SMART; SM00544; MA3; 1.
SMART; SM00543; MIF4G; 1.
SEQUENCE 1330 AA; 15163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.",
                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003659; AAF53667.3; -. FlyBase; FBgn003658; CG12750.
InterPro: TPP002000
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InterPro; IPR003891; IF_eIF4G_MA3
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89; Conserv
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D., Celniker
      IGGAANLYROSAMSFNIYFHALVCAVLTNOETITAEQV-KKVLFED-DERSTDSSQQCSS
                                                    EQRTYE----KFYGLLAQRFCNINKIYIPPFEEIFKDTYQTTHRLDTN-----RLRNVSK
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22.1%;
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to the EMBL/GenBank/DDBJ
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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PROSITE; PS00028; ZINC_FINGER_C2H2_1;
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249768 MW; !
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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Duzbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Duzbin K.J., Bevangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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Drosophila melanogaster (Fruit tly).
Eukaryota; Metazoa; Archropoda; Hexapoda; Inse
Eukaryota; Endopterygota; Diptera; Brachycera;
Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Stapleton M., Brokstein P.,
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era; Muscomorpha;
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A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
A Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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Science 287:2185-2195(2000).
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A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Friee E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
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A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
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"Sequencing of Drosophila melanogaster genome.";
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Best Local :
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Evans C.A., Gocayne J.D.,
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Pfam; PF03915;
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InterPro; IPR005613; AIP3.
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                                                                         EQAKLLQIQNLAKTHLNEMERLRQQADSLPHNVNGGEAPKYESVQQVQDDMASLVGRMKN
                                                                                                                                                         DVALSEMSDNRAQSIQSLHSVLETPTPDTTP--
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J.D., Amanatides P.G.,
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      RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Baril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Beeson K.Y., Bernos P.V., Bernann B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Bernann B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Duyan-Rocha S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandaz J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandaz J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Klang Y., Lin X.,
RA Merkulov G., Wilshina N.V., Wobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Wilshina N.V., Mobarry C., Morris J., Welson D.L.,
RA Melson D.R., Pettman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T.,
RA Shue E.C., Stardling A.C., Starbleton M., Skupski M.P., Smith T.,
RA Spier E., Sporadling A.C., Starbleton M., Strong R.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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NCBI_TaxID=7227;
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EMBL; ARO3538; ANAF49814.2; -
FlyBase; FBgn0036365; CG10732.

SEQUENCE 1657 AA; 183992 MW; FF55F036A233ECBD CRC64;
yeasts.";
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Q8TF17;
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                                                                                                                                                                                       Saccharomyces bayanus (Yeast) (Saccharomyces uvarum).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4931;
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                                             LIB533; TRANSPOSON=LTR-retrotransposon Tsu4;
se C., Feldmann H., Bon E., Gaillardin C., Casaregola S.;
evolution of the LTR-retrotransposons in hemiascomycetous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLSVSVRDAEAQIQAWTN 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGP--ELLRQDKRPRSGSTGS
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ilarity 21.1%; Pred. No. 0.37;
Conservative 72; Mismatches 181;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 1110 AA;
                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team: "Analysis of the mouse transcriptome based on functional annot 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                       EMBL; AK029994; BAC26722.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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78; Conser
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VSLLSH--QVLLQNLYDILLEE---
                                               SLRDDLIMLGYGDRRGQLETPNYLEDPASQKAISPIPNEVICPESP-GNLWRNYEFLVNR
                                                                                               AMAQQVFML---DTQCSPKTPNNFDHAQSCQLIIELPPD----EKPNGHTKKSVSFREIV
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                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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19.9%;
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18.8%;
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                                                                                                                                                                                                                                                       128516 MW;
                                                                                                                                                  94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation updat
                                                                                                                                               Score 116; DB 11;
Pred. No. 0.69;
14; Mismatches 227;
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                                                                                                                                                  227;
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  FVKGPSPGEEKTIQVPEAKLAGF
                                                                                                                                                                                                  Length 1110;
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                                                                                                                                                  Indels 142;
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                                                                                                                                                                                 Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8WZV3;
Q8WZV3;
01-MAR-2002
                                                                                                                                                                                                                                                                                     German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; AL669986; CAD21060.1; -.
InterPro; IPR001611; LRR.
Pfam; PF00560; LRR; 6.
Hypothetical protein.
SEQUENCE 2309 AA; 252994 MW; 583ACF6D3A12E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., I
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conserved hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCYLENLIQSLKMNIFHLQTEKESNPQKTAFLNDQLNIIQGEHSKGLKLLQLEVMNLRQQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAESKEDINVLNONLOTLMEENKHLTNKMASLEHHKATSDYOGKVEKAL----EKITDSK 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDAAHASITGELQAVQNEKAQLQIHLDH-----LILEHNQCLQKSQEAEKR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGKAQV-LNDQLSKXCSEL-TSMLQV-VKMENSRIJAEHQAILKVEQKMITETFQEQNLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLFEDDERSTDSSQQCSSEDED-----IFEE--TAQVSPPRGKEKRQWRARMPLLSVQPV
   EFDTSPGLKCLLKKVS----GIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVK 179
                                                                                                                LQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGF--LRYISMQNLAVIFDLLLDSYRTAR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPRSGSTGSSLSVSVRDAEAQIQAWTNMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KGEPLGPRGQD-SPLLQRPQHLMD------QGQMRHSFSAGPELLRQDK 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TVVQKELLESTIARLQGELKASLQEKKSLLEKNEWFQREINKTEKEVAKEKCNLEKE
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                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                          4.3%; Score 115; DB 3; Length 2309;
18.8%; Pred. No. 2.5;
vative 71; Mismatches 174; Indels 16
                                                                                                                                                                                                                                                                                              583ACF6D3A12B67C CRC64;
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ID QATE7
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GN EUCax
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OX NCB1 GN
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Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aerbajinai W., Miller J.L.;
Submitted (JAN-2002) to the EMBL/G
EMBL; AY074490; AAL71549.1; -.
InterPro; IPR001073; C1q.
Pfam; PF00386; C1q; 1.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
SEQUENCE 1077 AA; 120974 MW; 2
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01-JUN-2002
01-JUN-2002
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8TE71
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                                                                                                                                                                                                                                    74 LEEFVKGPSPGEEKTIQVPEAKLAGFLRYI------SMQNLAVIFDLLLDS 118
                                                                                                                                                                                                                                                                                                                                                     22 NNFDHAQSCQ-----LIIELPPDEKP---NGHTKKSVSFREIVVSLLSHQVLLQNLYDIL
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                                                                                                                                                                                                                                                                                              HNLEFÄKELQKTFSGLSLDLLKAQKKAQRREHMLKLEAEKKKLRTILQVQYVLQNLTQEH 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CMEEP--PIFKGDPFFILPSFQSESSTPSTGGFSG-----KETPSEDDRSQSREHMGES
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   KKVLFEDDERSTDSSQQCSSEDEDIFE-ETAQVSP-----
                                                         SEKAVVGTTYKHLKDLLSKLLNSG------YFESIPVPKNAKEKEVPLEE-
                                                                                                             YRTAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQV 178
                                                                                                                                                                             VQKDFKG---GLNGAVYLPSKELDYLIKFSKLTCPERNESLSVEDQMEQSSLYFWDLLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPSIKTEDFLIEA--NKIMAMIRK 932
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                                                                                                                                                                                                                                                                                                                                                                                                                                           4.2%;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 114; DB 4;
; Pred. No. 0.99;
91; Mismatches 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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Search completed: July 24, 2003, 11:56:56 Job time: 120.28 secs

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Result
No.
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 2000000000
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296
296
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518
1 RIRAMAQQVFMLDTO
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sp_bacteria:*
sp_fungi:*
sp_human:*
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sp_rvirus:*
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sp_virus:*
sp_vertebrate:*
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_mammal:*
  GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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16
 Q9ULH6
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Q97R75
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                                                                       Q9ulh6 homo sapien Q8n4y4 homo sapien Q8n4y4 homo sapien Q96ch9 homo sapien Q8hd83 panulirus j O85197 streptococc Q97r75 streptococc Q97r75 streptococc Q97rW8 homo sapien Q81254 proteus vul
Q8ivl3 homo sapien
Q8y7t3 listeria mo
Q9xvn2 caenorhabdi
Q9pfc6 xylella fas
                                                                                                                                                                                    Description
                                          Q8ci16 mus musculu
Q8btx3 mus musculu
Q9m035 arabidopsis
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1.4	1.4	1.4	1.4	1.4	1.4	1.4		1.4	1.4	1.4		1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	4	1.4	1.4	1.4	1.4	1.4	1.4	1.5
176	175	174	174	174	174	166	164	164	161	149	147	143	143	143	142	141	137	137	129	113	90	88		82	76	67	33	1532
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Q8WKQN8	Q8WKS8	Q8WL48	Q8WKR5	Q8WKQ0	Q8WKP7	Q96NM6	Q8Z4U4	016292	Q92HT4	P74153	Q8JUX8	Q9YDK3	P93272	015660	Q8IMK8	Q9JWS0	Q9RZT7	Q9HU07	050122	Q8VXR5	Q99XM6	ОЭННМЗ	Q92ZV9	Q8X345	Q8VR56	Q8GVS0	Q945D4	Q9SRD9
	Q8wks8 syringodea	Q8wl48 doryanthes	Q8wkr5 tecophilaea	5	zeph	Q96nm6 homo sapien	4 salı	G	Q92ht4 rickettsia		macaca fas		N	O15660 plasmodium		0	Q9rzt7 deinococcus	7	O50122 pyrococcus	-		Q9hhm3 halobacteri	_		æ	_	castanea	Q9srd9 arabidopsis

ALIGNMENTS

RESULT 1 Q9ULH6

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Best Local Similarity
Matches 518; Conserv
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SMART; SM00222; Sec7; 1.
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Q9ULH6; Q96P46;
Q1-000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 1770 AA;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                             1 RIRAMAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLL
TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK 180
                                                                       SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR 120
                                                                                                             RIRAMAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLL
                                                       SHQVLLQNLYDILLESFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR 1372
                                                                                                                                                                  100.0%; Score 518; I larity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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Last sequence update)
Last annotation update)
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Q8N4Y4;
Q8N4Y4;
Q1-Q1-Q1-Q1 (TrEMBLrel. 22, Created)
Q1-Q1-Q1-Q1 (TrEMBLrel. 22, Last sequence update)
Q1-Q1-Q1-Q1 (TrEMBLrel. 22, Last annotation update)
Similar to KIAA1244 protein (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-2002) to the
EMBL; BC033191; AAH33191.1;
NON_TER 1
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Local
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       TPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD
                                                                                                                                   SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR
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                                                                                                         VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW
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                                                                                                                                                                                                                                                                                                                        589 AA;
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99.6%;
                                                                                                                                                                                                                                                                          Score 296; DB 4;
Pred. No. 2.4e-299;
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Matches 516
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (SEP-2001) to the
EMBL; BC014227; AAH14227.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
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                                                                                                                       KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
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Pred. No. 2.4e-299;
0; Mismatches 1;
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InterPro; IPR004509; COMEA HHH.
InterPro; IPR000445; HhH. 1.
InterPro; IPR003583; HHH 1.
Pfam; PP00633; HHH; 2.
SMART; SM00278; HhH1; 2.
TIGRPAMS; TIGR01259; COME; 1.
TIGRPAMS; TIGR00426; TIGR00426; 1.
SEQUENCE 216 AA; 23244 MW; C90
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O85197;
O1-NOV-1998
O1-NOV-1998
O1-MAR-2003
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Q8HD83;
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MEDLINE=2226630; PubMed=12242015;
Yamauchi M.M., Miya M.U., Nishida M.;
"Complete mitochondrial DNA sequence of Panulirus japonicus (Crustacea: Decapogene 295:89-96(2002).
                                                                                                                                                                                                                                                                      Pestova E.V., Morrison D.A.; "Isolation and characterization of three Streptococcus pneumoniae transformation-specific loci by use of a lacZ reporter insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eumalacostraca; Eucarida; Palinuroidea; Palinuroidea;
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Panulirus japonicus (Japanese spiny lobster).
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                                                                                                                                                                                                                                                                                                                                             MEDLINE=98241533; PubMed=9573156;
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                                                                                                                                                                                   InterPro; IPR004787; ComE
                                                                                                                                                                                                                                                          vector."
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9; Conserv
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B (TrEMBLrel. 08, 1
CTREMBLrel. 23, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zoa; Arthropoda; Crustacea; Malacostraca;
Bucarida; Decapoda; Pleocyemata; Palinura;
alinuridae; Panulirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactobacillales;
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
       C96DA17761B81938 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nence of the Japanese spiny lobster,
Decapoda).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcaceae;
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Q8DQ41
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Best Local Similarity
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Best Local
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                                                                  Q8DQ41;
Q8DQ41;
Q1-MAR-2003
Q1-MAR-2003
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                   Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam I.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald I.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q97R75;
01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
       Streptococcus.
NCBI_TaxID=171101;
                             Bacteria; Firmicutes;
                                       Streptococcus
                                                CELA OR SPR0856.
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR01259; comE; 1.
TIGRFAMS; TIGR00426; TIGR00426; 1.
                                                                                                                                                                                                                                                                                                                                                    EMBL; AE007400;
TIGR; SP0954; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SP0954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Competence protein
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                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                 Pfam; PF00633; HHH;
                                                                                                                                                                                                                                                                                                                                                                        Science 293:498-506(2001).
                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21357209; PubMed=11463916;
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                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                        interPro;
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SM00278; HhH1; 2.
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9; Conserv
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IPR003583; HHH_1.
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                                                                    (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                              216 AA;
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                                                                                                             PRELIMINARY;
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                           pneumoniae (strain ATCC BAA-255 / R6)
nicutes; Lactobacillales; Streptococca
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                                                                                                                                                                                                                                               23181 MW;
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                                                                                                                                                                                                                                                                                                                          COMEA_HHH.
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Pred. No.
                                                                                                                                                                                                                                              291462B84608DB4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             virulent isolate
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                                                                    sequence up
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o. 1.6;
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                           Streptococcaceae;
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Q9H7WB
ID Q9H7WB
ID Q9H7WB
ID Q9H7WB
ID Q9H7
DT 01--P
DT 01--P
DT 01--P
DT 01--C
DM HOME
OC EURA
OC EURA
OC MAMM
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RN [1]
RN WAGA
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                                                                             RESULT 9
Q8L254
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Best Local S
Matches 8
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Best Local S
Matches
Q8L254;
Q8L254;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuxi I.,
Isogai T., Ota T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Kondo H., Sugawara M.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.,
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
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                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (AUG-2001) to the
EMBL; AK024228; BAB14856.1;
EMBL; BC013353; AAH13353.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ14166.
                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Lung;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE008460; AAK99660.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome of the bacterium Streptococcus
J. Bacteriol. 183:5709-5717(2001).
                                                                                                                                                                                                                            436
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                                                                                                                                                                                                                            SCSTGSSL
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                                                                                                                                                                                                                                                                                                                                                                              121 AA; 1
     (TrEMBLrel. 22,
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larity 100.0%; I
Conservative 0;
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                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                              12905 MW;
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     Created)
                                                                                                                                                                                                                                                                           Score 8; DB 4; Pred. No. 10; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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o. 1.6;
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Tian Q.B., Ohnishi M., Tabuchi A., Terawaki Y.;
"A new plasmid-encoded proteic killer gene system: cloning, sequencing, and analyzing hig locus of plasmid Rts1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murata T., Hayashi T.
Submitted (SEP-2001)
[2]
                      MEDLINE=85234397; PubMed=2989253;
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"Organization of the Tn6-related kanamycin resistance transposon
                                                                                                                                                                                                                                                                                                       MEDLINE=91193219; PubMed=2013575; Mochida S., Tsuchiya H., Mori K., Kaji "Three short fragments of Rts1 DNA are temperature-sensitive growth phenotype J. Bacteriol. 173:2600-2607(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-22024716; PubMed=12029035;
Murata T., Ohnishi M., Ara T., Kaneko J., Han C.-G., Li Y.F.
Murata K., Nojiana H., Nakayama K., Kaji A., Kamio Y., Mik
Mori H., Ohtsubo E., Terawaki Y., Hayashi T.;
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01-MAR-2003
           Tn2680
                                                                                                                          MEDLINE=88139175; PubMed=3277947;
Tanaka M., Okawa N., Mori K., Suy
"Nucleotide sequence of an Rtsl f
                                                                                                                                                                                                                 Nozue H., Tsuchiya K., Kamio Y.; "Nucleotide sequence and copy control incl region (incl-b) of Rtsl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    Janosi L., Yonemitsu H., Hong H., Kaji "Molecular cloning and expression of a specific restriction enzyme (PvuRtslI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid
                                                              STRAIN=UR-75;
                                                                          SEQUENCE FROM N.A.
                                                                                                               Tanaka M., Okawa N., "Nucleotide sequence instability.";
                                                                                                                                                                                                     Plasmid 19:46-56(1988).
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Enterobacteriaceae; Prote
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                                                                                                                                                                                                                                                      MEDLINE=88289863; PubMed=2840681;
2680 carrying two copies of Bacteriol. 163:55-60(1985).
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                                                                                                   Bacteriol.
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Last annotation update)
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RESULT 11
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Q8CI16;

Q1-MAR-2003 (TrEMBLrel. 23, Created)

Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)

Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Q1-MAR-2003 (Tremblrel. 23, Last annotation update)
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SEQUENCE FROM N.A.
STRAIN=UR-75;
MEDLINE=84185439; P
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STRAIN-FVB/N; TISSUE=Kidney;
Strausberg R;
Strausberg R;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037708; AAH37708.1; -.
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SEQUENCE
    Q8BTX3
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Terawaki Y., Kakizawa Y., Takayyasu H., Yoshikawa M.;
"Temperature sensitivity of cell growth in Escherichia
with the temperature sensitive R(KM) factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
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Pfam; PF02195; ParBc; 1.
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J. Bacteriol. 155:1185-1191(1983).
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Kamio Y., Tabuchi A., Itoh Y., Katagiri H., Terawaki Y.;
"Complete nucleotide sequence of mini-Rts1 and its copy |
J. Bacteriol. 158:307-312(1984).
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RESULT
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P SEQUENCE FROM N.A.

C STRAIN=NOD; TISSUB=Thymus;

XX MEDLINE=22354683; PubMed=12466851;

X4 The FANTOM Consortium,

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X5 THE FANTOM Consortium,

X6 THE FANTOM CONSORTIUM

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Best Local :
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01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
MGD5 protein homolog.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chord
Mammalia; Eutheria; Roden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9M035
Q9M035;
01-OCT-2000
01-OCT-2000
01-OCT-2002
  01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/G EMBL; AL161746; CABB1920.1; -. Hypothetical protein.
SEQUENCE: 427 AA; 48124 MW; 4B8
                                                                    Q8IV13;
                                                                                              Q81V13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger T.,
Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical 48.1 kDa protein.
T1008_80.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
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8; Conserv
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                                                                                                                                                                                                            SVSFREIV 152
  (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
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Rodentia;
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Pred. No.
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Sciurognathi;
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thi; Muridae; Murinae; Mus.
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Best Local S
Matches 8
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WA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng B., Nedjari H.,

Madueno E., Maitournam A., Mata Vicente J., Ng B., Nedjari H.,

Madueno E., Maitournam A., Mata Vicente J., Ng B., Nedjari H.,

Madueno E., Maitournam A., Simoes N., Tierrez A.,

Nordsiak G., Novella S., de Pablos B., Perze-Diaz J.-C., Purcell R.,

Na Nacquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

Science 294 849-852 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 8
  Q9XVN2;
01-NOV-1999
01-NOV-1999
01-MAR-2003
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01-MAR-2002
01-MAR-2002
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Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC035871; AAH35871.1; -.
Hypothetical protein.
SEQUENCE 434 AA; 48274 MW; 01D44EBED823426D CRC64;
                                                                                                         Q9XVN2
                                                                                                                                                                                                                                                                                                                                                                                                                                          ListiList; LMO01188; --
Hypothetical protein; (
SEQUENCE 483 AA; 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL591978; CAC99266.1; -.
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STRAIN=EGD-e / Ser
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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483 AA; 56753 MW;
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434 AA; 48274 MW;
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                         Search completed: July 24, Job time: 163.268 secs
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                               investigating biology,",
Science 282:2012-2018(1998).
EMBL, Z81086; CRB03116.1; -.
WormPep; FS3B6.6; CE10900.
InterPro; IPR001507; Endoglin/CD105.
Pfam; PF00100; zona pellucida; 1.
SMART; SM00241; ZP; 1.
                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                              none;
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                        MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                            Submitted (OCT-1996)
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  Genome sequence of the nematode C.elegans: A platform for
                                               481
                                                                     286
                                              SESSTPST
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                                                                                                                                         610 AA;
                                                                                            Conservative
                                               488
                                                                                                                                         68585 MW; 09819DC5C3741329 CRC64;
                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                       100.0%;
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            2003, 12:25:43
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                                                                                                      DB 5;
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